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OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 08:20:34 ; Search time 5521 Seconds
(without alignments)
10938.045 Million cell updates/sec

Title: US-10-612-668-18
1277
Sequence: 1 GAATTTCTTAGGCCCCCAGGTC.....CAGACGGCGCGCCGGAATTC 1277

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_stb:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 1277 | 100.0 | 1277 | 6 AR083391 | AR083391 Sequence |
| 2 | 1277 | 100.0 | 1277 | 6 AR164500 | AR164500 Sequence |
| 3 | 1277 | 100.0 | 1277 | 6 AR423678 | AR423678 Sequence |
| 4 | 885.8 | 69.4 | 2112 | 6 AR083393 | AR083393 Sequence |
| 5 | 885.8 | 69.4 | 2112 | 6 AR164502 | AR164502 Sequence |
| 6 | 885.8 | 69.4 | 2112 | 6 AR423680 | AR423680 Sequence |
| 7 | 885.6 | 69.4 | 2109 | 6 AR083392 | AR083392 Sequence |
| 8 | 885.6 | 69.4 | 2109 | 6 AR164501 | AR164501 Sequence |
| 9 | 885.6 | 69.4 | 2109 | 6 AR423679 | AR423679 Sequence |
| 10 | 876.2 | 68.6 | 2600 | 6 CR456543 | CR456543 Homo sapi |
| 11 | 876.2 | 68.6 | 2755 | 6 AX834211 | AX834211 Sequence |
| 12 | 876.2 | 68.6 | 2755 | 6 AK096521 | AK096521 Homo sapi |
| 13 | 876.2 | 68.6 | 3098 | 9 AF102989 | AF102989 Homo sapi |
| 14 | 876.2 | 68.6 | 3223 | 6 CO730527 | CO730527 Sequence |
| 15 | 876.2 | 68.6 | 3235 | 9 HSM800709 | HSM800709 Homo sapi |
| 16 | 876.2 | 68.6 | 3240 | 6 AR215869 | AR215869 Sequence |
| 17 | 876.2 | 68.6 | 3257 | 9 AF064594 | AF064594 Homo sapi |
| 18 | 876.2 | 68.6 | 3257 | 9 BC036742 | BC036742 Homo sapi |
| 19 | 876 | 68.6 | 2936 | 9 AF102988 | AF102988 Homo sapi |

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| 20 | 876 | 68.6 | 3080 | 9 BC051904 | BC051904 Homo sapi |
| 21 | 809.8 | 63.4 | 2392 | 6 AX876424 | AX876424 Sequence |
| 22 | 809.8 | 63.4 | 2392 | 6 BD156121 | BD156121 Primer fo |
| 23 | 809.8 | 63.4 | 2392 | 9 AK001290 | AK001290 Homo sapi |
| 24 | 717.8 | 56.2 | 3021 | 10 AF259401 | AF259401 Mus muscu |
| 25 | 717.8 | 56.2 | 3352 | 10 BC057209 | BC057209 Mus muscu |
| 26 | 716 | 56.1 | 2259 | 10 NMU86824 | U86824 Mus musculi |
| 27 | 716 | 56.1 | 2918 | 10 BC003487 | BC003487 Mus muscu |
| 28 | 716 | 56.1 | 2950 | 10 BC052845 | BC052845 Mus muscu |
| 29 | 716 | 56.1 | 3113 | 10 BC049778 | BC049778 Mus muscu |
| 30 | 708 | 55.4 | 2935 | 6 AR059699 | AR059699 Sequence |
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| 32 | 708 | 55.4 | 2935 | 6 AR164498 | AR164498 Sequence |
| 33 | 708 | 55.4 | 2935 | 6 I15470 | I15470 Sequence 1 |
| 34 | 708 | 55.4 | 2935 | 6 I132484 | I132484 Sequence 1 |
| 35 | 708 | 55.4 | 2935 | 6 AR429676 | AR429676 Sequence |
| 36 | 698.6 | 54.7 | 70000 | 6 RNU51898 | U51898 Rattus norv |
| 37 | 472.2 | 37.0 | 70000 | 6 AR215862 | AR215862 Sequence |
| 38 | 472.2 | 37.0 | 73317 | 9 AY522921 | AY522921 Homo sapi |
| 39 | 472.2 | 37.0 | 95375 | 9 HS22849 | AL022322 Human DNA |
| 40 | 411 | 32.2 | 3442 | 5 BC077558 | BC077558 Xenopus l |
| 41 | 373.2 | 29.2 | 688 | 9 F116252S09 | F116260 Homo sapi |
| 42 | 353.4 | 27.7 | 3967 | 9 AK128862 | AK128862 Homo sapi |
| 43 | 275.8 | 21.6 | 3775 | 5 BC067375 | BC067375 Danio rer |
| 44 | 223 | 17.5 | 2331 | 3 AY122192 | AY122192 Drosophi |
| 45 | 223 | 17.5 | 2634 | 6 CQ586905 | CQ586905 Sequence |

ALIGNMENTS

| | | | | | |
|------------|--|-------------------------------------|-----|--------|-----------------|
| RESULT 1 | AR083391 | 1277 bp | DNA | linear | PAT 01-SEP-2000 |
| LOCUS | AR083391 | Sequence 18 from patent US 5976854. | | | |
| DEFINITION | AR083391 | | | | |
| ACCESSION | AR083391 | | | | |
| VERSION | AR083391.1 | GI:10010181 | | | |
| KEYWORDS | Unknown. | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unclassified. | | | | |
| REFERENCE | 1 (bases 1 to 1277) | | | | |
| AUTHORS | Jones S. and Tang J. | | | | |
| TITLE | Calcium independent cytosolic phospholipase A. sub.2 / B enzymes | | | | |
| JOURNAL | Patent: US 5976854-A 18 02-NOV-1999; | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1..1277 | | | | |
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ORIGIN

| | |
|----------------------------|--|
| Query Match | 100.0%; Score 1277; DB 6; Length 1277; |
| Best Local Similarity | 100.0%; Pred. No. 6e-252; |
| Matches 1277; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 GAATTTCTTAGGCCCCCAGGTCGATTCGAGCATCGGCTCCGATGCAAGAAAGCACTTT 60 |
| DB | 1 GAATTTCTTAGGCCCCCAGGTCGATTCGAGCATCGGCTCCGATGCAAGAAAGCACTTT 60 |
| QY | 61 GTCTGAAGAGACACGCAAGGATTCATGCGCTTGAGGTTTCAAGAGAAAGATTGAGG 120 |
| DB | 61 GTCTGAAGAGACACGCAAGGATTCATGCGCTTGAGGTTTCAAGAGAAAGATTGAGG 120 |
| QY | 121 GGAACCTGGAGCTGGCTGGGAGGGTGGGAGCCCTTCCAGAGAGAGTGCGGCCCTTT 180 |
| DB | 121 GGAACCTGGAGCTGGCTGGGAGGGTGGGAGCCCTTCCAGAGAGAGTGCGGCCCTTT 180 |
| QY | 181 TCACATCCAGCCCATTTCTCTCTGCGCTGCGCTGAGCTTCTCCCTGGGACAGAGTC 240 |
| DB | 181 TCACATCCAGCCCATTTCTCTCTGCGCTGCGCTGAGCTTCTCCCTGGGACAGAGTC 240 |
| QY | 241 CTTCCGTGGGAGGAGAGATGACAGAGGAGAGTGGGGAGATGAGGGGCTGGCG 300 |
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 Db 301 CGAGGACAGAGCCAGGTTGATCTAGGGGACCTCTGGGGGTAGCAGGGCTTGGGGACCCACC 360
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 Db 421 GGGCCCCGAGAGCCAGGCTTATCTCTGGGCTCCATGAGGGAGCAGAGCCGACCCAGACC 480
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 Db 1021 ACCCAAGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 QY 1081 GTACAGGCAAGAGTGAAGAACTCTCCATGCTGTCTTCCCTGGGAGCAGGAGGTCTCC 1140
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 QY 1141 CACAAGTGCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 Db 1141 CACAAGTGCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 QY 1201 AGACTGTGTTTGGGGCAAGAACTGGGCAAGATGATGATGATGATGATGATGATGATG 1260
 Db 1201 AGACTGTGTTTGGGGCAAGAACTGGGCAAGATGATGATGATGATGATGATGATGATG 1260
 QY 1261 ACGGGCGGCGGGAATTC 1277
 Db 1261 ACGGGCGGCGGGAATTC 1277

RESULT 2
 ARI64500

LOCUS ARI64500 1277 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 18 from patent US 6274140.
 ACCESSION ARI64500
 VERSION ARI64500.1 GI:16237548
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1277)
 AUTHORS Jones S. and Tang J.
 TITLE Calcium independent cytosolic phospholipase A2/B enzymes
 JOURNAL Patent: US 6274140-A 18 14-AUG-2001;
 FEATURES
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 1..1277
 /organism="Unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Query Match 100.0%; Score 1277; DB 6; Length 1277;
 Best Local Similarity 100.0%; Pred. No. 6e-252;
 Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAATTTTGGGCCCCAGGTGTTATGTCAGCATCGGCTCCAGTGCAGAGAAAGCACTT 60
 Db 1 GAATTTTGGGCCCCAGGTGTTATGTCAGCATCGGCTCCAGTGCAGAGAAAGCACTT 60
 QY 61 GTCTGAAGAGGACACGCAAGGATATTCATGCTTGGGGTTCAGAGAGAAAGATTGAG 120
 Db 61 GTCTGAAGAGGACACGCAAGGATATTCATGCTTGGGGTTCAGAGAGAAAGATTGAG 120
 QY 121 GGAAGCTGGAGTGGCTGGGCGAGGGGTGGGAGACCTTCCAGAGCAGTGGGCCCCCTT 180
 Db 121 GGAAGCTGGAGTGGCTGGGCGAGGGGTGGGAGACCTTCCAGAGCAGTGGGCCCCCTT 180
 QY 181 TCCACTCCAGCCCATTTCTCTCTGTGGCTGTGAGCTTCTCCCTGGGAGAGATC 240
 Db 181 TCCACTCCAGCCCATTTCTCTCTGTGGCTGTGAGCTTCTCCCTGGGAGAGATC 240
 QY 241 CTTCTGTGGGAGAGGAGACAGATGACAGGGGAGTGGGGGATGAGGGGCTTGGG 300
 Db 241 CTTCTGTGGGAGAGGAGACAGATGACAGGGGAGTGGGGGATGAGGGGCTTGGG 300
 QY 301 CGAGGACAGCCAGGTTTGAATCTAGGAGCTCTGGGGTTAGCAAGGCTTGGGAGCCAC 360
 Db 301 CGAGGACAGCCAGGTTTGAATCTAGGAGCTCTGGGGTTAGCAAGGCTTGGGAGCCAC 360
 QY 361 TGACCAAGAGTCCCTGCTCTGTGCTCAGAGACTAGAGATCTCATGCAATCTCAC 420
 Db 361 TGACCAAGAGTCCCTGCTCTGTGCTCAGAGACTAGAGATCTCATGCAATCTCAC 420
 QY 421 GGGCCCCGAGAGCCAGGCTTATCTCTGGGCTCCATGAGGGAGCAGAGCCGACCCAGACC 480
 Db 421 GGGCCCCGAGAGCCAGGCTTATCTCTGGGCTCCATGAGGGAGCAGAGCCGACCCAGACC 480
 QY 481 ACCTGCTGTGCTGTGATGAGAGAGTGAAGAGGCTCATCATCTCATGCTCTCATG 540
 Db 481 ACCTGCTGTGCTGTGATGAGAGAGTGAAGAGGCTCATCATCTCATGCTCTCATG 540
 QY 541 CCATCGAAGAGGCTCTGGGGTGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGGACCA 600
 Db 541 CCATCGAAGAGGCTCTGGGGTGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGGACCA 600
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 Db 601 GCACTGAGGAGCATCTGGGCGCTGGCCATCTGCAAGTATGCTCATGCGCTTACATGCGCG 660
 QY 661 GCATGTACTTTCGATGAGAGATGAGGTGTTCGGGGCTCCAGGCCCTACGATCGGGGC 720
 Db 661 GCATGTACTTTCGATGAGAGATGAGGTGTTCGGGGCTCCAGGCCCTACGATCGGGGC 720
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 Db 721 CCTGTGAGAGATTCTGAGCGGAGTGTGGGAGCACCAGATGACGAGCTCAGAG 780

[illegible]

| | | | |
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| QY | 181 | TCGACCTCAGGCCATTTCTCTCCCTGATGAGCCCTGATGCTTCTCTCTGGGACAGAGTC | 240 |
| Db | 181 | TCGACTCAGGCCATTTCTCTCTGATGAGCCCTGATGCTTCTCTCTGGGACAGAGTC | 240 |
| QY | 241 | CTTCTCTGAGGGAAGGACAGATGACAGGGGAGATGGGGGATGAGGGCCGTGGCCTTGGG | 300 |
| Db | 241 | CTTCTCTGAGGGAAGGACAGATGACAGGGGAGATGGGGGATGAGGGCCGTGGCCTTGGG | 300 |
| QY | 301 | CGAGGCACAGCCCAAGGTTTGAATCTAGGGAACCTCTGGGGATAGCAGGCTTGGGGACCAAC | 360 |
| Db | 301 | CGAGGCACAGCCCAAGGTTTGAATCTAGGGAACCTCTGGGGATAGCAGGCTTGGGGACCAAC | 360 |
| QY | 361 | TGAGCCACAGCATGACCTCTGCTCTGAGCTTCAAGAACTTACAGATCTCATGACATCTTCAAC | 420 |
| Db | 361 | TGAGCCACAGCATGACCTCTGCTCTGAGCTTCAAGAACTTACAGATCTCATGACATCTTCAAC | 420 |
| QY | 421 | GGGCCCCGGAAGCCAGCGTTTCATCTCTGGGCTTCATAGAGGACGAGAGCCGACCAAC | 480 |
| Db | 421 | GGGCCCCGGAAGCCAGCGTTTCATCTCTGGGCTTCATAGAGGACGAGAGCCGACCAAC | 480 |
| QY | 481 | ACCGCTGTGCTGATGAGAGGAGATGAAAGGCGCTCATGATCAGATCCCTCATG | 540 |
| Db | 481 | ACCGCTGTGCTGATGAGAGGAGATGAAAGGCGCTCATGATCAGATCCCTCATG | 540 |
| QY | 541 | CCATCGAAGAGCCCTCGGCTGTGCGCACAGAGACCTGTTTGAATGAGGTGGCGGGACCA | 600 |
| Db | 541 | CCATCGAAGAGCCCTCGGCTGTGCGCACAGAGACCTGTTTGAATGAGGTGGCGGGACCA | 600 |
| QY | 601 | GCACTGAGAGCATCTCTGGCCCTTGCCCAATCTTGCAACAATAGTCCATAGGCTTCATATGCGCG | 660 |
| Db | 601 | GCACTGAGAGCATCTCTGGCCCTTGCCCAATCTTGCAACAATAGTCCATAGGCTTCATATGCGCG | 660 |
| QY | 661 | GCATGTACTTTCGATGAGAGATAGAGTGTTCGGGGGCTCCAGGCGCTCAAGTCAGGCGG | 720 |
| Db | 661 | GCATGTACTTTCGATGAGAGATAGAGTGTTCGGGGGCTCCAGGCGCTCAAGTCAGGCGG | 720 |
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| Db | 721 | CCCTGAGAGATTCCTGAAAGCGGAGTTTGGGGAGCACACCAAGATGACGAGCCTCAGGA | 780 |
| QY | 781 | AAACCAAGATGATGCTTGAACAGGACCACTGTGTGACCGGACCGGCGTAACTCCACGCT | 840 |
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| Db | 841 | TCCGGAACCTAGATGCTTCAAGAACTGTCCGGGAGCCTCTGTTTCAACAGAACGTTAAC | 900 |
| QY | 901 | TCAGGCTCTCAGCTCAGGCTTCAAGCAAGCTGTGTGTGGCGGGCGGCTCGAAGACGCGGG | 960 |
| Db | 901 | TCAGGCTCTCAGCTCAGGCTTCAAGCAAGCTGTGTGTGGCGGGCGGCTCGAAGACGCGGG | 960 |
| QY | 961 | CAGCTCCTACTTACTTCCGACCCCAATGGGCGCTTCTTGACGATGGGCTGTGGCCAAACA | 1020 |
| Db | 961 | CAGCTCCTACTTACTTCCGACCCCAATGGGCGCTTCTTGACGATGGGCTGTGGCCAAACA | 1020 |
| QY | 1021 | ACCCCAAGCTGATGCAATGACCGAGATCCATGAGTAAATCAGAGCCTGATCCGCAAGG | 1080 |
| Db | 1021 | ACCCCAAGCTGATGCAATGACCGAGATCCATGAGTAAATCAGAGCCTGATCCGCAAGG | 1080 |
| QY | 1081 | GTCAGGCGCAAAAGTGAAGAACTTCTCCATCGTTGTCTCCCTGGGGACAGGAGGTGCC | 1140 |
| Db | 1081 | GTCAGGCGCAAAAGTGAAGAACTTCTCCATCGTTGTCTCCCTGGGGACAGGAGGTGCC | 1140 |
| QY | 1141 | CACAAAGTCCCTGTGACCTGTGTGATGTCTTCCGTCCAGCAACCCCTGGAGCTGGCCA | 1200 |
| Db | 1141 | CACAAAGTCCCTGTGACCTGTGTGATGTCTTCCGTCCAGCAACCCCTGGAGCTGGCCA | 1200 |
| QY | 1201 | AGACTGTTTTTGGGGCCCAAGAACTGGGCAAGATGATGTGTGATCTTGTGACCGATCCAG | 1260 |
| Db | 1201 | AGACTGTTTTTGGGGCCCAAGAACTGGGCAAGATGATGTGTGATCTTGTGACCGATCCAG | 1260 |

| | | | | |
|------------|--|-------------------|---------|--------|
| cy | 1261 | ACGGCGCGCCGGAATTC | 1277 | |
| | | | | |
| Db | 1261 | ACGGCGCGCCGGAATTC | 1277 | |
| RESULT 4 | | | | |
| AR083393 | | | | |
| LOCUS | AR083393 | | 2112 bp | DNA |
| DEFINITION | Sequence 22 from patent US 5976854. | | | linear |
| ACCESSION | AR083393 | | | |
| VERSION | AR083393.1 | GI:10010183 | | |
| KEYWORDS | | | | |
| SOURCE | Unknown. | | | |
| ORGANISM | Unknown. | | | |
| REFERENCE | Unclassified. | | | |
| AUTHORS | 1 (bases 1 to 2112) | | | |
| TITLE | Jones, S. and Tang, J. | | | |
| JOURNAL | Calcium independent cytosolic phospholipase A ₂ sub.2 / B enzymes | | | |
| FEATURES | Patent: US 5976854-A 22 02-NOV-1999; | | | |
| | Location/Qualifiers | | | |
| | 1..2112 | | | |

ORIGIN

| | | | | |
|---------------------------|-------|------------------|----------|-------------|
| Query Match | 69.4% | Score 885.8 | DB 6 | Length 2112 |
| Best Local Similarity | 99.8% | Pred. 1.1-2e-171 | | |
| Matches 887; Conservative | 0 | Mismatches 2 | Indels 0 | Gaps 0 |

[illegible]

| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|
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| 47 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 510 |
| 48 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 511 |
| 49 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 512 |
| 50 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 513 |
| 51 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 514 |
| 52 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 515 |
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| 54 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 517 |
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| 57 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 520 |
| 58 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 521 |
| 59 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 522 |
| 60 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 523 |
| 61 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 524 |
| 62 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 525 |
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| 64 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 527 |
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| 66 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | C | T | T | G | A | T | 529 |
| 67 | C | C | C | A | T | G | A | G | A | G | C | G | A | C | C | A | C | G | A | C | | | | | | | |

Qy 509 GAAAGGCTCATCATCATCAGCTCTCTCATCGCCATCGAAGGCTCTCGGGTGTGGCCAC 568

1344 GAAAGGCTCATCATCATCAGCTCTCTCATCGCCATCGAAGGCTCTCGGGTGTGGCCAC 1403

QY 569 CAAGGACCTGTTTGACTGGGTGGCGGGCAACAGCACTGGAGGCACTCTGGCCCTGGCCAT 628

1404 CAAGGACCTGTTTGACTGGGTGGCGGGCAACAGCACTGGAGGCACTCTGGCCCTGGCCAT 1463

QY 629 TCTGCACAGTAAGTCATG6CCTTACATGCGCGCATGTACTTTGGCATGAAGTAGAGT 688

1464 TCTGCACAGTAAGTCATG6CCTTACATGCGCGCATGTACTTTGGCATGAAGTAGAGT 1523

Qy 689 GTTCCGGGCTCAAGCCCTACGATCGGCGCCCTTGAGAGATTCTGAAGCCGAGATT 748

QY 749 TGGGAGCACCAAGATGATGCGAGCGTACAGAAACCAAGGTGATGCTGACAGGGACACT 808
1584 TGGGGAGGACACCTAAGATTGCGGCGCTCGAGAACTCCAGGCTGATGCTACAGGGACACT 1643

Oy GTCGACCGGACGGCGGTGAATCCACTCTTCGGAACTACGATGCTCCAGAACTGT 868
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 1644 GTTTGACCTGGCAAGCGCTGATCTTCACTTCTTCTGGAACTACGATGCTCCAGAACTGT 1739

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| OY | 869 | CCGGAGCCTCGTTCAACCGAAGCTTAACCTCAGGCGCTCCAGCTCAGCGCTCAGACCA | 928 |
| 1704 | CGGCGAGCCTCGTTCAACCGAAGCTTAACCTCAGGCGCTCCAGCTCAGCGCTCAGACCA | 1763 | |

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| OY | GCTGGTGTGGCGGCGCCCGAAGCAGACGGGGAGACTCTCACTTAATTCCGACCCCAATGG | 988 |
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989 GCGCTTCCTGACGCTGGGCTGTGGCCAAACCCACGCTGGATGCCATGACCGAGAT 1048

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| QY | 1049 | CCATGAGATCATATGAGGACCTGATCCCTCCAGAGGGTCTCAGGCCCAACAAGGTGAAGAAATCTCTC | 1108 |
| Db | 1884 | CCATGAGATCATATGAGGACCTGATCCCTCCAGAGGGTCTCAGGCCCAACAAGGTGAAGAAATCTCTC | 1943 |
| QY | 1109 | CATCGTTGTCTCCCTGGGGGACAGGGAGGTCCCAACAATGCTCTGTGATCTGTGTGATGT | 1168 |
| Db | 1944 | CATGTTGTGTCTCCCTGGGGGACAGGGAGGTCCCAACAATGCTCTGTGATCTGTGTGATGT | 2003 |
| QY | 1169 | CTTCCGTCCTCCAGCAACCCCTGAGGACTGTGGCCAAAGCTGTTTTTTGGGGCCAAAGAACTGTGG | 1228 |
| Db | 2004 | CTTCCGTCCTCCAGCAACCCCTGAGGACTGTGGCCAAAGCTGTTTTTTGGGGCCAAAGAACTGTGG | 2063 |
| QY | 1229 | CAAGATGTGTGTGACTGTTGCCAAGGATCCAGAGGGGCGGCGCGGAATTC | 1277 |
| Db | 2064 | CAAGATGTGTGTGACTGTTGCCAAGGATCCAGAGGGGCGGCGCGGAATTC | 2112 |

RESULT 5

| | | | | | |
|------------|-------------------------------------|-------------|-----|--------|-----------------|
| LOCUS | AR164502 | 2112 bp | DNA | linear | PAT 17-OCT-2001 |
| DEFINITION | Sequence 22 from patent US 6274140. | | | | |
| ACCESSION | AR164502 | | | | |
| VERSION | AR164502.1 | GI:16237550 | | | |

KEYWORDS
SOURCE
ORGANISM
unknown.
unknown.
unclassified.

| REFERENCE | AUTHORS | TITLE | JOURNAL |
|----------------------|------------------------|--|---------|
| 1 (Pages 1 to 2112) | Jones, S. and Tang, J. | Calcium independent cytosolic phospholipase A2/B enzymes | |
| Patent: US 6271410-A | | 22 14-AUG-2001; | |

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FEATURES
source
location/Qualifiers
1..2112
/organisms="unknown"
/mol_type="unassigned DNA"

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| ORIGIN | Query Match | Score | DB 6: | length |
|-----------------------|-------------------|-------|-------|--------|
| Best local similarity | 69.4% | 885.8 | 6: | 2112 |
| | 99.8% | | | |
| | Prod. No. 12e-171 | | | |

| QY | 389 | CACAGAACTACAGAGATCTCATGCACATCTACGGGCCCCGGAAGCAGAGTTATCCTCTGGG | 448 |
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| Matches | 887; | Conservative 0; Mismatches 2; Indels 0; Gaps 0; | |

Db 1234 CAGACMACTACAGGATCTCATGACACATCTCACCGGGCCCGGAMGCGACGCTTCCCTCTGG 12833
Qy 449 CTCCTAGGGGAGAGAGGCGGCCACGACCACTGCTGTGCTTGATGTTGAGAGAGAGT 508

Db 1289 CTCATGAGGGAGCGAAGCGGACCCAGCCACTGCTGTGCTGTAGTAGAGAGGAGT 13433

Qy 509 GAAAGGCTTCATCATCCAGTCTTCATTCGATCGAGAAGGCTCGGGTGGCCAC 568

Db 1344 GAAAGGCTCATCATCAGCTCCTCATGCCCATCGAAGAGGCTCGGCTGGCCAC 14033

Db 1404 CAAAGGACCTGTTGACCTGGGTGGCGGGGACACAGCACTGGAGGCATCTGGCCCTGGCCCAT 1463

Db 1464 TCTGCACAGTAATGCCATGGCCCTACATGGCGGCGCATGTAACTTTTCGCATGGAAGATGAGGT 1523

Db 1524 GTTCCGGGCTCCAGCCCTACAGTCGGGGCCCTGAGAGATTCCTGAGGGGAGATT 1593

Qy 749 TGGGAGCACCAACAGATGACGGAGCTACAGAAACCCAGGTGATGCTGCACAGGACACT 808

[illegible]

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|------------|--|--|------|
| QY | 869 | CCGGAGGCTGTTTCAACGAAAGTTAACTCAGAGGCTCAGCTCAGCCCTCAGACCA | 928 |
| Db | 1704 | CCGGAGGCTGTTTCAACGAAAGTTAACTCAGAGGCTCAGCTCAGCCCTCAGACCA | 1763 |
| QY | 929 | GCTGTGTGTGGCGGCGGCGCCCGAAGCAGCGGGGCAgCTCTTACTTACTTCCAGCCAATATG | 988 |
| Db | 1764 | GCTGTGTGTGGCGGCGGCGCCCGAAGCAGCGGGGCAgCTCTTACTTACTTCCAGCCAATATG | 1823 |
| QY | 989 | GCGCTTCTTGACCGGTGGGGCTGTGGCCAAACAACCCCAAGCTGATGGCAATGACCGAGAT | 1048 |
| Db | 1824 | GCGCTTCTTGACCGGTGGGGCTGTGGCCAAACAACCCCAAGCTGATGGCAATGACCGAGAT | 1883 |
| QY | 1049 | CCATAGTATCAATCAGACCTGATCCGCAAGGGTCAGGCAACAAGTGAAGAAACTCTC | 1108 |
| Db | 1884 | CCATAGTATCAATCAGACCTGATCCGCAAGGGTCAGGCAACAAGTGAAGAAACTCTC | 1943 |
| QY | 1109 | CATGCTTGTCTCTCTTGGGAGCAGGGAGGTCCCCACAAGTGCTGTGACTGTGTGATGT | 1168 |
| Db | 1944 | CATGCTTGTCTCTCTTGGGAGCAGGGAGGTCCCCACAAGTGCTGTGACTGTGTGATGT | 2003 |
| QY | 1169 | CTTCCGTCCTCCAGCAACCCCTGGGAGCTG3CCCAAGACTGTTTTTGGGGGCAAGAACTGG | 1228 |
| Db | 2004 | CTTCCGTCCTCCAGCAACCCCTGGGAGCTG3CCCAAGACTGTTTTTGGGGGCAAGAACTGG | 2063 |
| QY | 1229 | CAAGTGTGTGTGACTGTTGTGACGGAATCCAGACGG3CGGCGGAATTC | 1277 |
| Db | 2064 | CAAGTGTGTGTGACTGTTGTGACGGAATCCAGACGG3CGGCGGAATTC | 2112 |
| RESULT 6 | | | |
| AR429680 | | | |
| LOCUS | AR429680 | 2112 bp | mRNA |
| DEFINITION | Sequence 22 from patent US 6645736. | | |
| ACCESSION | AR429680 | | |
| VERSION | AR429680.1 | GI:40189998 | |
| KEYWORDS | . | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | Unclassified. | | |
| AUTHORS | 1 (bases 1 to 2112) | | |
| TITLE | Jones, S. and Tang, J. | | |
| JOURNAL | Calcium independent cytosolic phospholipase A2/B enzymes | | |
| FEATURES | Patent: US 6645736-A 22.11.NOV-2003; | | |
| | Location/Qualifiers | | |
| | 1..2112 | | |
| source | /organism="unknown" | | |
| | /mol_type="mRNA" | | |

| Query Match | 69.4% | Score 885.8 | DB 6 | Length 2112 |
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| Best Local Similarity | 99.8% | Pred. No. 1.2e-17 | | |
| Matches 887 | Conservative | 0 | Mismatches 12 | Indels 0 |
| | | | Gaps 0 | |
| QY | 389 | CACAGAACTCAGGATCTCATGCAATCTCAGGGGCCGGAAAGCAGGCTTCATCTTGG | 448 | |
| Db | 1224 | CAGACAACTACAGATCTCATGCAATCTCAGGGGCCGGAAAGCAGGCTTCATCTTGG | 1283 | |
| QY | 449 | CTCCATGAGGAGCGAAGCGGACCAGACCACTGTGTGCTCGATGAGAGAGAGT | 508 | |
| Db | 1284 | CTCCATGAGGAGCGAAGCGGACCAGACCACTGTGTGCTCGATGAGAGAGAGT | 1343 | |
| QY | 509 | GAAAGGCTCATCATCTCAGCTCTTCATGCGCATGAGAAAGGCTTCGGGTGTGGCAC | 568 | |
| Db | 1344 | GAAAGGCTCATCATCTCAGCTCTTCATGCGCATGAGAAAGGCTTCGGGTGTGGCAC | 1403 | |
| QY | 569 | CAGGACCTGTTTGACTGGGTGGCGGCAACAGCACTGAGGCACTCTGGCCCTTGGCCAT | 628 | |
| Db | 1404 | CAGGACCTGTTTGACTGGGTGGCGGCAACAGCACTGAGGCACTCTGGCCCTTGGCCAT | 1463 | |
| QY | 629 | TCTGACAGTAGTCATGAGGCTTAATGAGCGGCAATGATCTTTGSCATGAAGAGTAGAGT | 688 | |
| Db | 1464 | TCTGACAGTAGTCATGAGGCTTAATGAGCGGCAATGATCTTTGSCATGAAGAGTAGAGT | 1523 | |

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|------------|------|--|-----------------|
| QY | 689 | GTTCGGGGGGCTCCACAGGCGCCCTACAGATGAGGGGGCCCTGGAGGAGTTCCTGAAGCCGGAGTT | 748 |
| Db | 1524 | GTTCGGGGGGCTCCACAGGCGCCCTACAGATGAGGGGGCCCTGGAGGAGTTCCTGAAGCCGGAGTT | 1583 |
| QY | 749 | TGGGAGAGCACACCAAGATGACGAGACGTACAGAGAAACCAAGGTGATGTGACACAGGACACT | 808 |
| Db | 1584 | TGGGAGAGCACACCAAGATGACGAGACGTACAGAGAAACCAAGGTGATGTGACACAGGACACT | 1643 |
| QY | 809 | GTTTGACCGGACGCGGCTGAACTTCCACTTCTTCCGGAATTACGATGTCTCCAGAACTGT | 868 |
| Db | 1644 | GTTTGACCGGACGCGGCTGAACTTCCACTTCTTCCGGAATTACGATGTCTCCAGAACTGT | 1703 |
| QY | 869 | CCGGAGGCGCTGTTTCAACCAAGACGTAACTCAAGGCGCTCCAGCTAGGCGCTCAGACCA | 928 |
| Db | 1704 | CCGGAGGCGCTGTTTCAACCAAGACGTAACTCAAGGCGCTCCAGCTAGGCGCTCAGACCA | 1763 |
| QY | 929 | GCTGGTGTGGCGGGCGGGCCCGAAGCAGCGGGGCGAGCTCTACTTACTTCCGACCCCAATGG | 988 |
| Db | 1764 | GCTGGTGTGGCGGGCGGGCCCGAAGCAGCGGGGCGAGCTCTACTTACTTCCGACCCCAATGG | 1823 |
| QY | 989 | GCGCTCTCTGAGCGGTGGGCTGTTGGCCCAACACCACGCTGATGCGCATGACCGAGAT | 1048 |
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| QY | 1049 | CCATGAGTACATCAGACGACTGTATCCGCAAGGGTCAAGGCGCAACAAAGTGAAGAAACTTTC | 1108 |
| Db | 1884 | CCATGAGTACATCAGACGACTGTATCCGCAAGGGTCAAGGCGCAACAAAGTGAAGAAACTTTC | 1943 |
| QY | 1109 | CATGTTGTCTCCCTGGGGGACAGGGAAGGTCCCCCAAGTGCCTGTGACTGTGTGATGT | 1168 |
| Db | 1944 | CATGTTGTCTCCCTGGGGGACAGGGAAGGTCCCCCAAGTGCCTGTGACTGTGTGATGT | 2003 |
| QY | 1169 | CTTCGCTCCACGACAAACCCCTGGGAGCTGGCCMAAGACTGTTTTTGGGGCCAAAGAACTGGG | 1228 |
| Db | 2004 | CTTCGCTCCACGACAAACCCCTGGGAGCTGGCCMAAGACTGTTTTTGGGGCCAAAGAACTGGG | 2063 |
| QY | 1229 | CAAGATGTTGTGTACTGTTGCACGGAATCCAGACGGGGCGCCGGAAATTC | 1277 |
| Db | 2064 | CAAGATGTTGTGTACTGTTGCACGGAATCCAGACGGGGCGCCGGAAATTC | 2112 |
| RESULT 7 | | | |
| AR083392 | | 2109 bp | DNA |
| LOCUS | | | linear |
| DEFINITION | | Sequence 20 from patent US 5976854. | PAT 01-SEP-2000 |
| ACCESSION | | AR083392 | |
| VERSION | | AR083392.1 | GI:10010182 |
| KEYWORDS | | | |
| SOURCE | | Unknown. | |
| ORGANISM | | Unknown. | |
| REFERENCE | | 1 (bases 1 to 2109) | |
| AUTHORS | | Jones,S. and Tang,J. | |
| TITLE | | Calcium independent cytosolic phospholipase A. sub.2 /B enzymes | |
| JOURNAL | | Patent: US 5976854-A 20 02-NOV-1999; | |
| FEATURES | | Location/Qualifiers | |
| | | 1..2109 | |
| source | | /organism="Unknown" /mol_type="unassigned DNA" | |

| | Query Match | Best Local Similarity | Score | DB | Length |
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| | Matches | 897 | Conservative | 0 | Mismatches 19; Indels 0; Gaps 0; |
| QY | 362 | GACCACAGCATGCGCTGCTGTGTCACAGAACTACAGATCTCATGTCATCTTCACG | 421 | | |
| DB | 1194 | GACTCTACATTCCTCAGGCTCCAAAATGCGCAAACTACAGATCTCATGTCATCTTCACG | 1253 | | |
| QY | 422 | GGCCCGAAGGACAGGCTCATCTCTGGGCTCATGAGGACAGAGAAGCGGACCCACGACCA | 481 | | |
| DB | 1254 | GGCCCGAAGGACAGGCTCATCTCTGGGCTCATGAGGACAGAGAAGCGGACCCACGACCA | 1313 | | |

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| Oy | 482 | CCTGGTGTGACCTGATGTGGAGGAGAGTGAAGAAGCCTCATCATCATCAAGCTTCCTCATGCG | 541 |
| Db | 1314 | CCTGCTGTGCTCTGGATGTGAGGAGAGTGAAGAAGCCTCATCATCATCAAGCTTCCTCATGCG | 1373 |
| Oy | 542 | CATCGAAGAAGCCTCGGGTGTGGCCACCAAGACCTGTTTGACTGGTGTGGCGGACCAAG | 601 |
| Db | 1374 | CATCGAAGAAGCCTCGGGTGTGGCCACCAAGACCTGTTTGACTGGTGTGGCGGACCAAG | 1433 |
| Oy | 602 | CACGTGGAAGCATCCGTGGCCCTGTGGCCATTCTGCAACAGTAAGTCCATGGGCTCATGTGGGG | 661 |
| Db | 1434 | CACGTGGAAGCATCTGGCCCTGTGGCCATTCTGCAACAGTAAGTCCATGGGCTCATGTGGGG | 1493 |
| Oy | 662 | CATGTACTTTGCGCATGAAGAAGATGAGTGTTCGGGGGCTTCAAGGCCCTTCAAGTGGGGCC | 721 |
| Db | 1494 | CATGTACTTTGCGCATGAAGAAGATGAGTGTTCGGGGGCTTCAAGGCCCTTCAAGTGGGGCC | 1553 |
| Oy | 722 | CCTGGAAGAGTTCCTGGAAGCCGGGAATTTGGGGAGCAACACMAAGATGAAGGACGTGAGGA | 781 |
| Db | 1554 | CCTGGAAGAGTTCCTGGAAGCCGGGAATTTGGGGAGCAACACMAAGATGAAGGACGTGAGGA | 1613 |
| Oy | 782 | ACCCAAGGTGATGCTGACAGAGGACACTGTCTGACCGGGAGCCGGCTGAATCTCAACTCTT | 841 |
| Db | 1614 | A0CCAAGGTGATGCTGACAGAGGACACTGTCTGACCGGGAGCCGGCTGAATCTCAACTCTT | 1673 |
| Oy | 842 | CCGGAACCTACGATGCTCCGAAGAACTGTCCGGGAGCCTTGTTCAACCAAGAACGTTAACCT | 901 |
| Db | 1674 | CCGGAACCTACGATGCTCCGAAGAACTGTCCGGGAGCCTTGTTCAACCAAGAACGTTAACCT | 1733 |
| Oy | 902 | CAGGCTCTCAGCTCAGCCCTCAGACACAGCTGGTGTGTGGCGGGCGGCCGGAAGAGAGCGGGC | 961 |
| Db | 1734 | CAGGCTCTCAGCTCAGCCCTCAGACACAGCTGGTGTGTGGCGGGCGGCCGGAAGAGAGCGGGC | 1793 |
| Oy | 962 | AGCTCTCTACTTAATTCCGAGCCCAATGAGGCGCTTCTGTGACGGTGGGCTGTTGGCCACA | 1021 |
| Db | 1794 | AGCTCTCTACTTAATTCCGAGCCCAATGAGGCGCTTCTGTGACGGTGGGCTGTTGGCCACA | 1853 |
| Oy | 1022 | CCCCACGCTGATGTGCATGACCCGANAATCCATGAGATGACAACTAGACCTGATCCGCAAGG | 1081 |
| Db | 1854 | CCCCACGCTGATGTGCATGACCCGANAATCCATGAGATGACAACTAGACCTGATCCGCAAGG | 1913 |
| Oy | 1082 | TCAGGCCCAACAAGTGAAGAAACTCTCATCGTTGCTCCCTGGGAGACAGGAGGTCCTCC | 1141 |
| Db | 1914 | TCAGGCCCAACAAGTGAAGAAACTCTCATCGTTGCTCCCTGGGAGACAGGAGGTCCTCC | 1973 |
| Oy | 1142 | ACAAGTGCCTGTGACCTGTGTGGATGTCTTCCGTCCAGCAACCCCTGGAGACTGGCCAA | 1201 |
| Db | 1974 | ACAAGTGCCTGTGACCTGTGTGGATGTCTTCCGTCCAGCAACCCCTGGAGACTGGCCAA | 2033 |
| Oy | 1202 | GACTGTGTTTTGGGGGCAAGGAACGTGGGCAAGATGTGTGGTGAAGCTGTTSCACAGATCCAGA | 1261 |
| Db | 2034 | GACTGTGTTTTGGGGGCAAGGAACGTGGGCAAGATGTGTGGTGAAGCTGTTSCACAGATCCAGA | 2093 |
| Oy | 1262 | CGGGCGGCGGGAATTC 1277 | |
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| RESULT 8 | | | |
| AR164501 | | | |
| LOCUS | AR164501 | 2109 bp | DNA linear |
| DEFINITION | Sequence 20 from patent US 6274140. | | |
| ACCESSION | AR164501 | | |
| VERSION | AR164501.1 GI:16237549 | | |
| KEYWORDS | . | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unclassified. | | |
| REFERENCE | 1 (bases 1 to 2109) | | |
| AUTHORS | Jones, S. and Tang, J. | | |
| TITLE | Calcium independent cytosolic phospholipase A2/B enzymes | | |
| JOURNAL | Patent: US 6274140-A 20 14-AUG-2001; | | |
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| Query Match Similarity | | 97.9% | Pred. No. 1.3e-171 | | | |
| Matches 8977 | | Conservative | 0 | Mismatches 19 | Indels 0 | Gaps 0 |
| QY | 362 | GACCAAGCATGCCCTCTGTGCTTCAAGAACTACAGAGTTCATGACATCTCAG | 421 | | | |
| DB | 1194 | GACTCTACATCTTCAAGCTTCAAAATCGGCAACTACAGATCTCATGCACTCTCAG | 1253 | | | |
| QY | 422 | GGCCCGGAAGCCAGCCTTCACTCTGGGCTCCATAGGAGCGAAGAGGGACCAGCA | 481 | | | |
| DB | 1254 | GGCCCGGAAGCAACCTTCACTCTGGGCTCCATAGGAGCGAAGAGGGACCAGCA | 1313 | | | |
| QY | 482 | CCTGCTGTGCTGGATGAGAGGAGTGAAGAGGCTCATCATCATCCAGCTCATGCG | 541 | | | |
| DB | 1314 | CTGCTGTGCTGGATGAGAGGAGTGAAGAGGCTCATCATCATCCAGCTCATGCG | 1373 | | | |
| QY | 542 | CATCGAAGAGCCTCGGAGTGTGGCCACCAAGAACCTGTTTGACTGGGTGGGCGCACG | 601 | | | |
| DB | 1374 | CATCGAAGAGCCTCGGAGTGTGGCGCAACCAAGAACCTGTTTGACTGGGTGGGCGCACG | 1433 | | | |
| QY | 602 | CATCGAGAGGATCCTGGCCCTGGGCACTTTCGACAGTAAGTCATAGGCTCATGCGCG | 661 | | | |
| DB | 1434 | CATCGAGAGCATCTTGCCCTTGCCATTTTCGACAGTAAGTCATAGGCTCATGCGCG | 1493 | | | |
| QY | 662 | CATGTACTTTGCGATGAGAGTAGTGTCTCCGGGCTCCAGGCTTACAGAGTCGGGCG | 721 | | | |
| DB | 1494 | CATGTACTTTGCGATGAGAGTAGTGTCTCCGGGCTCCAGGCTTACAGAGTCGGGCG | 1553 | | | |
| QY | 722 | CTTGAAGAGATTCTTGAAGCGGAGTTTGGGAGACACCAAGATGACGACCTCAGAA | 781 | | | |
| DB | 1554 | CTTGAAGAGATTCTTGAAGCGGAGTTTGGGAGACACCAAGATGACGACCTCAGAA | 1613 | | | |
| QY | 782 | ACCCAAGGTATGCTGAACGAGGACACTGTCTGACCCGAGCGGCTGAATCTCCACTCTT | 841 | | | |
| DB | 1614 | ACCCAAGGTATGCTGAACGAGGACACTGTCTGACCCGAGCGGCTGAATCTCCACTCTT | 1673 | | | |
| QY | 842 | CCGGAACCTAAGATCTCTCAGAACTGTCCGGAGCCTTGTTCACAGAACTTTAACTT | 901 | | | |
| DB | 1674 | CCGGAACCTAAGATCTCTCAGAACTGTCCGGAGCCTTGTTCACAGAACTTTAACTT | 1733 | | | |
| QY | 902 | CAGGCTTCCAGCTAAGCCCTCAGACCAAGCTGTGTGCGGGCGGCGGCAACAGCGGGC | 961 | | | |
| DB | 1734 | CAGGCTTCCAGCTAAGCCCTCAGACCAAGCTGTGTGCGGGCGGCGGCAACAGCGGGC | 1793 | | | |
| QY | 962 | AGCTCTCACTTACTTCCGACCACAATGAGGCGCTTCTGGAACGATGAGGCTGTGTGCCAACAA | 1021 | | | |
| DB | 1794 | AGCTCTCACTTACTTCCGACCACAATGAGGCGCTTCTGGAACGATGAGGCTGTGTGCCAACAA | 1853 | | | |
| QY | 1022 | CCCCACGCTGGATGCCATGACCGAGATCCATAGTACATCAGACCTGATCCGCAAGGG | 1081 | | | |
| DB | 1854 | CCCCACGCTGGATGCCATGACCGAGATCCATAGTACATCAGACCTGATCCGCAAGGG | 1913 | | | |
| QY | 1082 | TCAGGCCAACAGGTGTAAGAACTCTCATCTGTGTCTCCCTGTGGGACAGGGAAGTCCCG | 1144 | | | |
| DB | 1914 | TCAGGCCAACAGGTGTAAGAACTCTCATCTGTGTCTCCCTGTGGGACAGGGAAGTCCCG | 1973 | | | |
| QY | 1142 | ACAAGTCCCTGTGACTGTGTGATGTCTTCCGTCCAGCAACCCCTGGAGCTGGCCCA | 1201 | | | |
| DB | 1974 | ACAAGTCCCTGTGACTGTGTGATGTCTTCCGTCCAGCAACCCCTGGAGCTGGCCCA | 2033 | | | |
| QY | 1202 | GACTGTTTTTGGGGCCAAAGAACCTGGGCAAGATGTGTGTGATCTGTTGCACGATCCAGA | 1261 | | | |
| DB | 2034 | GACTGTTTTTGGGGCCAAAGAACCTGGGCAAGATGTGTGTGATCTGTTGCACGATCCAGA | 2093 | | | |
| QY | 1262 | CGGCGGCGCGGAATTC 1277 | | | | |
| DB | 2094 | CGGCGGCGCGGAATTC 2109 | | | | |

| RESULT 9 | AR429679 | 2109 bp | mRNA | linear | PAT 18-DEC-2003 |
|---------------------------|--|-------------------------------------|------|--------|-----------------|
| LOCUS | AR429679 | Sequence 20 from patent US 6645736. | | | |
| DEFINITION | Sequence 20 from patent US 6645736. | | | | |
| ACCESSION | AR429679 | | | | |
| VERSION | AR429679.1 | GI:40189997 | | | |
| KEYWORDS | . | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | 1 (bases 1 to 2109) | | | | |
| AUTHORS | Jones, S. and Tang, J. | | | | |
| JOURNAL | Calcium independent cytosolic phospholipase A2/B enzymes | | | | |
| FEATURES | Patent: US 6645736-A 20.11-NOV-2003; | | | | |
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| Query Match | 69.4%; Score 885.6; DB 6; Length 2109; | | | | |
| Best Local Similarity | 97.9%; Pred. No. 1.3e-171; | | | | |
| Matches 897; Conservative | 0; Mismatches 19; Indels 0; Gaps 0; | | | | |
| QY | 362 GACCAACAGATGCCCTGCTGTGTGCTCCAGAACTACAGATTCATGACATCTCACG | 421 | | | |
| DB | 1194 GACTCTTACATTCCTTCAAGCTTCCAAATGCGCAACTACAGATTCATGACATCTCACG | 1255 | | | |
| QY | 422 GGCCCGAAGCAGCGCTTCATCTGGGCTCCATGAGGACGAGAACCGACCAAGCA | 481 | | | |
| DB | 1254 GGCCCGAAGCAGCGCTTCATCTGGGCTCCATGAGGACGAGAACCGACCAAGCA | 1313 | | | |
| QY | 482 CCTGCTGTGCTGATGAGAGAGAGTAAAGCCTCATCATCATCAGCTCTCATGC | 541 | | | |
| DB | 1314 CCTGCTGTGCTGATGAGAGAGAGTAAAGCCTCATCATCATCAGCTCTCATGC | 1373 | | | |
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| DB | 1374 CATGAGAAAGCCCTCGGGTGTGGCCACCAAGACCTGTTTACATGGGTGGGGGACAG | 1433 | | | |
| QY | 602 CACTGAGAGCATCTCGGCCCTTGACCATTCGTGACAGTAAAGTTCATAGGCTCATACGCGG | 661 | | | |
| DB | 1434 CACTGAGAGCATCTCGGCCCTTGACCATTCGTGACAGTAAAGTTCATAGGCTCATACGCGG | 1499 | | | |
| QY | 662 CATGTACTTTGCGATGAAGATGAGTGTTCGGGGCTCAAGGCCCTTACAGTGGGGCC | 721 | | | |
| DB | 1494 CATGTACTTTGCGATGAAGATGAGTGTTCGGGGCTCAAGGCCCTTACAGTGGGGCC | 1553 | | | |
| QY | 722 CCTGAGAGAGTTCCTGAAGCCGGAGATTGGGGACACACCAAGATGACGAGCTCAGAA | 781 | | | |
| DB | 1554 CCTGAGAGAGTTCCTGAAGCCGGAGATTGGGGACACACCAAGATGACGAGCTCAGAA | 1613 | | | |
| QY | 782 ACCCAAGGTGATGCTGACAGGGGACCTGTCTGACCGGGAGCGGTGAATCTCACTCTT | 841 | | | |
| DB | 1614 ACCCAAGGTGATGCTGACAGGGGACCTGTCTGACCGGGAGCGGTGAATCTCACTCTT | 1673 | | | |
| QY | 842 CCGGAACTACGATGCTCCAGAACTGTCCGGAGGCTCTGTTTCAACACGAACTTTAACT | 901 | | | |
| DB | 1674 CCGGAACTACGATGCTCCAGAACTGTCCGGAGGCTCTGTTTCAACACGAACTTTAACT | 1733 | | | |
| QY | 902 CAGGCTTCAAGTCAAGCCCTCAGACCAAGCTGTGTGGCGGGCGGCCCAAGCAGCGGGC | 961 | | | |
| DB | 1734 CAGGCTTCAAGTCAAGCCCTCAGACCAAGCTGTGTGGCGGGCGGCCCAAGCAGCGGGC | 1793 | | | |
| QY | 962 AGCTCTTACTTACTTCCGACCCCAATAGGGGGCTTCTGGAACGGTGGGCTGTGGCCAA | 1022 | | | |
| DB | 1794 AGCTCTTACTTACTTCCGACCCCAATAGGGGGCTTCTGGAACGGTGGGCTGTGGCCAA | 1855 | | | |
| QY | 1022 CCCCACGCTGATGTCATGACCGAGATCCATAGTACATCAGACCTGATCCGCAAGG | 1081 | | | |
| DB | 1854 CCCCACGCTGATGTCATGACCGAGATCCATAGTACATCAGACCTGATCCGCAAGG | 1913 | | | |
| QY | 1082 TCAGGCCAACAGGTGAAGAACTCTTCATCGTTGTCTTCCTGGGGAACGAGGATCCCC | 1141 | | | |

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| Db | 1914 | TCAGGCCAACAGGTGAAGAACTCTCATGTGTCTCCCTGGGGACAGGAGTCCCC | 1973 |
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| Db | 1974 | ACAAGTCCCTGTGACCTGTGTGATGTCTTCCGTCCAGCAACCCTGGAGCTGGCCAA | 2033 |
| QY | 1202 | GACTGTTTTTGGGGCCAAAGAACTGGGCCAAGATGTGTGTGACTGTTGCACGATCCAGA | 1261 |
| Db | 2034 | GACTGTTTTTGGGGCCAAAGAACTGGGCCAAGATGTGTGTGACTGTTGCACGATCCAGA | 2093 |
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| Db | 2094 | CGGCGGCGCGAATTC | 2109 |

| | RESULT | 10 |
|------------|---|-------------------------------------|
| CR456543 | | |
| LOCUS | | |
| DEFINITION | CR456543 | 2600 bp mRNA linear PRI 25-MAY-2004 |
| | (Homo sapiens PLA2G6 full length open reading frame (ORF) cDNA clone) | |
| | (cDNA clone C220RF:PGEM.PLA2G6.V4). | |
| ACCESSION | CR456543 | |
| VERSION | CR456543.1 | GI:47678616 |
| KEYWORDS | CDNA; chromosome 22; | ORF. |
| SOURCE | Homo sapiens (human) | |
| ORGANISM | Homo sapiens | |

REFERENCE
1 (bases 1 to 2600)
Collins, J. B., Wright, C. L., Edwards, C. A., Davis, M. P., Grinham, J. A.,
et al. 1991. The structure of the human genome. *Nature* 350: 1-13.

| | |
|---------|--|
| TITLE | Direct Submission |
| JOURNAL | Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript Sanger Institute name : pGEM_PLA2G6_V4 |
| COMMENT | |

Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see <http://www.sanger.ac.uk/HGP/Chr22/>.

| FEATURES | location/qualifiers |
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CDS
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LIQULPLSP"

ORIGIN

| | | | |
|------------|---|---|--------|
| QY | 1172 | CCGTCGCCGACCAACCCCTGGAGACTGGCCCAAGACTCTTTTGTGGGGCCAGAACTGGGGCAA | 1233 |
| Db | 1796 | CCGTCGCCGACCAACCCCTGGAGACTGGCCCAAGACTCTTTTGTGGGGCCAGAACTGGGGCAA | 1855 |
| QY | 1232 | GATGATGTGTGAGACTGTGTGCACGGATCCAGACGGCGCGCCGG | 1272 |
| Db | 1856 | GATGATGTGTGAGACTGTGTGCACGGATCCAGACGGCGCGCCCTGG | 1896 |
| RESULT 12 | | | |
| AK096521 | 2755 bp | mRNA | linear |
| LOCUS | | | |
| AK096521 | | | |
| DEFINITION | Homo sapiens CDNA FJ39202 file, clone OCEBF2005373, highly similar to 85 KDA CALCITON- INDEPENDENT PHOSPHOLIPASE A2 (EC 3.1.1.4). | | |
| ACCESSION | AK096521.1 | GI:21756036 | |
| VERSION | AK096521.1 | | |
| KEYWORDS | oligo capping; fts (full insert sequence). | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | |
| AUTHORS | Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohtsuka, M., Nishi, T., Shibahara, T., Tanaka, T., Ichii, S., Yamamoto, J., Saito, K., Kawii, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwamaga, T., Watanabe, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Iehbasashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoa, S., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Hoota, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kunikida, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tachio, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiraoka, M., Omori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kakumaru, T., Noguchi, S., Itoh, T., Shigetani, K., Senda, T., Matsunaga, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaishi, T., Oyama, M., Hara, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Maehuo, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isegaki, T. and Sugano, S. | | |
| TITLE | Complete sequencing and characterization of 21,243 full-length human cDNAs | | |
| JOURNAL | Nat. Genet. 36 (1), 40-45 (2004) | | |
| PUBMED | 14702039 | | |
| REFERENCE | 2 | | |
| AUTHORS | Tachio, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, T., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawii, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Nagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Maehuo, Y., Nagai, K. and Isegaki, T. | | |
| TITLE | NEO human cDNA sequencing project | | |
| JOURNAL | Unpublished | | |
| REFERENCE | 3 (bases 1 to 2755) | | |
| AUTHORS | Isegaki, T. and Yamamoto, J. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (04-JUL-2002) Takao Isegaki, FUJ Project (HRI Team); 2-6-7 | | |
| REFERENCE | Kawakami, K., Kikuchi, H., Isegaki, T., Chiba, 292-0812, Japan | | |
| AUTHORS | (E-mail: genomat@hri.co.jp; Tel: 81-438-52-3975, Fax: 81-438-52-3986) | | |

| COMMENT | ORIGIN |
|---|--|
| NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology (RAB), cDNA library construction: Helix Research and Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'- and one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB. | location/Qualifiers 1. 2/55 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="OCBBP2005373" /issue_type="brain" /clone_id="OCBBP2" /dev_stage="fetal" /note="Cloning vector: pME18SFL3" |
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| Qy 512 AGGCTTCATCATCTCCAGCTCTTCATCGCCATGAGAAAGGCTCGGGTGTGGCCACCA 571 | |
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| Db 1676 TGAAGTCAATCAGGACCTGATCCGCAAGGCTCAGGCCAAACAAGGTGAAGAACTCTCCAT 1739 | |
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| ACCESSION | AF102989 | | |
| VERSION | AF102989.1 | GI:5305595 | |
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| SOURCE | | | |
| ORGANISM | Homo sapiens (human) | | |
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| AUTHORS | Ma,Z., Wang,X., Nowatke,W., Ramanadham,S. and Turk,J. | | |
| TITLE | Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (lPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the lPLA2 gene on chromosome 22q13.1 | | |
| JOURNAL | J. Biol. Chem. 274 (14), 9607-9616 (1999) | | |
| MEDLINE | 99194813 | | |
| PUBMED | 10092647 | | |
| REFERENCE | 2 (bases 1 to 3098) | | |
| AUTHORS | Ma,Z. | | |
| JOURNAL | Direct Submission | | |
| TITLE | Submitted (30-OCT-1998) Internal Medicine, Washington University School of Medicine, 660 S. Euclid Ave., St. Louis, MO 63110, USA | | |
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| | | | | | | | | | |
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| Beet Local Similarity 99.7%; Pred. No. 1e-169; Indels 0; Gaps 0; | | | | | | | | | |
| Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | | | | | | | | |
| OY | 392 | AGAACTACAGGATCTCAATGCAATCTCAACGGGCCCGGAAAGCCACCTTCATCTCGGGCTC | 451 | | | | | | |
| Db | 1347 | AGAACTACAGGATCTCAATGCAATCTCAACGGGCCCGGAAAGCCACCTTCATCTCGGGCTC | 1406 | | | | | | |
| OY | 452 | CATAGAGGAGCAGAAAGGSGAACCCACAGCAACCTGCTGTGCTGTGATGAGAGAGAGTGAA | 511 | | | | | | |
| Db | 1407 | CATAGAGGAGCAGAAAGGSGAACCCACAGCAACCTGCTGTGCTGTGATGAGAGAGTGAA | 1466 | | | | | | |
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| OY | 572 | GGACCTGTGTTGACCTGGGAGGCGGACACAGACCTGAGAGCATCTCTGGCCCTGGCCATTCT | 631 | | | | | | |
| Db | 1527 | GGACCTGTGTTGACCTGGGAGGCGGACACAGACCTGAGAGCATCTCTGGCCCTGGCCATTCT | 1586 | | | | | | |
| OY | 632 | GCACAGTAGTCCATGAGCCTTACATGCGCGGAGTACTCTTTGGCATGAAAGATGAGTGT | 691 | | | | | | |
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| OY | 692 | CCGGGGCTCCAGGGCCCTTACAGAGTGGGGGCCCTGAGAGAGTTCCTGAAAGCGGGAGTTGG | 751 | | | | | | |
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| OY | 752 | GGAGCACAACCAAGATGACGGAAGTCAGAGAAACCAAGGTGATGTGTGACAGGAGCACTGTC | 811 | | | | | | |
| Db | 1707 | GGAGCACAACCAAGATGACGGAAGTCAGAGAAACCAAGGTGATGTGTGACAGGAGCACTGTC | 1766 | | | | | | |
| OY | 812 | TGACCCGGAGCCGGGCTGAATCTCCACTCTTTCGGGAATGATGCTCCAGAACTGTGTGG | 871 | | | | | | |
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| Db | 1827 | GGAGCCTCGTGTTCACAGAACGTTAAACCTCAGGCTTCAGCTCAGCCCTCAGACCAAGCT | 1886 | | | | | | |
| OY | 932 | GGTGTGGCGGGCGGCCCGGAAAGCAGCGGGGCAAGCTCTTACTTTCCGCAATGAGGCG | 991 | | | | | | |
| Db | 1887 | GGTGTGGCGGGCGGCCCGGAAAGCAGCGGGGCAAGCTCTTACTTTCCGCAATGAGGCG | 1946 | | | | | | |
| OY | 992 | CTTCTCTGAGCGGTGGGCTGTGGCCAAACCCACGCTGATGTCGATGCAACCGAGATCA | 1051 | | | | | | |
| Db | 1947 | CTTCTCTGAGCGGTGGGCTGTGGCCAAACCCACGCTGATGTCGATGCAACCGAGATCA | 2006 | | | | | | |
| OY | 1052 | TGAGTACATACAGGACCTGATCCGCAAGGGTCAGGCGCAACAGGTGAAAGAACTCTCCAT | 1111 | | | | | | |
| Db | 2007 | TGAGTACATACAGGACCTGATCCGCAAGGGTCAGGCGCAACAGGTGAAAGAACTCTCCAT | 2066 | | | | | | |
| OY | 1112 | CGTTGTCTCTCTGGGGACAGGGAAGTCCCCCAAGTGCCTGTGACTGTGTGAGTGTCTT | 1177 | | | | | | |
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| OY | 1172 | CCGTCACAGCAACCCCTGGGAGCTGGGCCAAAGTCTGTTTGGGGCCAAAGAACTGGGCAA | 1231 | | | | | | |
| Db | 2127 | CCGTCACAGCAACCCCTGGGAGCTGGGCCAAAGTCTGTTTGGGGCCAAAGAACTGGGCAA | 2186 | | | | | | |
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| VERSION | CQ730527.1 | GI:42304590 | | | | | | | |
| KEYWORDS | | | | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | | | | |
| ORGANISM | Homo sapiens | | | | | | | | |

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 Kites, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 Patent: WO 02068579-A 16461 06-SEP-2002;
 JOURNAL
 PB Corporation (NY) (US)
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 452 CATGAGGAG 511
 1543 CATGAGGAG 1602
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 752 GAG 811
 1843 GAG 1902
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 ACCESSION AL080187
 VERSION AL080187.1 GI:5262666
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3235)
 Anborg, W., Winkler, U., Wewes, H.W., Gassenhuber, J. and Wiemann, S.
 Direct Submission
 Submitted (16-JUN-1999) MIPS, Am Klopferplatz 18a, D-82152
 Martinsried, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@kfz-heidelberg.de;
 sequenced by EMBL (European Molecular Biology Laboratory),
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 This clone (DKFZp434A102) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
 information about the clone and the sequencing project is available
 at <http://www.mips.biochem.mpg.de/proj/cDNA/>.
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| DB | 1483 AGAAGCTACAGGATCTCATGCAATCTCCAGGGCCCGGAAGCCAGCGTTCACTTGGGCTC | 1542 |
| QY | 452 CATGAGGAGCAGAAAGCGGAGCCCAAGACCACTCTGTGCTTGGATGGAAGAGTGA | 511 |
| DB | 1543 CATGAGGAGCAGAAAGCGGAGCCCAAGACCACTCTGTGCTTGGATGGAAGAGTGA | 1602 |
| QY | 512 AGGCTCATCATCATCCAGCTCCTCATGCGCCATCGAAGAGGCTCGGGTGTGGCCACAA | 571 |
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| QY | 632 GCACAGTAAGTCCATGGGCTTCAATGGCGGCAATGTAATTTGGCATGAAAGATGAGGTGT | 691 |
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| QY | 752 GGAACACACCAAGATGAGCGGAGCTCAGAGAAACCAAGGTGATGTGACAGGAGCACTGTC | 811 |
| DB | 1843 GGAACACACCAAGATGAGCGGAGCTCAGAGAAACCAAGGTGATGTGACAGGAGCACTGTC | 1902 |
| QY | 812 TGACCGGAGCGGCTGTAATCTTCCGGAATGAGATGCTCCAGAACTGTGTCCG | 871 |
| DB | 1903 TGACCGGAGCGGCTGTAATCTTCCGGAATGAGATGCTCCAGAACTGTGTCCG | 1962 |
| QY | 872 GGAGCGTGGTTCAACCGAAGGTTAACTCAGGCTCAGCTCAGCCCTCAGACCACTC | 931 |
| DB | 1963 GGAGCGTGGTTCAACCGAAGGTTAACTCAGGCTCAGCTCAGCCCTCAGACCACTC | 2022 |
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| QY | 1172 CCGTCCAGCAACCCCTGGAGCTGGGCGCAACCTGTTTTTTGGGGCCAAAGAACTGGGCA | 1231 |
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Job time : 5528 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 08:16:24 / Search time 678 Seconds
(without alignments)
9887.184 Million cell updates/sec

Title: US-10-612-668-18

Perfect score: 1277

Sequence: 1 GAATCTTAGCCCGCCGATG.....CAGACGGCGCCCGAATTC 1277

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 21 | 268 | 21.0 | 411 | 9 | ACH47835 |

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| 22 | 223 | 17.5 | 2634 | 4 | ABU11615 | ABU11615 Drosophila |
| 23 | 157.8 | 12.4 | 5498 | 4 | ABU11614 | ABU11614 Drosophila |
| 24 | 131.6 | 10.3 | 348 | 4 | AAH98967 | AAH98967 Human EST |
| 25 | 60 | 4.7 | 60 | 6 | ABN36726 | ABN36726 Human sp1 |
| 26 | 60 | 4.7 | 60 | 6 | ABN59116 | ABN59116 Human sp1 |
| 27 | 53.6 | 4.2 | 2000 | 8 | ADA71938 | ADA71938 Rice gene |
| 28 | 50 | 3.9 | 3798 | 6 | ABZ13238 | ABZ13238 Arabidops |
| 29 | 48.4 | 3.8 | 2000 | 8 | ADA71938 | ADA71938 Rice gene |
| 30 | 45 | 3.5 | 36955 | 6 | ABV73608 | ABV73608 S. albula |
| 31 | 43.2 | 3.4 | 2237 | 6 | ABU70109 | ABU70109 Pancreas |
| 32 | 43.2 | 3.4 | 3126 | 3 | AAH6740 | AAH6740 Humanised |
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| 35 | 42.6 | 3.3 | 3074 | 10 | ADG93414 | ADG93414 Maize 11p |
| 36 | 42.4 | 3.3 | 9369 | 10 | ADG75175 | ADG75175 Human her |
| 37 | 42.4 | 3.3 | 9369 | 10 | ADG75118 | ADG75118 Human her |
| 38 | 42.4 | 3.3 | 21034 | 2 | AAV62154 | AAV62154 HSV-2 str |
| 39 | 42.4 | 3.3 | 26338 | 2 | AAV62134 | AAV62134 HSV-2 str |
| 40 | 42.4 | 3.3 | 117213 | 2 | AAV62176 | AAV62176 HSV-2 str |
| 41 | 42.4 | 3.3 | 154746 | 6 | AAD25519 | AAD25519 Human her |
| 42 | 42 | 3.3 | 110000 | 11 | ADM27081_11 | Continuation (12 o |
| 43 | 41.8 | 3.3 | 670 | 4 | AAH15649 | AAH15649 Human RXR |
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ALIGNMENTS

| | | |
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| RESULT 1 | AAT68824 | AAT68824 standard; cDNA; 1277 BP. |
| ID | AAT68824 | |
| AC | AAT68824 | |
| DT | 07-AUG-1997 | (first entry) |
| XX | | |
| DE | Cytosolic phospholipase A2/B clone 19D. | |
| XX | | |
| KW | Cytosolic phospholipase A2/B; gPLA2/B; arachidonic acid cascade; | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| FT | Key | Location/Qualifiers |
| FT | CDS | 396..1271 |
| FT | | /*tag= a |
| XX | | |
| PN | WO9717448-A2. | |
| XX | | |
| PD | 15-MAY-1997. | |
| XX | | |
| PF | 07-NOV-1996; | 96WO-US017794. |
| XX | | |
| PR | 08-NOV-1995; | 95US-00555568. |
| XX | | |
| PA | (GEMV) GENETICS INST INC. | |
| XX | | |
| PI | Jones S, Tang J; | |
| XX | | |
| DR | WPI: 1997-281037/25. | |
| DR | P-PSDB; AAW17846. | |
| PT | Calcium independent phospholipase A2/B - used to reduce inflammation in a | |
| PT | mammalian subject. | |
| XX | | |
| PS | Claim 6; Page 46-47; 74pp; English. | |
| XX | | |
| CC | A cDNA clone (AAT68824), designated 19b and deposited as ATCC 69949. | |
| CC | codes for a novel human cytosolic phospholipase A2/B (gPLA2/B) (AAW17845) | |
| CC | involved in the arachidonic cascade. Clones 19b and 19a (see also | |
| CC | AAT68823) were isolated from a Raji cell DNA library derived from | |
| CC | Burkitt's lymphoma (ATCC CCR86) using a probe derived from a CHO-derived | |

CC clone (see also AAT6827). Clones 19a and 19b are both partial clones of the full-length enzyme. Splice variants (see also AAT6825-26) of 19a and CC 19b have also been identified. The isolated polynucleotides can be used to identify full-length clones and to produce recombinant sPLA2/B. CC polypeptides in transfected host cells. sPLA2/B polypeptides can be used to identify PLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade

XX Sequence 1277 BP; 262 A; 362 C; 411 G; 242 T; 0 U; 0 Other;

Query Match 100.0%; Score 1277; DB 2; Length 1277;
Best Local Similarity 100.0%; Pred. No. 2.8e-295;
Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

ABV73009
ID ABV73009 standard; cDNA; 1277 BP.

XX ABV73009;

DT 08-JAN-2003 (first entry)

XX Calcium independent phospholipase A2/B (cPLA2/B) cDNA (clone 19b).

XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; gene;

KW antiinflammatory; antiatheritic; antipsoriatic; antineumatic; cytotoxic;

KW antilesthetic; human; ss.

XX Homo sapiens.

OS

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XX

XX

XX

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XX

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XX

US2002106364-A1.
08-AUG-2002.
09-AUG-2001, 2001US-00927180.
27-JUL-1994, 94US-00281193.
14-APR-1995, 95US-00422106.
14-APR-1995, 95US-00422420.
26-JUN-1995, 95WO-US008069.
08-NOV-1995, 95US-00555568.
09-SEP-1998, 98US-00149988.
06-MAR-2000, 2000US-00519223.
(GENY) GENETICS INST INC.
Jones S, Tang J;
WPI, 2002-739923/80.
P-PDB; ABB82230.

PF 07-NOV-1996; 96MO-US017794.
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 PR 08-NOV-1995; 95US-00555568.
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 XX
 PI Jones S, Tang J;
 XX
 DR WPI; 1997-281037/25.
 P-PSDB; AAM17848.
 XX
 PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 mammalian subject.
 XX
 PS Claim 6; Page 54-56; 74pp; English.
 XX
 CC A cDNA clone (AAT68826) codes for a novel human cytosolic phospholipase
 A2/B (sPLA2/B) (AAM17848) that is involved in the arachidonic acid
 CC cascade. It is a splice variant of clone 19b (see also AAT68824), the
 CC splice occurring after nucleotide 1228. Isolated sPLA2/B polynucleotides
 CC can be used to produce recombinant sPLA2/B polypeptides in transformed
 CC host cells. The sPLA2/B polypeptides can be used to identify PLA2/B
 CC inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic
 CC acid cascade
 CC
 SQ Sequence 2112 BP; 451 A; 645 C; 630 G; 386 T; 0 U; 0 Other;

Query Match 69.4%; Score 885.8; DB 2; Length 2112;

Best Local Similarity 99.8%; Pred. No. 1.1e-201; Matches 88; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

389 CACAGACTACAGAGATCTCATGACATCTCAGCGGCCCGAAGCCAGCTTCATCTGGG 448
 1224 CAGACACTACAGAGATCTCATGACATCTCAGCGGCCCGAAGCCAGCTTCATCTGGG 1283
 449 CTCCTAGAGGAG 508
 1284 CTCCTAGAGGAG 1343
 509 GAAAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 568
 1344 GAAAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1403
 569 CAAAGACTTGTGACTGAGTGGGCGGACACAGCATGAGAGCATCTGGCCCTGGCCAT 628
 1404 CAAAGACTTGTGACTGAGTGGGCGGACACAGCATGAGAGCATCTGGCCCTGGCCAT 1463
 629 TCTGCACAGTAAGTCCATGGCTTCAATGCGCGGATATTAATCTTGGCATGAAAGATGAGT 688
 1464 TCTGCACAGTAAGTCCATGGCTTCAATGCGCGGATATTAATCTTGGCATGAAAGATGAGT 1523
 689 GTTCCGCGGCTCCAGGCTTCAAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 748
 1524 GTTCCGCGGCTCCAGGCTTCAAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1583
 749 TGGGAGACACACCAAGATGACGACGTCAGAGAAACCAAGATGATGCTGACAGGACAT 808
 1584 TGGGAGACACACCAAGATGACGACGTCAGAGAAACCAAGATGATGCTGACAGGACAT 1643
 809 GTTGCACCGGACCGGCTGAACTCCACCTTTCGGAATCAGATCTCCAGAACTGT 868
 1644 GTTGCACCGGACCGGCTGAACTCCACCTTTCGGAATCAGATCTCCAGAACTGT 1703
 869 CCGGAGACCTGTTTCAACGAGAACGTTAATCTCAGGCTCCAGCTCAGGCTCCAGACCA 928
 1704 CCGGAGACCTGTTTCAACGAGAACGTTAATCTCAGGCTCCAGCTCAGGCTCCAGACCA 1763
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 1764 GCTGTGTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1823
 989 GCGCTTCTTGAAGGTTGGCTTTGGGCAACACCCAGCTGATCCATGACCGAGAT 1048

Db 1824 GCGCTTCTTGAAGGTTGGCTTTGGGCAACACCCAGCTGATCCATGACCGAGAT 1883
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 Db 1884 CCATGAGTACATCAGGACCTGATCCGCAAGGCTCAGGCCAAGGTGAAGAACTCTC 1943
 Qy 1109 CATGTTGTCTCCCTGGGAGCAGGAGGTCCCAAGATGCTGTGACCTGTGTGATGT 1168
 Db 1944 CATGTTGTCTCCCTGGGAGCAGGAGGTCCCAAGATGCTGTGACCTGTGTGATGT 2003
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 Db 2004 CTTCGGTCCAGAACCCCTGGGAGCTGGCCAGACTGTTTGGGCGCCAGGAATTC 2063
 Qy 1229 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1277
 Db 2064 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2112

RESULT 4

ABV73011
 ID ABV73011 standard; cDNA; 2112 BP.

ABV73011;

08-JAN-2003 (first entry)

Human cPLA2/B splice variant cDNA (clone 19b).

Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; gene;
 antiinflammatory; antithrombotic; antiprostaglandin; antipneumatic; cytosolic;
 antileukemic; human; ss.

Homo sapiens.

Key Location/Qualifiers
 CDS 43..2106
 /tag= a
 /product= "cPLA2/B"
 /partial
 /note= "splice variant"

US2002106364-A1.

08-AUG-2002.

09-AUG-2001; 2001US-00927180.

27-JUL-1994; 94US-00281193.
 14-APR-1995; 95US-00422106.
 14-APR-1995; 95US-00422420.
 26-JUN-1995; 95MO-US008069.
 08-NOV-1995; 95US-00555568.
 09-SEP-1998; 98US-00149988.
 06-MAR-2000; 2000US-00519223.

(GEMV) GENETICS INST INC.

Jones S, Tang J;

WPI; 2002-739923/80.

P-PSDB; ABB82232.

Novel composition comprising purified mammalian calcium independent
 phospholipase enzyme, useful for the screening of inhibitors of
 phospholipase activity, is active in the absence of calcium.

Claim 6; Page 28-30; 41pp; English.

The invention relates to a purified mammalian calcium independent
 cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 characterized by activity in the absence of calcium and has a molecular
 weight of 86 kD on SDS-PAGE. A composition (i) comprising a purified

QY 482 CTTGCTGCTGCTGATGAGAGAGTGAAGGCTCATCATCATCCAGCTCCTCATCGC 541
 DB 1314 CTTGCTGCTGCTGATGAGAGAGTGAAGGCTCATCATCATCCAGCTCCTCATCGC 1373
 QY 542 CATCGAAGAGGCTCGGCTGTGCTCACCAAGACCTGTTGACTGGGTGGCGGACACAG 601
 DB 1374 CATCGAAGAGGCTCGGCTGTGCTCACCAAGACCTGTTGACTGGGTGGCGGACACAG 1433
 QY 602 CATCGAAGAGGCTCGGCTGTGCTCACCAAGACCTGTTGACTGGGTGGCGGACACAG 661
 DB 1434 CATCGAAGAGGCTCGGCTGTGCTCACCAAGACCTGTTGACTGGGTGGCGGACACAG 1493
 QY 662 CATGATCTTTCGATGAGAGTGAAGTGTTCGCGGGCTCCAGAGCTCAGAGTCCGCGGC 721
 DB 1494 CATGATCTTTCGATGAGAGTGAAGTGTTCGCGGGCTCCAGAGCTCAGAGTCCGCGGC 1553
 QY 722 CTTGAGAGAGTTCCTGAAGCGGAGTTTGGGAGACACCAAGATGACGGAAGTCCAGAA 781
 DB 1554 CTTGAGAGAGTTCCTGAAGCGGAGTTTGGGAGACACCAAGATGACGGAAGTCCAGAA 1613
 QY 782 ACCCAAGGTATGCTGACAGAGACACTGTCTGACCGGAGCTCGGCTGAATCCACCTCTT 841
 DB 1614 ACCCAAGGTATGCTGACAGAGACACTGTCTGACCGGAGCTCGGCTGAATCCACCTCTT 1673
 QY 842 CCGGAACTACGATGCTCAGAAACTGTCCGAGAGCTCGTTTCAACCAAGACGTTAACT 901
 DB 1674 CCGGAACTACGATGCTCAGAAACTGTCCGAGAGCTCGTTTCAACCAAGACGTTAACT 1733
 QY 902 CAGGCTCCAGCTCAGAGCTCAGACCCAGCTGTGTGTGCGGGCGGCGCGGAGACGCGGGC 961
 DB 1734 CAGGCTCCAGCTCAGAGCTCAGACCCAGCTGTGTGTGCGGGCGGCGCGGAGACGCGGGC 1793
 QY 962 AGCTCTACTACTTCCGACCCCAATGAGGCGCTTCTTGAAGGTGTGTCGCAACAA 1021
 DB 1794 AGCTCTACTACTTCCGACCCCAATGAGGCGCTTCTTGAAGGTGTGTCGCAACAA 1053
 QY 1022 CCCCACGCTGATGCCATGACCCAGATCATGATGATACATCAGAGCTGATCCGCAAGG 1081
 DB 1854 CCCCACGCTGATGCCATGACCCAGATCATGATGATACATCAGAGCTGATCCGCAAGG 1913
 QY 1082 TCAGGCCCAAGAGTGAAGAACTCTTCATCTGTTGTCCTCTGGGAGACAGAGGTCTCC 1141
 DB 1914 TCAGGCCCAAGAGTGAAGAACTCTTCATCTGTTGTCCTCTGGGAGACAGAGGTCTCC 1973
 QY 1142 ACAAGTGCCTGTGACCTGTGTGATGCTTCCGTCAGCAACCCCTGGAGCTGGCCAA 1201
 DB 1974 ACAAGTGCCTGTGACCTGTGTGATGCTTCCGTCAGCAACCCCTGGAGCTGGCCAA 2033
 QY 1202 GACTGTTTTTGGGCGCAAGAACTGGGCAAGATGTGTGACTGTTGACGGAATCCAGA 1261
 DB 2034 GACTGTTTTTGGGCGCAAGAACTGGGCAAGATGTGTGACTGTTGACGGAATCCAGA 2093
 QY 1262 CGGCGCGCGGGAATTC 1277
 DB 2094 CGGCGCGCGGGAATTC 2109
 RESULT 6
 ABV73010
 ID ABV73010 standard; cDNA; 2109 BP.
 XX
 AC ABV73010;
 XX
 DT 08-JAN-2003 (first entry)
 DE Human cPLA2/B splice variant cDNA (clone 19a).
 XX
 KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; gene;
 KM antiinflammatory; antiarthritic; antiapoptotic; antirheumatic; cytosolic;
 XX antiesthematic; human; ss.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 43..2103
 FT /tag= a
 FT /product= "cPLA2/B"
 FT /partial
 FT /note= "splice variant"
 US2002106364-A1.
 XX
 PN 08-AUG-2002.
 PD
 XX
 XX 09-AUG-2001; 2001US-00927180.
 PF
 XX 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422420.
 PR 26-JUN-1995; 95MO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 XX WPI; 2002-739923/80.
 DR P-PSDB; ABB82231.
 XX
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX
 PS Claim 6; Page 23-25; 41pp; English.
 XX
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotrienes or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant encoding
 CC cDNA (clone 19a)
 XX
 SQ Sequence 2109 BP; 450 A; 644 C; 629 G; 386 T; 0 U; 0 Other;
 Query Match 69.4%; Score 885.6; DB 6; Length 2109;
 Best Local Similarity 97.9%; Pred. No. 1.2e-201;
 Matches 897; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 362 GACCAACAGATGCCCTGCTCTGTGCTCACAAGACTACAGATCTATGACATCTCAG 421
 DB 1194 GACTCTTACTATCTTGCTCTCCAAATTCGCAAACTACAGATCTATGACATCTCAG 1253
 QY 422 GGCCTGGAAGCCAGCTTATCTGAGCTCCATGAGAGAGAGAGCGAGCCAGACCA 481
 DB 1254 GGCCTGGAAGCCAGCTTATCTGAGCTCCATGAGAGAGAGAGCGAGCCAGACCA 1313
 QY 482 CTTGCTGCTGCTGATGAGAGAGTGAAGGCTCATCATCATCCAGCTCCTCATCGC 541
 DB 1314 CTTGCTGCTGCTGATGAGAGAGTGAAGGCTCATCATCATCCAGCTCCTCATCGC 1373
 QY 542 CATCGAAGAGGCTCGGCTGTGCTCACCAAGACCTGTTGACTGGGTGGCGGACACAG 601


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XX
DB 1374 CATCGAAGAGGCTCGGGTGTGGCCACAGACCTGTTGATCTGGGTGGGGACACAG 1433
QY 602 CACTGAGGAGCATCTGGCCCTGGCCATTCTGACAGTAAGTCAATGGCTTACATGGCGG 661
DB 1434 CACTGAGGAGCATCTGGCCCTGGCCATTCTGACAGTAAGTCAATGGCTTACATGGCGG 1493
QY 662 CANTGACTTTCGATGAAGATGAAGGTGTCCGGGGCTCCAGGCCCTTAAGATCGGGGCC 721
DB 1494 CATGACTTTCGATGAAGATGAAGGTGTCCGGGGCTCCAGGCCCTTAAGATCGGGGCC 1553
QY 722 CCTGAGAGATTCTTAAGAGCGGAGTTTGGGAGACACACCAAGATGACGAGCTCAGAA 781
DB 1554 CCTGAGAGATTCTTAAGAGCGGAGTTTGGGAGACACACCAAGATGACGAGCTCAGAA 1613
QY 782 ACCCAAGGTGATGCTGACAGAGACACTGTCTGACCGGACCGGCTGAACCTCACTCTT 841
DB 1614 ACCCAAGGTGATGCTGACAGAGACACTGTCTGACCGGACCGGCTGAACCTCACTCTT 1673
QY 842 CCGGAATCTAGATGCTCCAGAAATCTGTCCGGGAGCTCTTTCACCAAGACCTTAACCT 901
DB 1674 CCGGAATCTAGATGCTCCAGAAATCTGTCCGGGAGCTCTTTCACCAAGACCTTAACCT 1733
QY 902 CAGGCTCTCAGCTCAGGCTCAGACCAAGCTGTGTGGCGGGCGGCGGAGACGCGGGC 961
DB 1734 CAGGCTCTCAGCTCAGGCTCAGACCAAGCTGTGTGGCGGGCGGCGGAGACGCGGGC 1793
QY 962 AGCTCTACTTACTTCCGACCCCAATGGCGCTTCTGAGCGGTGTGGCCCAAA 1021
DB 1794 AGCTCTACTTACTTCCGACCCCAATGGCGCTTCTGAGCGGTGTGGCCCAAA 1853
QY 1022 CCCAGGCTGAGATGCGCATGACCGAATCCATGATGATCAATCAGACCTGATCCGCAAGG 1081
DB 1854 CCCAGGCTGAGATGCGCATGACCGAATCCATGATGATCAATCAGACCTGATCCGCAAGG 1913
QY 1082 TCAGGCAACAGAGTGAAGAACTCTCATGTTGCTCCCTGGGAGCAGGAGTCCCG 1141
DB 1914 TCAGGCAACAGAGTGAAGAACTCTCATGTTGCTCCCTGGGAGCAGGAGTCCCG 1973
QY 1142 ACAAGTCTGTGATGCTGTGTGATGTTCTCCGTCCAGAACCCCTGGAGCTGGCAA 1201
DB 1974 ACAAGTCTGTGATGCTGTGTGATGTTCTCCGTCCAGAACCCCTGGAGCTGGCAA 2033
QY 1202 GACTGTTTTTGGGCGCAAGAACTGGGCAAGATGATGATGATGATGATGATGATGATGAT 1261
DB 2034 GACTGTTTTTGGGCGCAAGAACTGGGCAAGATGATGATGATGATGATGATGATGATGAT 2093
QY 1262 CGGCGGCGCGGAAATTC 1277
DB 2094 CGGCGGCGCGGAAATTC 2109

```

RESULT 7

ADM02650
ID ADM02650 standard; cDNA; 2755 BP.

AC ADM02650;

XX 20-MAY-2004 (first entry)

DE Human cDNA of the invention SEQ ID NO:1335.

KW 88; gene; human; gene therapy; diagnostic marker; pharmaceutical.

OS Homo sapiens.

PN BP1347046-A1.

XX 24-SEP-2003.

PF 12-APR-2002; 2002BP-00008400.

PR 22-MAR-2002; 2002JP-00137785.

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XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hito Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;
XX
DR WPI: 2003-723558/59.
DR P-PSDB; ADM05093.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 1335; 305bp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC cDNA sequence of the invention.
XX
SQ Sequence 2755 BP; 578 A; 887 C; 787 G; 503 T; 0 U; 0 Other;

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Query Match 68.6%; Score 876.2; DB 11; Length 2755;
Best Local Similarity 99.7%; Pred. No. 2.3e-199;
Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 392 AGAATCAAGATCTCATCATCTCAGCGGCGGGAAGCCATCTTCTGAGCTC 451
DB 1016 AGAATCAAGATCTCATCATCTCAGCGGCGGGAAGCCATCTTCTGAGCTC 1075
QY 452 CATTGAGGAGCGAAGCGGACCGACCAAGCACTGCTGTGCTGAGGAGGAGATGAA 511
DB 1076 CATTGAGGAGCGAAGCGGACCGACCAAGCACTGCTGTGCTGAGGAGGAGATGAA 1135
QY 512 AGGCTCATCATCATCTCCTCATCTGCGCATTCAGAAAGGCTCGGGTGTGGCCAA 571
DB 1136 AGGCTCATCATCATCTCCTCATCTGCGCATTCAGAAAGGCTCGGGTGTGGCCAA 1195
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QY 632 GCACATGATGATCATGATGCTTCAATGCGCGCATGTACTTTCCATGAAGATGATGTT 691
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DB 1316 CCGGGGCTCAGGCGCTTACGAGTCCGGGCGGCTTGAAGAGTTCTTAAGCGGAGTTTGG 1375
QY 752 GAGACACACCAAGATGACGAGCGTGAAGAAACCAAGGTGATGCTGACAGGACATGTC 811
DB 1376 GAGACACACCAAGATGACGAGCGTGAAGAAACCAAGGTGATGCTGACAGGACATGTC 1435
QY 812 TGAACCGGAGCGGCGTGAAGTCACTCTTCCGGGACCTAAGATGCTCAAGAACTGTCG 871
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QY 872 GAGAGCTGTTTCAACAGAGATTAACTCAGGCTCCAGTCAAGCTCAGACCAAGCT 931
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QY 932 GGTGTGGCGGCGGCGGCGGAGGAGCGGCGGAGCTCTTACTTACCTTCCAGATGGGCG 991
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QY 992 CTTCTGAGCGGTGGCTGTTGGCAACACCCGCGTGGATGCCATGACCGAGATCCA 1051
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 QY 1052 TAGGTCAATCAGAGACTGATCCGCAAGGCTCAGGCCAACAAAGTGAAGAACTTCCAT 1111
 DB 1676 TGAATCAATCAGAGACTGATCCGCAAGGCTCAGGCCAACAAAGTGAAGAACTTCCAT 1735
 QY 1112 CGTTGTCTCCCTGGGACAGAGAGGTCCCAAGTGCCTGTGACCTGTGTGATGCTT 1171
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 QY 1172 CGGTCCAGCAACCCCTGGGAGCTGGCCAAAGACTGTTTGGGCGCAAGAACTGGGCAA 1231
 DB 1796 CGGTCCAGCAACCCCTGGGAGCTGGCCAAAGACTGTTTGGGCGCAAGAACTGGGCAA 1855
 QY 1232 GATGTGTGAGTGTGCACTGTTGCACTGATCCAGACGGGCGGCGCG 1272
 DB 1856 GATGTGTGAGTGTGCACTGTTGCACTGATCCAGACGGGCGGCGCG 1896

RESULT 8

AAD42941
 ID AAD42941 standard; DNA; 3240 BP.

XX AAD42941;

DT 15-NOV-2002 (first entry)

DE Human PLA2 group VI (Ca2+-independent) DNA #1.

KW Human; antisense; phospholipase A2; infection; inflammation; tumour;

XX antisense therapy; PLA2; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 137..2557

XX /product= "Human phospholipase 2 protein"

PN US6410325-B1.

PD 25-JUN-2002.

PF 09-MAY-2001; 2001US-00851896.

PR 09-MAY-2001; 2001US-00851896.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Freiler SM, Watt AT;

XX MPI; 2002-616513/66.

DR P-PSDB; AAE25968.

PT Novel antisense compounds useful for inhibiting gene expression of human
 phospholipase A2, group VI and for treating diseases associated with
 expression of phospholipase A2, group VI.

XX Example 15; Col 109-116; 72pp; English.

CC The present invention relates to novel antisense compounds which inhibit
 the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 (Ca2+-independent) in human cells or tissues and for treating an animal,
 CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnostics, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) DNA

SQL Sequence 3240 BP; 681 A; 1048 C; 912 G; 598 T; 0 U; 1 Other;

Query Match 68.6%; Score 876.2; DB 6; Length 3240;

Best Local Similarity 99.7%; Pred. No. 2.4e-199;

Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 392 AGAATCAAGATCTCATCAATCTCAGGCGCCGGAAAGCCAGCTTATCTGGGCTC 451
 DB 1483 AGAATCAAGATCTCATCAATCTCAGGCGCCGGAAAGCCAGCTTATCTGGGCTC 1542
 QY 452 CATGAGGAGAGAAACCGAACCCAGACCACTGCTGTGCTGATGAGAGAGATGAA 511
 DB 1543 CATGAGGAGAGAAACCGAACCCAGACCACTGCTGTGCTGATGAGAGAGATGAA 1602
 QY 512 AGGCTCATCATCATCATCATCTCTCATTCGCATTCGAAAGGCTCGGCTGTGGCCAA 571
 DB 1603 AGGCTCATCATCATCATCTCTCATTCGCATTCGAAAGGCTCGGCTGTGGCCAA 1662
 QY 572 GGACTGTTGACTGAGTGGGCGGAGCCAGACACTGGAAGCATCTGGCCATTCT 631
 DB 1663 GGACTGTTGACTGAGTGGGCGGAGCCAGACACTGGAAGCATCTGGCCATTCT 1722
 QY 632 GCACTAGTATCATGAGCTTACATGCGCGGCAATGTACTTTCGATGAAAGATGAGTGT 691
 DB 1723 GCACTAGTATCATGAGCTTACATGCGCGGCAATGTACTTTCGATGAAAGATGAGTGT 1782
 QY 692 CCGGAGCTCAGGCGCTTACAGAGTGGGAGCCCTGTGAGAGATTCTGAAAGCGGAGTTTG 751
 DB 1783 CCGGAGCTCAGGCGCTTACAGAGTGGGAGCCCTGTGAGAGATTCTGAAAGCGGAGTTTG 1842
 QY 752 GGAGCACACCAAGATGACGAGTCAAGAAACCCAAAGTGAATGCTGACAGGAGCACTGTC 811
 DB 1843 GGAGCACACCAAGATGACGAGTCAAGAAACCCAAAGTGAATGCTGACAGGAGCACTGTC 1902
 QY 812 TGACCGGAGCGGCGGAGTCACTCACTCTTCCGGAATGATGCTCCAGAAATGTCGG 871
 DB 1903 TGACCGGAGCGGCGGAGTCACTCACTCTTCCGGAATGATGCTCCAGAAATGTCGG 1962
 QY 872 GGAGCTCGTTTCAACAGAAAGTTAACTCAGGCTCCAGGCTCAGCTCAGACCAAGCT 931
 DB 1963 GGAGCTCGTTTCAACAGAAAGTTAACTCAGGCTCCAGGCTCAGCTCAGACCAAGCT 2022
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 QY 1052 TGAATCAATCAGAGACTGATCCGCAAGGCTCAGGCCAACAAAGTGAAGAACTTCCAT 1111
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 QY 1112 CGTTGTCTCCCTGGGACAGAGAGTCCCAAGTGCCTGTGACTGTGTGATGCTT 1171
 DB 2203 CGTTGTCTCCCTGGGACAGAGAGTCCCAAGTGCCTGTGACTGTGTGATGCTT 2262
 QY 1172 CGGTCCAGCAACCCCTGGGAGCTGGCCAAAGCTGTTTGGGGCCAAAGAACTGGGCAA 1231
 DB 2263 CGGTCCAGCAACCCCTGGGAGCTGGCCAAAGCTGTTTGGGGCCAAAGAACTGGGCAA 2322
 QY 1232 GATGTGTGAGTGTGCACTGTTGCACTGATCCAGACGGGCGGCGCG 1272
 DB 2323 GATGTGTGAGTGTGCACTGTTGCACTGATCCAGACGGGCGGCGCG 2363

RESULT 9

AD019775
 ID AD019775 standard; cDNA; 3240 BP.

XX AD019775;
 XX

| Query Match | Best Local Similarity | Score | DB | Length | Matches | Conservative | Mismatches | Indels | Gaps |
|---|-----------------------|-------|--------|--------|---|--------------|------------|--------|------|
| 27-MAR-2003; 2003WO-US009755. | 68.6%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 29-MAR-2002; 2002US-0368722P. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 03-MAY-2002; 2002US-0377576P. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 05-JUL-2002; 2002US-039934P. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 27-SEP-2002; 2002US-0414269P. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| (INCY-) INCYTE CORP. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| Emerling BM, Margulis JP, Chawla NK, Lee SY, Duggan BM, Warren BA; Baughn MR, Lee EA, Griffin JA, Kable AE, Elliott VS, Chang H; Lee S, Ramkumar J, Bulloch SA, Hefalla AJA, Khare R, Jiang X; Jackson AS; | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| WPI: 2003-788347/74. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| P-PSDB; ADD93407. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| New LIPM polypeptides, useful for diagnosing, preventing, and treating disorders associated with abnormal expression or activity of LIPM, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| Claim 88; Page 232-233; 238p; English. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| The present sequence is the nucleotide sequence of human lipid-associated molecule LIPM-14 (Incyte polynucleotide 7512662CB1), which encodes a protein that shows homology to human Ca ²⁺ -independent phospholipase A2 short isoform. This is one of 19 LIPM polynucleotides of the invention. The invention relates to novel LIPMs and the nucleic acids encoding them, and to the use of nucleic acids and proteins in the diagnosis, treatment and prevention of disorders associated with abnormal expression or activity of LIPM such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy, catatonias), endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g. leukemias, cervical or breast cancers), immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention also relates to the assessment of the effects of exogenous compounds on the expression of nucleic acids and LIPMs. The invention provides expression vectors, host cells, antibodies, agonists and antagonists, transgenic organisms, and arrays and microarrays of the polynucleotides. | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| Sequence 3215 BP; 666 A; 1021 C; 923 G; 605 T; 0 U; 0 Other; | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| Query Match | Best Local Similarity | Score | DB | Length | Matches <td>Conservative</td> <td>Mismatches</td> <td>Indels</td> <td>Gaps</td> | Conservative | Mismatches | Indels | Gaps |
| 389 CACAGAACTACAGAGATCTCATGCAATCTCACGGGCCGGAAGCAGAGCTTCATCTGGG | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 1469 CAGACAACTACAGATCTCATGCAATCTTCACGGGCCGGAAGCAGAGCTTCATCTGGG | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 449 CTCATGAGGAGCAGAAAGCAGACCCACGACCACTGCTGTGCTTGATGAGAGAGAGT | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 1529 CTCATGAGGAGCAGAAAGCAGACCCACGACCACTGCTGTGCTTGATGAGAGAGAGT | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 509 GAAAGGCTCATCATCATCCAGCTCCATGCGCATGAGAAAGGCTGGGTGGCCAC | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 1589 GAAAGGCTCATCATCATCCAGCTCCATGCGCATGAGAAAGGCTGGGTGGCCAC | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 569 CAAAGGACTGTTTGACTGGGTGGCGGAGCAGACACTGAGAGCACTCGGCGCTGGCCAT | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 1649 CAAAGGACTGTTTGACTGGGTGGCGGAGCAGACACTGAGAGCACTCGGCGCTGGCCAT | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 629 TCTGCACTGAATGCTCAGTCCCTACATGCGGCGAGTGAATCTTGGCATGAAGATAGGT | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |
| 1709 TCTGCACTGAATGCTCAGTCCCTACATGCGGCGAGTGAATCTTGGCATGAAGATAGGT | 99.4%; | 876; | DB 10; | 3215; | 879; | 0; | 5; | 0; | 0; |

| | | | | | | |
|-----------|---|-----------------|---|------|--|--|
| OY | | 689 | GTTCCGCGGGCTTCAAGGCCCTTAACAAGTGCGGGGCCCTGTGAAGAATTCCTGAAGCGGAGTT | 748 | | |
| Dd | | 1769 | GTTCCGCGGGACTTCAAGGCCCTTAACAAGTGCGGGGCCCTGTGAAGAATTCCTGAAGCGGAGTT | 1828 | | |
| OY | | 749 | TGGGAGACACAACAAGATGACGACGTCACAGAAACCCAAGGTGATGCTGACAGGGACACT | 808 | | |
| Dd | | 1829 | TGGGAGACACAACAAGATGACGACGTCACAGAAACCCAAGGTGATGCTGACAGGGACACT | 1888 | | |
| OY | | 809 | GTCGACCCGGCAGCCGGCTGAATCTTCAACCTTCTCCGAACTAAGATGCTCTCAAAAATTGT | 868 | | |
| Dd | | 1889 | GTCGACCCGGCAGCCGGCTGAATCTTCAACCTTCTCCGAACTAAGATGCTCTCAAAAATTGT | 1948 | | |
| OY | | 869 | CCGGAGAGCTGTTTCAAACCAAGACGTTAACCTTAGGCCTTCAGACTCAGCCCTCAGACCA | 928 | | |
| Dd | | 1949 | CCGGAGAGCTGTTTCAAACCAAGACGTTAACCTTAGGCCTTCAGACTCAGCCCTCAGACCA | 2008 | | |
| OY | | 929 | GCTGGTGTGCGGGCGGGCCCGAAGCACGCGGGGACGTCCTACTTACTTCTCCGACCACATGG | 988 | | |
| Dd | | 2009 | GCTGGTGTGCGGGCGGGCCCGAAGCACGCGGGGACGTCCTACTTACTTCTCCGACCACATGG | 2068 | | |
| OY | | 989 | GCGCTTCTTGGAACGCTGGGCTGTGGCCACAAACCCCAAGCTGATGACATGACCCAGAT | 1048 | | |
| Dd | | 2069 | GCGCTTCTTGGAACGCTGGGCTGTGGCCACAAACCCCAAGCTGATGACATGACCCAGAT | 2128 | | |
| OY | | 1049 | CCATGAGTACAAATGAGAACCTGATCCCGCAAGGGTCAGAGCCCAACAAGGTGAAGAAACTCTC | 1108 | | |
| Dd | | 2129 | CCATGAGTACAAATGAGAACCTGATCCCGCAAGGGTCAGAGCCCAACAAGGTGAAGAAACTCTC | 2188 | | |
| OY | | 1109 | CATCGTGTGTCTCCCTGGGGACAGGGAGGTCCCCAANAAGTCCCTGTGACTCTGTGTGATGT | 1168 | | |
| Dd | | 2189 | CATCGTGTGTCTCCCTGGGGACAGGGAGGTCCCCAANAAGTCCCTGTGACTCTGTGTGATGT | 2248 | | |
| OY | | 1169 | CTTCCGCTCCCAACAACCCCTGGGGACGTCGGCCAAAGACTGTTTTGGGGGCCCAAGAACTGGG | 1228 | | |
| Dd | | 2249 | CTTCCGCTCCCAACAACCCCTGGGGACGTCGGCCAAAGACTGTTTTGGGGGCCCAAGAACTGGG | 2308 | | |
| OY | | 1229 | CAAGATGATGATGAGACTGTTGCAACGATTCAGACGCGGCGGACCGG | 1272 | | |
| Dd | | 2309 | CAAGATGATGATGAGACTGTTGCAACGATTCAGACGCGGCGGCGGCTG | 2352 | | |
| <hr/> | | | | | | |
| RESULT 11 | | | | | | |
| AAH14129 | | | | | | |
| ID | AAH14129 | standard; cdna; | 2392 BP. | | | |
| <hr/> | | | | | | |
| XX | AAH14129; | | | | | |
| AC | | | | | | |
| XX | | | | | | |
| DT | 26-JUN-2001 | (first entry) | | | | |
| XX | | | | | | |
| DE | Human cDNA sequence SEQ ID NO:11329. | | | | | |
| XX | | | | | | |
| KM | Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. | | | | | |
| XX | | | | | | |
| OS | Homo sapiens. | | | | | |
| XX | | | | | | |
| PN | EP1074617-A2. | | | | | |
| XX | | | | | | |
| PD | 07-FEB-2001. | | | | | |
| XX | | | | | | |
| PF | 28-JUL-2000; 2000EP-00116126. | | | | | |
| XX | | | | | | |
| PR | 29-JUL-1999; 99JP-00248036. | | | | | |
| PR | 27-AUG-1989; 99JP-00300253. | | | | | |
| PR | 11-JAN-2000; 2000JP-00118776. | | | | | |
| PR | 02-MAY-2000; 2000JP-00183767. | | | | | |
| PR | 09-JUN-2000; 2000JP-00241899. | | | | | |
| XX | | | | | | |
| PA | (HELI-) HELIX RES INST. | | | | | |
| XX | | | | | | |
| FI | Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J; | | | | | |
| PI | Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T; | | | | | |
| XX | | | | | | |

CC phospholipase enzyme recombinantly. Host cells include animal cells,
 CC insect cells, eukaryotes, prokaryotes, etc. The sequence may also be
 CC expressed in transgenic animals (e.g. milk of transgenic cow). The
 CC encoded protein is used to screen for agents which inhibit phospholipase
 CC activity for use as antiinflammatory agents

XX Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 U; 0 Other;

Query Match 55.4%; Score 708; DB 2; Length 2935;
 Best Local Similarity 87.6%; Pred. No. 3.8e-159;
 Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 389 CACAGAACTACAGAGATTCATGCACATCTCAAGGAGCCCGAAGCCAGCTTACTCTGGG 448
 DB 1277 CAAACAGCTTCAGAGACTCATGCCCCTCCCGAGCCCGAAGCCAGCATTCCTGAG 1336
 QY 449 CTCATGAGGAG 508
 DB 1337 CTCATGAGGAG 1396
 QY 509 GAAAGCCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 568
 DB 1397 GAAAGCCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1456
 QY 569 CAAAGACTTGTGACTGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628
 DB 1457 CAAAGACTTGTGACTGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1516
 QY 629 TCTGCAAGTAATCCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 688
 DB 1517 TCTGCAAGTAATCCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1576
 QY 689 GTTCGGGAGCTCCAGAGGCTTACAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 748
 DB 1577 GTTCGGGAGCTCCAGAGGCTTACAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1636
 QY 749 TGGGAGAGACACCAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 808
 DB 1637 TGGGAGAGACACCAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1696
 QY 809 GTCGACCGGAG 868
 DB 1697 GTCGACCGGAG 1756
 QY 869 CCGGAGAGCTCTGTTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 928
 DB 1757 TCGGAGAGCTCTGTTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1816
 QY 929 GCTGAGTGGGAG 988
 DB 1817 ACTGATATGGGAG 1876
 QY 989 GCGCTTCCTGAG 1048
 DB 1877 AGCTTTCCTGAG 1936
 QY 1049 CCATGATACATACAG 1108
 DB 1937 CCATGATACATACAG 1996
 QY 1109 CATGCTGTGTTCTCTGAG 1168
 DB 1997 CATGCTGTGTTCTCTGAG 2056
 QY 1169 CTCCTGAG 1228
 DB 2057 CTCCTGAG 2116
 QY 1229 CAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1272
 DB 2117 CAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160

RESULT 13
 AAT44578
 ID AAT44578 standard; cDNA; 2935 BP.
 XX
 AC AAT44578;

XX 25-MAR-2003 (revised)
 DT 11-FEB-1997 (first entry)
 XX
 DE Calcium-independent cytosolic phospholipase A2/B coding sequence.
 XX
 KW cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
 KW arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;
 KW anti-inflammatory; screen; rheumatoid arthritis; de.

OS Synthetic.

FN Key Location/Qualifiers
 FT CDS 96..2354
 FT /*tag= a

PN US5554511-A.

PD 10-SEP-1996.

XX 14-APR-1995; 95US-00422420.

XX 27-JUL-1994; 94US-00281193.

XX (GENE) GENETICS INST INC.

PI Tang J, Jones S;

XX WPI; 1996-424653/42.

DR P-PSDB; AAW01479.

PT Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing
 PT host cells contg. the phospholipase gene, useful for screening anti-
 PT inflammatory agents for treating e.g. rheumatoid arthritis.

XX Claim 1; Col 15-22; 24pp; English.

XX The present sequence encodes a calcium-independent cytosolic
 CC phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release
 CC of arachidonic acid in specific tissues characterized by unique membrane
 CC phospholipids. The invention provides a process for producing such an
 CC enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence
 CC of one or more amino acid sequences selected from AAW01480-92. cPLA2/B
 CC has activity in a mixed micelle assay with 1-palmitoyl-2-[14C]-
 CC arachidonyl-phosphatidylcholine. The enzyme is useful for screening anti-
 CC -inflammatory agents mediated by the arachidonic acid cascade, for
 CC treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF
 CC field.)

XX Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 U; 0 Other;

Query Match 55.4%; Score 708; DB 2; Length 2935;
 Best Local Similarity 87.6%; Pred. No. 3.8e-159;
 Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 389 CACAGAACTACAGAGATTCATGCACATCTCAAGGAGCCCGAAGCCAGCTTACTCTGGG 448
 DB 1277 CAAACAGCTTCAGAGACTCATGCCCCTCCGAGCCCGAAGCCAGCATTCCTGAG 1336
 QY 449 CTCATGAGGAG 508
 DB 1337 CTCATGAGGAG 1396
 QY 509 GAAAGCCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 568
 DB 1397 GAAAGCCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1456
 QY 569 CAAAGACTTGTGACTGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628

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Db      1457 CAAGGACCTTCTGACCTGGGTGGGAGGAGCAGACCTGGGGGCACTCTGGCCAT 1516
Qy      629 TCTGCA CAGTAAGTCCATGCGCTCAATGCGGGCATGTACTTTCCATGAGGATGAGT 688
Db      1517 TCTGCA CAGTAAGTCCATGCGCTCAATGCGGGCATGTACTTTCCATGAGGATGAGT 1576
Qy      689 GTTCCGGGGCTCCAGGCGCTCAATGCGGGCATGTACTTTCCATGAGGATGAGT 748
Db      1577 GTTCCGGGGCTCCAGGCGCTCAATGCGGGCATGTACTTTCCATGAGGATGAGT 1636
Qy      749 TGGGAGACACCAAGATGACGACGTCAGAGAAACCAAGATGATGTCAGAGACACT 808
Db      1637 TGGGAGACACCAAGATGACGATGTCAAAAAACCAAGATGATGTCAGAGACACT 1696
Qy      809 GTCTGACCGGACCGCGCTGAACTCCACTTTCCGGAACCTAGATGCTCCAGAACTGT 868
Db      1697 GTCTGACCGGACCGCGCTGAACTCCACTTTCCGGAACCTAGATGCTCCAGAGGTCAT 1756
Qy      869 CCGGGAGCCTCTTTCATACCAAGAACCTTAACCTCAGGCTCCAGGCTCCAGACCA 928
Db      1757 TCGGGAACCTCGCTTCAACCAAAACATTAACCTGAAGCTCCCACTCAGCTCAGACCA 1816
Qy      929 GCTGATGCGGCGGCGCGCCGGAAGACGCGGAGCTCTACTTACTTCCAGCCCAATGG 988
Db      1817 ACTGATATGGCGGACGACCGCGGACGATGCGGAGACCCCACTACTTCCGCGCCATGG 1876
Qy      989 GCGCTTCTGACGCGTGGGCTGTTGGCAACACCCCAAGCTGATGCCATGACCAAT 1048
Db      1877 ACCTTCTCTGATGATGCGGCTGCTGGCCCAACCCCACTAGATGCCATGACTGAAAT 1936
Qy      1049 CCATGATGTCATACAGACCTGATCCGCAAGGTCAGGCGCAACCAAGTGAAGAACTCTC 1108
Db      1937 CCATGATGTCATACAGACCTGATCCGCAAGGTCAGGCGCAACCAAGTGAAGAACTCTC 1996
Qy      1109 CATGTTGTTCTCCCTGGGAGACAGAGAGTCCCAAGTCCCTGATGCTGTGTGATGT 1168
Db      1997 CATGTTGTTCTCCCTGGGAGACAGAGAGTCCCAAGTCCCTGATGCTGTGTGATGT 2056
Qy      1169 CTTCCTGCTCCAGACCCCTGGAGAGCTGGCAAGACTGTTTTGGGGCCCAAGAACTGGG 1228
Db      2057 CTTCCTGCTCCAGACCCCTGGAGAGCTGGCAAGACTGTTTTGGAGCCCAAGAACTGGG 2116
Qy      1229 CAAGATGCTGTCGATCTGTCGACGATCCAGACGCGCGCGCG 1272
Db      2117 CAAGATGCTGTCGATCTGTCGACGATCCAGATGCTGCGGCTG 2160

RESULT 14
AAT59199
ID      AAT59199 standard; cDNA; 2935 BP.
XX
AC      AAT59199;
XX
DT      17-OCT-2003 (revised)
DT      25-MAR-2003 (revised)
DT      20-MAY-1997 (first entry)
XX
DE      Ca-independent phospholipase A2/B gene.
XX
KW      Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
KW      chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
KW      heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;
KW      CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade; ds.
XX
OS      Cricetus griseus; ovary cells.
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
FT      96..2354
FT      /tag= a
FT      /product= "ca-independent phospholipase A2/B"
XX
PN      US5589170-A.

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XX
PD      31-DEC-1996.
XX
PF      14-APR-1995; 95US-00422106.
XX
PR      27-JUL-1994; 94US-00281193.
XX
PA      (GBM ) GENETICS INST INC.
XX
PI      Tang J, Jones S;
XX
DR      WPI; 1997-076789/07.
XX
DR      P-PSDB; AAW13163.
XX
PT      Compden. comprising calcium-independent phospholipase enzyme - for
PT      screening for anti-inflammatory agents.
PS      Claim 5; Col 15-22; 24pp; English.
XX
CC      This is the nucleotide sequence encoding the Ca-independent phospholipase
CC      A2/B from Chinese hamster ovary cells. The protein was isolated from
CC      these cells by conventional chromatographic methods e.g. DEAE anion
CC      exchange, hydrophobic interaction, heparin Toyopearl and Mono P 5/20
CC      chromatofocusing chromatography. The purified protein has mol. wt. of 86
CC      kD and an optimum pH 6. The protein was used for amino acid sequencing
CC      from which pools of degenerate probes were synthesised. The probes were
CC      used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 40000
CC      recombinant phages screened, 12 positive plaques were isolated. One of
CC      these, designated clone 9, contained this sequence. The phospholipase
CC      gene can be inserted into eukaryotic vectors for expression in COS or CHO
CC      cells. The protein, or peptides derived from it e.g. AAW13164-76, can be
CC      used to identify phospholipase inhibitors that can be used as anti-
CC      inflammatory agents, esp. against components of the arachidonic acid
CC      cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT
CC      -2003 to standardise OS field)
XX
SQ      Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 U; 0 Other;
XX
Query Match 55.4%; Score 708; DB 2; Length 2935;
Best Local Similarity 87.6%; Pred. No. 3,8e-159;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy      389 CACGAGACTACAGGATCTCATGACATCTCAGGGCGCGGAGCCGATTCCTGGG 448
Db      1277 CAAACGCTTCAGAGCCTCATGCTCCTCCAGGCCGAGACCACTTCACTCTGAG 1336
Qy      449 CTCATGAGGAGACGAGAGCGGACCCAGACCACTGTGTGCTGCTGATGAGAGAGT 508
Db      1337 CTCATGAGGAGATGAGAGGAGATTCATGATCACTGCTGTGCTGAGAGGAGGCGT 1396
Qy      509 GAAAGGCTTCATCATCATCAAGTCTCTCATGCGCATGAGGAGGCTCGGGTGTGGCCAC 568
Db      1397 GAAAGGCTTCATCATCATCAAGTCTCTCATGCGCATGAGGAGGCTTCAGTGTGGCCAC 1456
Qy      569 CAAGGACCTGTTGATGAGGAGTGGCGGAGCAGACATGAGAGGACCTGCGCCCTGGCCAT 628
Db      1457 CAAGGACCTGTTGATGAGGAGTGGCGGAGCAGACATGAGAGGACCTGCGCCCTGGCCAT 1516
Qy      629 TCTGCA CAGTAAGTCCATGCGCTCAATGCGGGCATGTACTTTCCATGAGGATGAGT 688
Db      1517 TCTGCA CAGTAAGTCCATGCGCTCAATGCGGGCATGTACTTTCCATGAGGATGAGT 1576
Qy      689 GTTCCGGGGCTCCAGGCGCTCAATGCGGGCATGTACTTTCCATGAGGATGAGT 748
Db      1577 GTTCCGGGGCTCCAGGCGCTCAATGCGGGCATGTACTTTCCATGAGGATGAGT 1636
Qy      749 TGGGAGACACCAAGATGACGACGTCAGAGAAACCAAGATGATGTCAGAGACACT 808
Db      1637 TGGGAGACACCAAGATGACGATGTCAAAAAACCAAGATGATGTCAGAGACACT 1696
Qy      809 GTCTGACCGGACCGCGCTGAACTCCACTTTCCGGAACCTAGATGCTCCAGAACTGT 868
Db      1697 GTCTGACCGGACCGCGCTGAACTCCACTTTCCGGAACCTAGATGCTCCAGAGGTCAT 1756

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QY 869 CCGGAGACCTGTTTCAACGAGAACCTTAACCTCAGGCTCCAGCTCAGGCTCAGACCA 928
 DB 1757 TCGGGAACCTCGCTTCAACCAAAACATTAACCTGAGGCCCACTCAGCTCAGACCA 1816
 QY 929 GCTGTGTGGCGGCGCGCGGCAAGCAGCGGGGAGCTCTTAATTCTCCGACCAATGG 988
 DB 1817 ACTGTATGGCGAGCAGCGCGGAGCAGTGGGGGAGCCCAACTTCCGCGCCCAATGG 1876
 QY 989 GCGCTTCCTGAGAGGTGGGCTGTGGCCAAACACCCAGCTGATGGCCATGACCAAT 1048
 DB 1877 ACCTTTCCTGAGAGGTGGGCTGTGGCCAAACACCCAGCTGATGGCCATGACCAAT 1936
 QY 1049 CCATGATCAATCAGGACCTGATCCGCAAGGCTCAGGCGCAAGGTGAAGAACTCTC 1108
 DB 1937 CCATGATCAATCAGGACCTGATCCGCAAGGCGCAAGGTGAAGAACTCTC 1996
 QY 1109 CATGTTGTCTCCTTGGGGAAGAGAGTCCCAACAGTCTGTGATCTGTGTGATGT 1168
 DB 1997 CATAGTGTCTCTCTGGGGAAGAGAGTCCCTCAAGTCCCGTAACCTGTGTGATGT 2056
 QY 1169 CTTCGCTCCAGAACCCCTGGGAGGCTGGCCAAAGACTTTTGGGGCCAAAGAACTGG 1228
 DB 2057 CTTCGCTCCAGAACCCCTGGGAGGCTGGCCAAAGACTTTTGGGGCCAAAGAACTGG 2116
 QY 1229 CAAGATGTGTGAGTGTGACGATGTCAGACGATCCAGACGCGCGCGCG 1272
 DB 2117 CAAGATGTGTGAGTGTGACGATGTCAGACGATGTCAGACGCGCGCGCG 2160

RESULT 15

AAT68827
 ID AAT68827 standard; cDNA; 2935 BP.

XX AAT68827;

DT 27-AUG-2003 (revised)
 DT 07-AUG-1997 (first entry)

XX Hamster cytosolic phospholipase A2/B cDNA.

KM Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 KW Inflammation; inhibitor; antiinflammatory; CHO; ds.

OS Cricetus.

XX Key Location/Qualifiers
 FT CDS 96..2354
 FT /*tag= a

XX W09717448-A2.

XX 15-MAY-1997.

XX 07-NOV-1996; 96WO-US017794.

XX 08-NOV-1995; 95US-00555568.

XX (GEMV) GENETICS INST INC.

XX Jones S, Tang J;

XX MPI; 1997-281037/25.

XX P-PSDB; AAM17849.

XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PT mammalian subject.

XX Example 4; Page 33-36; 74p; English.

CC A cDNA clone (AAT68827), deposited as ATCC 6969, codes for a cytosolic
 CC phospholipase A2/B (sPLA2/B) (AAM17849) that is thought to be involved in
 CC the arachidonic acid cascade. It was obtd. by screening a CHO-DUX cDNA

CC library with probes based on isolated peptides of the enzyme. Recombinant
 CC sPLA2/B was expressed in COS and CHO cells. Probes based on the hamster
 CC sPLA2/B clone were used to identify human sPLA2/B partial cDNA clones
 CC (see also AAT68823-26). (Updated on 27-AUG-2003 to correct OS field.)
 XX

SQ Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 U; 0 Other;

Query Match 55.4%; Score 708; DB 2; Length 2935;

Best Local Similarity 87.6%; Pred. No. 3.8e-159;

Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 389 CACAGACTACAGGATCTCATGCACTTCACGGGCGCCGGAAGCCAGCGTTCTCTGGG 448
 DB 1277 CAACAGCTTCAGGACCTCATGCTCCATCTCCGAGCGCCGAAGCCAGCTTCACTCTGAG 1336
 QY 449 CTCATGAGGGAAGAGACCGGACCCAGACCACTCTGTGCTGTGATGAGAGAGAT 508
 DB 1337 CTCATGAGGGAAGAGACCGGACCCAGACCACTCTGTGCTGTGATGAGAGAGAT 1396
 QY 509 GAAAGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 568
 DB 1397 GAAAGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1456
 QY 569 CAAGACCTGTTGATGCTGGGTGGCGGCAACAGCACTGAGAGGCACTCTGCGCTGCGCAT 628
 DB 1457 CAAGACCTGTTGATGCTGGGTGGCGGCAACAGCACTGAGAGGCACTCTGCGCTGCGCAT 1516
 QY 629 TCTGCAAGTATGATCATGAGGCTCAATGCGCGGATGTACTTTCCGATGAGATGAGT 688
 DB 1517 TCTGCAAGTATGATCATGAGGCTCAATGCGCGGATGTACTTTCCGATGAGATGAGT 1576
 QY 689 GTTCGCGGCGCTCAGGCGCCCTAAGAGTGGGCGCCCTGAGAGATTCTGAAGCGGAGTT 748
 DB 1577 GTTCGCGGCGCTCAGGCGCCCTAAGAGTGGGCGCCCTGAGAGATTCTGAAGCGGAGTT 1636
 QY 749 TGGGGAAGCAACCAAGATGACGAGCTCAGGAAACCCAGAGTGTACTGACAGGCACT 808
 DB 1637 TGGGGAAGCAACCAAGATGACGAGTGTCAAAAAACCCAGAGTGTACTGACAGGCACT 1696
 QY 809 GTTCGCGGCGGAGCGGCTGAATCCACCTCTTCCGGAATCTCGATGCTCCAGAACTGT 868
 DB 1697 GTTCGCGGCGGAGCGGCTGAATCCACCTCTTCCGGAATCTCGATGCTCCAGAACTGT 1756
 QY 869 CCGGGAACCTCGTTTCAACAGAACGTTAACTCAGAGCTCCAGCTCAGCCCTCAGACCA 928
 DB 1757 TCGGGAACCTCGTTTCAACAGAACGTTAACTCAGAGCTCCAGCTCAGCCCTCAGACCA 1816
 QY 929 GCTGTGTGGCGGCGCGCCGGAAGCAGCGGGGCACTCTACTTACTTCCGACCCCAATGG 988
 DB 1817 ACTGTATGGCGAGCAGCGCGGAGCAGTGGGGAGCGCCCAACTTCTCCGCGCCCAATGG 1876
 QY 989 GCGCTTCCTGAGACGCTGGGCTGTGGCCAAACCCAGCTGATGGCCATGACCAATG 1048
 DB 1877 ACCTTTCCTGAGAGGTGGGCTGTGGCCAAACCCAGCTGATGGCCATGACCAATG 1936
 QY 1049 CCATGATCAATCAGGACCTGATCCGCAAGGCTCAGGCGCAAGGTGAAGAACTCTC 1108
 DB 1937 CCATGATCAATCAGGACCTGATCCGCAAGGCGCAAGGTGAAGAACTCTC 1996
 QY 1109 CATGTTGTCTCCTTGGGGAAGAGAGTCCCAACAGTCTGTGATCTGTGTGATGT 1168
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 QY 1169 CTTCGCTCCAGAACCCCTGGGAGGCTGGCCAAAGACTTTTGGGGCCAAAGAACTGG 1228
 DB 2057 CTTCGCTCCAGAACCCCTGGGAGGCTGGCCAAAGACTTTTGGGGCCAAAGAACTGG 2116
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 DB 2117 CAAGATGTGTGAGTGTGACGATGTCAGACGATGTCAGACGCGCGCGCG 2160

Search completed: December 16, 2004, 12:22:06

Thu Dec 16 19:13:25 2004

us-10-612-668-18.rng

Page 15

Job time : 685 secs

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Db 1 GAATTTTAAAGCCCAAGTGGTATATGACACATCGGCTCCGATGCAAGAAAGCACTTT 60
Qy GTCTGAAGAGACACGCAAGGATATTATGCTTGGGTTTCAAGAGAAAGATTGAG 120
Db 61 GTCTGAAGAGACACGCAAGGATATTATGCTTGGGTTTCAAGAGAAAGATTGAG 120
Qy 121 GGAACCTGGAGCTGGTGGGCAAGGATGGGAGCCCTTCCCAAGAGAGTGGGCCCCCTT 180
Db 121 GGAACCTGGAGCTGGTGGGCAAGGATGGGAGCCCTTCCCAAGAGAGTGGGCCCCCTT 180
Qy 181 TGCACTTCACAGCCATTTCTCTCTGTGGCTGTGGCTCACTTTTCTTCTGGGCAAGATC 240
Db 181 TGCACTTCACAGCCATTTCTCTCTGTGGCTGTGGCTCACTTTTCTTCTGGGCAAGATC 240
Qy 241 CTTCCTGTGGGGAAGGAGACAGATGACAGGGGAGTGGGGGATGAGGGGCTGGCCGTGG 300
Db 241 CTTCCTGTGGGGAAGGAGACAGATGACAGGGGAGTGGGGGATGAGGGGCTGGCCGTGG 300
Qy 301 CGAAGCAGACCCAGGTTTATCTAGGAGCTCTGGGTTAGCAAGGCTTGGGAGCCACC 360
Db 301 CGAAGCAGACCCAGGTTTATCTAGGAGCTCTGGGTTAGCAAGGCTTGGGAGCCACC 360
Qy 361 TGACCAAGAGATGCTGCTGTGCTCTCAAGAACTCAAGAGATCTGATGCAATCTCAC 420
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Qy 421 GGGCCCGGAAGCAGCCTTATCTCTGGGCTCAATGAGGAGCAGAAAGCCAGCCAGCC 480
Db 421 GGGCCCGGAAGCAGCCTTATCTCTGGGCTCAATGAGGAGCAGAAAGCCAGCCAGCC 480
Qy 481 ACCTGCTGTGCTGTGATGAGAGAGAGTGAAGGCTCATCATCTCAGCTCTCATCG 540
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Qy 541 CCATCGAAGAGGCTCGGGTGTGGCCCAAGAGCCTGTTGATGGGTGGCGGCGCA 600
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Qy 601 GCACTGAGAGCATCTGGCCCTGGCCATCTGCAAGATGATGATGATGATGATGATGATG 660
Db 601 GCACTGAGAGCATCTGGCCCTGGCCATCTGCAAGATGATGATGATGATGATGATGATG 660
Qy 661 GCACTGATCTTCCATGAGATGAGTGTTCGGGGCTCCAGGCTTACGAGTGGGGC 720
Db 661 GCACTGATCTTCCATGAGATGAGTGTTCGGGGCTCCAGGCTTACGAGTGGGGC 720
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Qy 781 AACCCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 AACCCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Qy 841 TCCGGAACCTAGATGCTCCAGAACTGTCCGGAGGCTTCCGTTCAACAGAAAGTTAAC 900
Db 841 TCCGGAACCTAGATGCTCCAGAACTGTCCGGAGGCTTCCGTTCAACAGAAAGTTAAC 900
Qy 901 TCAGGCTCCAGTCCAGGCTTCCAGACAGTGTGTGGGGGGGGGGGGGGGGGGGGGGGG 960
Db 901 TCAGGCTCCAGTCCAGGCTTCCAGACAGTGTGTGGGGGGGGGGGGGGGGGGGGGGGG 960
Qy 961 CAGCTCTTACTTATCTTCCGACCAATGGGGCTTCCGAGCGGTGGGCTTGGCCAA 1020
Db 961 CAGCTCTTACTTATCTTCCGACCAATGGGGCTTCCGAGCGGTGGGCTTGGCCAA 1020
Qy 1021 ACCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 ACCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Qy 1081 GTGAGGCAAGCAAGTGAAGAACTCTCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 GTGAGGCAAGCAAGTGAAGAACTCTCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

Qy 1141 CACAAGTGCCTGTGACCTGTGTGATGCTTCCGTCACAGCAACCCCTGGAGCTGGCA 1200
Db 1141 CACAAGTGCCTGTGACCTGTGTGATGCTTCCGTCACAGCAACCCCTGGAGCTGGCA 1200
Qy 1201 AGACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGATGATGATGATGATGATGATG 1260
Db 1201 AGACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGATGATGATGATGATGATGATG 1260
Qy 1261 ACGGCGCGCCGGAATTC 1277
Db 1261 ACGGCGCGCCGGAATTC 1277

RESULT 2

US-09-519-223-18

Sequence 18, Application US/09519223

Patent No. 6274140

GENERAL INFORMATION:

APPLICANT: Jones, Simon

APPLICANT: Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/519,223

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 1277 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 396..1271

US-09-519-223-18

Query Match 100.0%; Score 1277; DB 3; Length 1277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAATTTTAAAGCCCAAGTGGTATATGACACATCGGCTCCGATGCAAGAAAGCACTTT 60
Qy 61 GTCTGAAGAGACACGCAAGGATATTATGCTTGGGTTTCAAGAGAAAGATTGAG 120
Db 61 GTCTGAAGAGACACGCAAGGATATTATGCTTGGGTTTCAAGAGAAAGATTGAG 120

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QY 121 GGAACCTGGAGCTGCTGGGCAAGGAGTGGGAGGCTTCCAGAGCATGGGCCCCCTT 180
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DB 301 CGAGGACAGCCCAAGGTTTATCTAGGAGCTCTGGGCTAGCAGGCTTGGGAGCCCAAC 360
QY 361 TGAACCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TGAACCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 GGGGCGGGGAGGAGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GGGGCGGGGAGGAGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 CCATGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 CCATGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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DB 601 GCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 GCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 GCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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DB 721 CCCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 AACCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 AACCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 TCCGGAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 TCCGGAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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DB 901 TCAAGGCTTCAAGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTC 960
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DB 961 CAGCTCTCTACTTACTTCCAGCCCAATGAGGCTTCTGAGCGGTGGGCTGTTGGCCACA 1020
QY 1021 ACCCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1080
DB 1021 ACCCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1080
QY 1081 GTGAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1140
DB 1081 GTGAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1140
QY 1141 CAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1141 CAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 AGACTGTTTTGGGGCAAGGAGTGGGCAAGTGGTGGTGAAGTGGTGAAGTGGTGAAGT 1260

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DB 1201 AGACTGTTTTGGGGCAAGGAGTGGGCAAGTGGTGGTGAAGTGGTGAAGTGGTGAAGT 1260
QY 1261 ACCGGGCGCCGGAATTC 1277
DB 1261 ACCGGGCGCCGGAATTC 1277

RESULT 3
US-09-927-180-18
; Sequence 18, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 396..1271
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-927-180-18

Query Match 100.0%; Score 1277; DB 4; Length 1277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      241  CTTCTGTGGGAGGAGAGATGACAGGGGAGTGGGGGAGTGGGCGTGGCCGTGG 300
Qy      301  CGAGGACAGCCAGGTTTGTATCTAGGGACCTCTGGGGTACAGAGGCTTGGGAGCCCA 360
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Qy      361  TGACACAGATAGCCCTGTCTGTGTGCTCAGAGAACTACAGAGATCTATGCAATCTCAC 420
Db      361  TGACACAGATAGCCCTGTCTGTGTGCTCAGAGAACTACAGAGATCTATGCAATCTCAC 420
Qy      421  GGGCCGCGGAGGAGGCTTATCTCTGGGCTCAGTGAAGGAGCAGAGCCGAGCCAGACC 480
Db      421  GGGCCGCGGAGGAGGCTTATCTCTGGGCTCAGTGAAGGAGCAGAGCCGAGCCAGACC 480
Qy      481  ACCTGTGTGCTGTGATGAGAGAGATGAAAGGCTCATCATCTCAGCTCTCATCG 540
Db      481  ACCTGTGTGCTGTGATGAGAGAGATGAAAGGCTCATCATCTCAGCTCTCATCG 540
Qy      541  CCATCCAGAAAGGCTCGGGTGTGGCCACCAAGGACCTGTTGACTGGGTGGCGGACCA 600
Db      541  CCATCCAGAAAGGCTCGGGTGTGGCCACCAAGGACCTGTTGACTGGGTGGCGGACCA 600
Qy      601  GCACTGGAGGACATCTGTGGCCCTGAGCCATCTGCACTAGATGATGAGCTTACATGCG 660
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Qy      661  GCATGTATCTTTCATAGAGATGAGAGTGTTCGGGGCTCCAGGCTTACAGAGTGGGG 720
Db      661  GCATGTATCTTTCATAGAGATGAGAGTGTTCGGGGCTCCAGGCTTACAGAGTGGGG 720
Qy      721  CCTGTGAGAGGTTCTCGAAGCGGAGTGTGGGAGCACCAAGATGACGAGCTGAGGA 780
Db      721  CCTGTGAGAGGTTCTCGAAGCGGAGTGTGGGAGCACCAAGATGACGAGCTGAGGA 780
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Db      781  AACCCAGGTGATGCTGACAGGACACTGTCTGACCGGAGCGGCTGAACTCCACTCT 840
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Db      841  TCCGGAACCTACGATGCTCCAGAAACTGTCTCGGAGGCTCTGTTCAACAGAACTTAAC 900
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Db      901  TCAAGGCTCCAGTCAAGCTTCAAGCCAGACGAGTGTGGGCGGCGGCGGAGCAAGCGGG 960
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Db      961  CAGCTCTTACTTACTTCCGACCCCAATGGGGCTTCTGTGAGCGGTGGCTGTGGCCAA 1020
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Db      1021  ACCCCACGCTGTGATCCATGACGAGATCCATGATGATCAATCAAGACTTATCCGCAAG 1080
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Db      1081  GTAGGCGCAACAGGTGAAAGAACTCCATCGTGTCTCCCTGGGGGACAGGGAGGTCCC 1140
Qy      1141  CACAAGTCTGTGACCTGTGTGATCTTCCGTCCCAAGCAACCTCTGGGAGCTGGCCA 1200
Db      1141  CACAAGTCTGTGACCTGTGTGATCTTCCGTCCCAAGCAACCTCTGGGAGCTGGCCA 1200
Qy      1201  AGACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGTGTGAGTGTTCACGAGATCAG 1260
Db      1201  AGACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGTGTGAGTGTTCACGAGATCAG 1260
Qy      1261  ACGGGCGCGCGGAATTC 1277

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Db      1261  ACGGGCGCGCGGAATTC 1277

RESULT 4
US-08-555-568B-22
; Sequence 22, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..2106
; US-08-555-568B-22

Query Match      69.4%; Score 885.8; DB 2; Length 2112;
Best Local Similarity 99.8%; Pred. No. 2.7e-233;
Matches 887; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      1224  CACAGACTACAGATCTCATGCACTCTCACCGGGCCCGGAGCCAGCGTTCACTCTGG 1283
Qy      449  CTCATGAGGAGTGAAGAGGACCCAGACCACTGCTGTGCTGCTGATGAGAGAGT 508
Db      1284  CTCATGAGGAGTGAAGAGGAGCCAGACCACTGCTGTGCTGCTGATGAGAGAGT 1343
Qy      509  GAAAGGCTCATCATCATCAGCTCCTCATCGCATCGAAGAGGCTCGGGTGTGGCCAC 568
Db      1344  GAAAGGCTCATCATCATCAGCTCCTCATCGCATCGAAGAGGCTCGGGTGTGGCCAC 1403
Qy      569  CAAAGACTGTTTGAAGTGGTGGCGGACACAGACTGAGAGGATCTGGCCCTTGGCCAT 628
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Qy      629  TCTGCAAGTAACTCATGAGCTTCAATGCGCGGAGTACTTTGCAATGAAGATAGGT 688
Db      1464  TCTGCAAGTAACTCATGAGCTTCAATGCGCGGAGTACTTTGCAATGAAGATAGGT 1523
Qy      689  GTTCGGGGCTTCAGGCGCTTACGAGTGGGGGCGCTGAGAGAGTCTCTGAAGCGGAGTT 748

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Db 1524 GTTCCGGGGCTCCAGGCTTACGAGTGGGGCCCTGAGAGAGTTCTGAGGGAGTT 1583
Qy 749 TGGGAGACACCAAGTGAAGGAGTCTGAGGAAACCAAGGTGATCTGACAGGAGACT 808
Db 1584 TGGGAGACACCAAGTGAAGGAGTCTGAGGAAACCAAGGTGATCTGACAGGAGACT 1643
Qy 809 GTCTGACCGGACCGGCTGAATCCGACTCTTCCGGAACTGAGTCTCAGAACTGT 868
Db 1644 GTCTGACCGGACCGGCTGAATCCGACTCTTCCGGAACTGAGTCTCAGAACTGT 1703
Qy 869 CCGGAGACCTCGTTCAACCAAGAGCTTAACTTCAGGCTCTGAGCTCAGACCA 928
Db 1704 CCGGAGACCTCGTTCAACCAAGAGCTTAACTTCAGGCTCTGAGCTCAGACCA 1763
Qy 929 GCTGTGTGCGGGCGGCGCCGAGACCGGGGAGCTCTTACTTCTTCCGACCAATGG 988
Db 1764 GCTGTGTGCGGGCGGCGCCGAGACCGGGGAGCTCTTACTTCTTCCGACCAATGG 1823
Qy 989 GCGCTTCTGAGACGATGGGCTGTGGCCACACCCGCTGAGTGGCCAGTACCGAGT 1048
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Qy 1049 CCATGAGTAAATCAAGGACCTGATCCGCAAGGCTCAGGCCAACAAGGTGAAGAACTCTC 1108
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Qy 1109 CATGTTGTCTCTCTGGGAGACAGGAGGATCCCAAGTGCCTGTGATCTGTGTGATGT 1168
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Db 2064 CAAGATGATGATGATCTGTTGCAAGGATCCAGACGGGCGGCGGAACTTC 2112

RESULT 5

US-09-519-223-22
; Sequence 22: Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..2106
; US-09-519-223-22

Query Match 69.4%; Score 885.8; DB 3; Length 2112;
Best Local Similarity 99.8%; Pred. No. 2,7e-233;
Matches 887; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 389 CACAGAACTACAGAGATCTCATGACATCTCACAGGCGCCCGAAGCCAGCGTTCACTCTGGG 448
Db 1224 CAGACAACTACAGAGATCTCATGACATCTCACAGGCGCCCGAAGCCAGCGTTCACTCTGGG 1283
Qy 449 CTCATGAGGAGCAGAGAGCGAGCCCAAGCAACCTCTGTGCTGTGATGAGAGAGT 508
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Db 1344 GAAAGGCTCATATCATATCATAGCTCTCATGCGCATGAGAGAGCGCTCGGCTGTGCGCAC 1403
Qy 569 CAAGACCTGTTTGAATGAGGCTGGGCGGAGCAACAGCACTGAGAGCATCTGCGCTTGGCCAT 628
Db 1404 CAAGACCTGTTTGAATGAGGCTGGGCGGAGCAACAGCACTGAGAGCATCTGCGCTTGGCCAT 1463
Qy 629 TCTGCAAGTAACTCATGAGCTTACATGCGGCGCATGATCTTTCGATGAGAGTGAAGT 688
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Qy 689 GTTCGGGGCTCCAGGCTTCAAGAGTCCGGGCGGCTGGAGAGTTCTCTGAAGGGGAGTT 748
Db 1524 GTTCGGGGCTCCAGGCTTCAAGAGTCCGGGCGGCTGGAGAGTTCTCTGAAGGGGAGTT 1583
Qy 749 TGGGAGACACCAAGATGACGAGCTCAGAGAAACCAAGGTGATCTGACAGGAGACT 808
Db 1584 TGGGAGACACCAAGATGACGAGCTCAGAGAAACCAAGGTGATCTGACAGGAGACT 1643
Qy 809 GTCTGACCGGACCGGCTGAATCCGACTCTTCCGGAACTGAGTCTCAGAACTGT 868
Db 1644 GTCTGACCGGACCGGCTGAATCCGACTCTTCCGGAACTGAGTCTCAGAACTGT 1703
Qy 869 CCGGAGACCTCGTTCAACCAAGAGCTTAACTTCAGGCTCTGAGCTCAGACCA 928
Db 1704 CCGGAGACCTCGTTCAACCAAGAGCTTAACTTCAGGCTCTGAGCTCAGACCA 1763
Qy 929 GCTGTGTGCGGGCGGCGCCGAGACCGGGGAGCTCTTACTTCTTCCGACCAATGG 988
Db 1764 GCTGTGTGCGGGCGGCGCCGAGACCGGGGAGCTCTTACTTCTTCCGACCAATGG 1823
Qy 989 GCGCTTCTGAGACGATGGGCTGTGGCCACACCCGCTGAGTGGCCAGTACCGAGT 1048
Db 1824 GCGCTTCTGAGACGATGGGCTGTGGCCACACCCGCTGAGTGGCCAGTACCGAGT 1883
Qy 1049 CCATGAGTAAATCAAGGACCTGATCCGCAAGGCTCAGGCCAACAAGGTGAAGAACTCTC 1108
Db 1884 CCATGAGTAAATCAAGGACCTGATCCGCAAGGCTCAGGCCAACAAGGTGAAGAACTCTC 1943
Qy 1109 CATGTTGTCTCTCTGGGAGACAGGAGGATCCCAAGTGCCTGTGATCTGTGTGATGT 1168
Db 1944 CATGTTGTCTCTCTGGGAGACAGGAGGATCCCAAGTGCCTGTGATCTGTGTGATGT 2003
Qy 1169 CTTCGGGCGGAGCAACCCCTGGGAGCTGGGCAACGCTTTTGGGGCCCAAGAACTGGG 1228
Db 2004 CTTCGGGCGGAGCAACCCCTGGGAGCTGGGCAACGCTTTTGGGGCCCAAGAACTGGG 2063

1314 CTTGCTGCTGCTGATGAGAGAGAGTGAAGGCTCATCATCATCCAGCTCTCATGCG 1373
QY 542 CATGAGAAAGGCTCGGGGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGGACACAG 601
DB 1374 CATGAGAAAGGCTCGGGGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGGACACAG 1433
QY 602 CACTGAGAGGATCTGGGCTGGCCATTTCTGACAGTAACTGATGCTTCACTGACGCGG 661
DB 1434 CACTGAGAGGATCTGGGCTGGCCATTTCTGACAGTAACTGATGCTTCACTGACGCGG 1493
QY 662 CATGTAATTTTCGATGAAGATGAAGGTTCCTGGGGCTTCAAGGCTTCAAGTGGGGCC 721
DB 1494 CATGTAATTTTCGATGAAGATGAAGGTTCCTGGGGCTTCAAGGCTTCAAGTGGGGCC 1553
QY 722 CTTGAGAGAGTCTTGAAGGGAGTTTGGGAGACACCAAGATGACGAGCTGAGAA 781
DB 1554 CTTGAGAGAGTCTTGAAGGGAGTTTGGGAGACACCAAGATGACGAGCTGAGAA 1613
QY 782 ACCCAAGTATGCTGACAGGAGACCTGTCTGACCGGACCGGCTGAACTGCACTCTT 841
DB 1614 ACCCAAGTATGCTGACAGGAGACCTGTCTGACCGGACCGGCTGAACTGCACTCTT 1673
QY 842 CCGGAACTAGATGCTCCAGAAACTGTCCGGAGCTCTTTTCAACCAAGCTTAACTT 901
DB 1674 CCGGAACTAGATGCTCCAGAAACTGTCCGGAGCTCTTTTCAACCAAGCTTAACTT 1733
QY 902 CAGGCTTCAAGCTCAGGCTTCAAGCACTGTGTGAGCGGCGGCGCGGAGAGCGGCGG 961
DB 1734 CAGGCTTCAAGCTCAGGCTTCAAGCACTGTGTGAGCGGCGGCGGAGAGCGGCGG 1793
QY 962 AGCTCTTACTTACTTCTGAGCCCAATGGGCGCTTCTGAGCGGTGGGTGTTGGCCAA 1021
DB 1794 AGCTCTTACTTACTTCTGAGCCCAATGGGCGCTTCTGAGCGGTGGGTGTTGGCCAA 1853
QY 1022 CCCCAGCGTGAAGCCATGAACCAAGATCCATGATTAATCAAGAACTGTAATCCGCAAGG 1081
DB 1854 CCCCAGCGTGAAGCCATGAACCAAGATCCATGATTAATCAAGAACTGTAATCCGCAAGG 1913
QY 1082 TCAGGCAACAAAGTGAAGAACTCTCCATGTTGTCTCCCTGGGAGCAGAGAGTCCG 1141
DB 1914 TCAGGCAACAAAGTGAAGAACTCTCCATGTTGTCTCCCTGGGAGCAGAGAGTCCG 1973
QY 1142 ACAAGTGCCTGTGACCTGTGTGATGTCTTCCGTCCAGCAACCCCTGGAGCTGGCCAA 1201
DB 1974 ACAAGTGCCTGTGACCTGTGTGATGTCTTCCGTCCAGCAACCCCTGGAGCTGGCCAA 2033
QY 1202 GACTGTTTTTGGGCGCAAGAACTGGGCAAGATGTGTGATGATGCTTGGCAAGATCCAGA 1261
DB 2034 GACTGTTTTTGGGCGCAAGAACTGGGCAAGATGTGTGATGATGCTTGGCAAGATCCAGA 2093
QY 1262 CGGGCGGCGGAATTC 1277
DB 2094 CGGGCGGCGGAATTC 2109

RESULT 9
US-09-927-180-20

Sequence 20, Application US/09927180
Patent No. 6645736

GENERAL INFORMATION:
APPLICANT: Jones, Simon

Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.

ZIP: 02140
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927, 180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/519, 223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2109 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 43..2103
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-927-180-20
Query Match 69.4%; Score 885.6; DB 4; Length 2109;
Best Local Similarity 97.9%; Pred. No. 3e-233;
Matches 897; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 362 GACCAAGATGCGCTGCTGTGCTTCAAGAACTTCAAGATCTGATGACATCTCAGG 421
DB 1194 GACTCTTAATCTTCTGAGCTTCCCAAAATCGGCAACTTACAGATCTATGACATCTCAGG 1253
QY 422 GGGCCGGAAGCCAGCTTATCTGTGGCTCATGAGGAGAGAGAACCCAGACCA 481
DB 1254 GGGCCGGAAGCCAGCTTATCTGTGGCTCATGAGGAGAGAGAACCCAGACCA 1313
QY 482 CTGCTGTGCTGATGAGAGAGAGTGAAGGCTTCAATCATCTCACTCTCATGCG 541
DB 1314 CTGCTGTGCTGATGAGAGAGAGTGAAGGCTTCAATCATCTCACTCTCATGCG 1373
QY 542 CATGGAAGAGGCTCGGGGTGGCCACCAAGAACTGTTGACTGGGTGGCGGCGCAAG 601
DB 1374 CATGGAAGAGGCTCGGGGTGGCCACCAAGAACTGTTGACTGGGTGGCGGCGCAAG 1433
QY 602 CACTGAGAGCATCTGGCCCTGGCCATTTCTGACAGTAACTGATGCTTCACTGCGCG 661
DB 1434 CACTGAGAGCATCTGGCCCTGGCCATTTCTGACAGTAACTGATGCTTCACTGCGCG 1493
QY 662 CATGTAATTTTCGATGAAGATGAAGGTTCCTGGGGCTTCAAGGCTTCAAGTGGGGCC 721
DB 1494 CATGTAATTTTCGATGAAGATGAAGGTTCCTGGGGCTTCAAGGCTTCAAGTGGGGCC 1553
QY 722 CTTGAGAGAGTCTTGAAGGGAGTTTGGGAGACACCAAGATGACGAGCTGAGAA 781
DB 1554 CTTGAGAGAGTCTTGAAGGGAGTTTGGGAGACACCAAGATGACGAGCTGAGAA 1613
QY 782 ACCCAAGTATGCTGACAGGAGACCTGTCTGACCGGACCGGCTGAACTGCACTCTT 841
DB 1614 ACCCAAGTATGCTGACAGGAGACCTGTCTGACCGGACCGGCTGAACTGCACTCTT 1673
QY 842 CCGGAACTAGATGCTCCAGAAACTGTCCGGAGCTCTTTTCAACCAAGCTTAACTT 901
DB 1674 CCGGAACTAGATGCTCCAGAAACTGTCCGGAGCTCTTTTCAACCAAGCTTAACTT 1733
QY 902 CAGGCTTCAAGCTCAGGCTTCAAGCACTGTGTGAGCGGCGGCGGAGAGCGGCGG 961
DB 1734 CAGGCTTCAAGCTCAGGCTTCAAGCACTGTGTGAGCGGCGGCGGAGAGCGGCGG 1793

| | | | |
|----|------|---|------|
| Qy | 962 | AGCTCTCACTTACTTCGGAACCCAAATGGGAGGCTTCCTGGAACGTGGGCTGTGGCCAA | 1021 |
| Db | 1794 | AGCTCTCACTTACTTCGGAACCCAAATGGGAGGCTTCCTGGAACGTGGGCTGTGGCCAA | 1853 |
| Qy | 1022 | CCCCACGTGATGCGCATGACCCGAGATCATATGATCAATCAGGACTGATCCGCAAGG | 1081 |
| Db | 1854 | CCCCACGTGATGCGCATGACCCGAGATCATATGATCAATCAGGACTGATCCGCAAGG | 1913 |
| Qy | 1082 | TCAGGCCAACAAGGTGAAGAACTTCATCGTGTCTCCCTGGGACAGGAGGTCCTCC | 1141 |
| Db | 1914 | TCAGGCCAACAAGGTGAAGAACTTCATCGTGTCTCCCTGGGACAGGAGGTCCTCC | 1973 |
| Qy | 1142 | ACAAGTGCCTGTGACCTGTGTGAGATGTCTTCGTCCTCCAGCAACCCCTGGAGCTGGCCAA | 1201 |
| Db | 1974 | ACAAGTGCCTGTGACCTGTGTGAGATGTCTTCGTCCTCCAGCAACCCCTGGAGCTGGCCAA | 2033 |
| Qy | 1202 | GACTGTTTTTGGGGCACAAGAACTGGGCAAGATGGTGTGGAAGTTTGCACGAGATCCAGA | 1261 |
| Db | 2034 | GACTGTTTTTGGGGCACAAGAACTGGGCAAGATGGTGTGGAAGTTTGCACGAGATCCAGA | 2093 |
| Qy | 1262 | CGGGCGGCGCGAATTC | 1277 |
| Db | 2094 | CGGGCGGCGCGAATTC | 2109 |

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RESULT 10
US-09-851-896-10
; Sequence 10, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 3240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2770
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (137)...(2557)
; US-09-851-896-10

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| | | | | | | | | |
|----|-----------------------|------------------------------|---------------------------------------|---------------|------------|----|--------|-------|
| | Query Match | 68.6%; | Score | 876.2; | DB | 4; | Length | 3240; |
| | Best Local Similarity | 99.7%; | Pred. | No. 1.4e-230; | | | | |
| | Matches | 878; | Conservative | 0; | Mismatches | 3; | Indels | 0; |
| | Gaps | 0; | | | | | | |
| OY | 392 | AGAACTACAGATCTCATGCA | CATTCACGGGCCCGGAAGCCAGCATTATCTTGAGCTC | 451 | | | | |
| Db | 1483 | AGAACTACAGATCTCATGCA | CATTCACGGGCCCGGAAGCCAGCATTATCTTGAGCTC | 1542 | | | | |
| OY | 452 | CATGAGGACGAGAAGCGGACCACAGACA | CCCTGTGTGCCTGTGATGAGAGAGAGTGA | 511 | | | | |
| Db | 1543 | CATGAGGACGAGAAGCGGACCACAGACA | CCCTGTGTGCCTGTGATGAGAGAGAGTGA | 1602 | | | | |
| OY | 512 | AGGCCTCATCATCATCA | AGCTTCTCATGCGCATGAGAAGGCTTGAGCCACCAA | 571 | | | | |
| Db | 1603 | AGGCCTCATCATCATCA | AGCTTCTCATGCGCATGAGAAGGCTTGAGCCACCAA | 1662 | | | | |
| OY | 572 | GGAACCTGTTTGA | CTGGGTGGGGGACCAAGCATCTTGAGCCATCTT | 631 | | | | |
| Db | 1663 | GGAACCTGTTTGA | CTGGGTGGGGGACCAAGCATCTTGAGCCATCTT | 1722 | | | | |

| | | | |
|----|------|---|------|
| Qy | 632 | GCA CAGTAAAGCTCA TGGCCTCA TCAATGCCGGGATG TACTCTTTCG SCA TGAAGATGAGGTGTT | 691 |
| Db | 1723 | GCA CAGTAAAGCTCA TGGCCTCA TCAATGCCGGGATG TACTCTTTCG SCA TGAAGATGAGGTGTT | 1782 |
| Qy | 692 | CCGGGGGCTCCA GGCCTCA TCGAGTCGGGGCCCTTGAGAGATTCCTGAAAGCGGAGTTTGG | 751 |
| Db | 1783 | CCGGGGGCTCCA GGCCTCA TCGAGTCGGGGCCCTTGAGAGATTCCTGAAAGCGGAGTTTGG | 1842 |
| Qy | 752 | GGAGCA CACCAAGATGACGGACGTCA GAGAAACCAAGAGTATGCTGACAGGGACACTGTC | 811 |
| Db | 1843 | GGAGCA CACCAAGATGACGGACGTCA GAGAAACCAAGAGTATGCTGACAGGGACACTGTC | 1902 |
| Qy | 812 | TGACCGGACGCGGCTGAA CTCGACCTCTTCCGAACTACGATGCTCCAGAACTGTCCG | 871 |
| Db | 1903 | TGACCGGACGCGGCTGAA CTCGACCTCTTCCGAACTACGATGCTCCAGAACTGTCCG | 1962 |
| Qy | 872 | GGAGCCTCGTTTCAA CCAAGAACGTTTAACTTCAGGCTTCAGCTACGCTCCAGACGACT | 931 |
| Db | 1963 | GGAGCCTCGTTTCAA CCAAGAACGTTTAACTTCAGGCTTCAGCTACGCTCCAGACGACT | 2022 |
| Qy | 932 | GGTGTGGCGGGCGGCCCCGAAGCACCGGGGGACGCTCTACTTACTTCCGACCCTTGAAGGCG | 991 |
| Db | 2023 | GGTGTGGCGGGCGGCCCCGAAGCACCGGGGGACGCTCTACTTACTTCCGACCCTTGAAGGCG | 2082 |
| Qy | 992 | CTTCTCGGACGGTGGGCTGTTGGCCAA CAACCCACGCTGGATGCA TGA CCGAGATCCA | 1051 |
| Db | 2083 | CTTCTCGGACGGTGGGCTGTTGGCCAA CAACCCACGCTGGATGCA TGA CCGAGATCCA | 2142 |
| Qy | 1052 | TGAAGTACA TACAGACCTGATTCGCCAAGGGCTCAGGCCAA CAAGGTGAAAGAACTCTCAT | 1111 |
| Db | 2143 | TGAAGTACA TACAGACCTGATTCGCCAAGGGCTCAGGCCAA CAAGGTGAAAGAACTCTCAT | 2202 |
| Qy | 1112 | CGTGTCTCCCTGCGGAGCA GGGAGGTCGCCACAAGTGCCTGTGACTGTGTGATGTCCTT | 1171 |
| Db | 2203 | CGTGTCTCCCTGCGGAGCA GGGAGGTCGCCACAAGTGCCTGTGACTGTGTGATGTCCTT | 2262 |
| Qy | 1172 | CCGTCCAGCAACCCCTGGAGCTGGCCAGACTGTTTTTGGGGCCAAAGAACTGGGCAA | 1231 |
| Db | 2263 | CCGTCCAGCAACCCCTGGAGCTGGCCAGACTGTTTTTGGGGCCAAAGAACTGGGCAA | 2322 |
| Qy | 1232 | GATGTGTGTGACTGTTGACCGGATCCAGACGGGCGGCGG | 1272 |
| Db | 2323 | GATGTGTGTGACTGTTGACCGGATCCAGACGGGCGGCGG | 2363 |

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/ RESULT 11
/ US-08-281-193-1
/ Sequence 1, Application US/08281193
/ Patent No. 5466595
/ GENERAL INFORMATION:
/ APPLICANT: Jones, Simon
/ APPLICANT: Tang, Jim
/ TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
/ NUMBER OF SEQUENCES: 15
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/281,193
/ FILING DATE:
/ CLASSIFICATION: 435
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2935 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:

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NAME/KEY: CDS
LOCATION: 96..2352
US-08-281-193-1

Query Match 55.4%; Score 708; DB 1; Length 2935;
Best Local Similarity 87.6%; Pred. No. 2e-184;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

389 CACAGACTACAGAGTCTGACATCTCACGGGCGCCGAGACGCGCTTACCTCGG 448
1277 CAACAGCTTCAAGACCTTATGCCATCTCCGAGCCCGAAGCCAGATTCTCTGAG 1336
449 CTCATGAGGAGCAGAGAGGAGCCACGACCACTCTGCTGCTGAGTGAAGAGT 508
1337 CTCATGAGGAGTGAAGAGGAGTCCATGATCACTGCTGCTGAGCGAGGGCGCT 1396
509 GAAAGGCTTATCATCTATCCAGCTCTCATGCCATGAGAGGCTCGGGTGTGCCAC 568
1397 GAAAGGCTGCTATCATCTATCCAGCTCTCATGAGAGGCTCGAGGTGTGCCAC 1456
569 CAAGGACTGTTGACTGGGTGGCGGACAGAGCTGAGGATCCCTGGCGCTGAGCAT 628
1457 CAAGGACTTTCAGCTGGGTGGAGAGACAGAGCTGGGGCATCTTGGCCTTGGCAT 1516
629 TCTGCAAGTATGATGCTATGCTATGCTGCGGATGTACTTTGCGATGAGAGT 688
1517 TCTGCAAGTATGCTATGCTATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCT 1576
689 GTTCCGGGCTCCAGGCTTACAGAGTGGGGGCTTGGAGAGTCTTGAAGCGGAGTT 748
1577 GTTCCGGGCTCCAGGCTTACAGAGTGGGGGCTTGGAGAGTCTTGAAGCGGAGTT 1636
749 TGGGAGACACCAAGATGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGT 808
1637 TGGGAGACACCAAGATGACAGATGACAGAGAGAGAGAGAGAGAGAGAGAGT 1696
809 GTTGAACCGGACCGGCTGAGTCACTCTTCCGAGTACAGTCTTCAAGAACTGT 868
1697 GTTGAACCGGACCGGCTGAGTCACTCTTCCGAGTACAGTCTTCAAGAACTGT 1756
869 CCGGAGACCTCTGTTCAACAGAGAGTCACTTCAAGGCTTCAAGGCTTCAAGCA 928
1757 TCGGAGACCTCTGTTCAACAGAGAGTCACTTCAAGGCTTCAAGGCTTCAAGCA 1816
929 GCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 988
1817 ACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1876
989 GCGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1048
1877 AGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1936
1049 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1108
1937 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1996
1109 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1168
1997 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2056
2057 CTTCCGCGCCAGCAACCTCTGGGAGTGGCTAAGAGTGTGTTGGAGCCAAAGAGT 2116
1229 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272
2117 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160

RESULT 12
US-08-422-106-1
Sequence 1, Application US/08422106
Patent No. 5589170

GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,106
CLASSIFICATION: 435
FILING DATE: 14-APR-1995
PRIORITY DATE: 27-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-422-106-1

Query Match 55.4%; Score 708; DB 1; Length 2935;
Best Local Similarity 87.6%; Pred. No. 2e-184;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

389 CACAGACTACAGAGTCTGACATCTCACGGGCGCCGAGACGCGCTTACCTCGG 448
1277 CAACAGCTTCAAGACCTTATGCCATCTCCGAGCCCGAAGCCAGATTCTCTGAG 1336
449 CTCATGAGGAGCAGAGAGGAGCCACGACCACTCTGCTGCTGAGTGAAGAGT 508
1337 CTCATGAGGAGTGAAGAGGAGTCCATGATCACTGCTGCTGAGCGAGGGCGCT 1396
509 GAAAGGCTTATCATCTATCCAGCTCTCATGCGCATGAGAGAGGCTCGGGTGTGCCAC 568
1397 GAAAGGCTTATCATCTATCCAGCTCTCATGCGCATGAGAGAGGCTCGGGTGTGCCAC 1456
569 CAAGGACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 628
1457 CAAGGACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1516
629 TCTGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
1517 TCTGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1576
689 GTTCCGGGCTCCAGGCTTACAGAGTGGGGGCTTGAAGAGTCTTGAAGCGGAGTT 748
1577 GTTCCGGGCTCCAGGCTTACAGAGTGGGGGCTTGAAGAGTCTTGAAGCGGAGTT 1636
749 TGGGAGACACCAAGATGACGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGT 808
1637 TGGGAGACACCAAGATGACAGATGACAGAGAGAGAGAGAGAGAGAGAGT 1696
809 GTTGAACCGGACCGGCTGAGTCACTCTTCCGAGTACAGTCTTCAAGAACTGT 868
1697 GTTGAACCGGACCGGCTGAGTCACTCTTCCGAGTACAGTCTTCAAGAACTGT 1756
869 CCGGAGACCTCTGTTCAACAGAGAGTCACTTCAAGGCTTCAAGGCTTCAAGCA 928
1757 TCGGAGACCTCTGTTCAACAGAGAGTCACTTCAAGGCTTCAAGGCTTCAAGCA 1816
929 GCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 988

Db 1817 ACTGATGCGAGACGCCGAGACAGTGGGGGACGCCCAACTCTTCGCGCCCAATGG 1876
Qy 989 GCGCTTCCTGAGACGCTGGGCTGTTGGCCAAACACCCCAAGCTGATGACCGAGAT 1048
Db 1877 ACCTTCTCTGAGATGCTGGGCTGGGCTGAGCAACACCCCACTGATGCTGATGAAT 1936
Qy 1049 CCATGATGAATCAAGACCTGATCCGCAAGGGGTCAGGCCCAAGAGTGAAGAACTCTC 1108
Db 1937 CCATGATGAATCAAGACCTGATCCGCAAGGGGTCAGGCCCAAGAGTGAAGAACTCTC 1996
Qy 1109 CATGTTGCTCTCCCTGGGAGACAGGAGTCCCAAGTGCCTGTGACTGTGTGATGT 1168
Db 1997 CATAGTGTCTCTCTGGGAGACAGGAGTCCCTCAAGTGCCTGTAACCTGTGATGT 2056
Qy 1169 CTTCCTGCTCCAGCAACCTCTGGGAGTGGCCCAAGACTGTTTGGGGCCAAAGACTGGG 1228
Db 2057 CTTCCTGCTCCAGCAACCTCTGGGAGTGGCCCAAGACTGTTTGGGGCCAAAGACTGGG 2116
Qy 1229 CAAGATGCTGTGAGACTGTGCAACGATCCAGACGGGCGGCGG 1272
Db 2117 CAAGATGCTGTGAGACTGTGCAACGATCCAGATGCTGGGCTG 2160

RESULT 13

US-08-735-716-1
Sequence 1, Application US/08735716
Patent No. 5840511
GENERAL INFORMATION:
APPLICANT: Jones, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735, 716
FILING DATE: 23-OCT-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-735-716-1

Query Match 55.4%; Score 708; DB 2; Length 2935;
Best Local Similarity 87.6%; Pred. No. 2e-184;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 389 CACGAACTACAGATCTCATGACATCTCAAGGCGCCGGAAGCCAGCGTTTCCTGGG 448
Db 1277 CAACACCTTCAGAGACCTCATGCCCCTCCGAGCCCGAAGCACAATTCATCTGAG 1336
Qy 449 CTCATGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 508
Db 1337 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1396
Qy 509 GAAAGGCTCATCATCATCCAGCTCTCATCGCCATCGAGAGAGGCTCGGGTGTGGCAC 568
Db 1397 GAAAGGCTGTATCATCATCACTCTCATTTGCAATGAGAGAGGCTCAAGGTGTGGCAC 1456

Qy 569 CAAGACCTGTTGATGCGGTGGCGGGCAACAGCACTGAGAGGATCTCGGCGCTGGCCAT 628
Db 1457 CAAGACCTGTTGATGCGGTGGCGGGCAACAGCACTGAGAGGATCTCGGCGCTGGCCAT 1516
Qy 629 TCTGCAAGTAACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 688
Db 1517 TCTGCAAGTAACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1576
Qy 689 GTTCCGCGCTCGAGGCTTCAGAGTGGGCGCCCTGAGAGAGTCTCTGAGCGGAGTT 748
Db 1577 GTTCCGCGCTCGAGGCTTCAGAGTGGGCGCCCTGAGAGAGTCTCTGAGCGGAGTT 1636
Qy 749 TGGGAGACACCAAGATGACGAGTCCAGAGAAACCAAGGTGATGCTGACAGGACAT 808
Db 1637 TGGGAGACACCAAGATGACGAGTCCAGAGAAACCAAGGTGATGCTGACAGGACAT 1696
Qy 809 GTCTGACCGGACCGGCTGTAACCTCCAGCTCTTCCGGAATACAGATGCTCCAGAACTGT 868
Db 1697 GTCTGACCGGACCGGCTGTAACCTCCAGCTCTTCCGGAATACAGATGCTCCAGAACTGT 1756
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Db 1757 TCGGAACTCGCTTCAACCAAGACCTTAACTCAGGCTCCAGCTCAGACCA 1816
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RESULT 14

US-08-555-568B-1
Sequence 1, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-555-5688-1

Query Match 55.4%; Score 708; DB 2; Length 2935;

Best Local Similarity 87.6%; Pred. No. 2e-184;

Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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US-09-519-223-1
Sequence 1, Application US/09519223

Patent No. 6274140

GENERAL INFORMATION:

APPLICANT: Jones, Simon

APPLICANT: Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSER: Genetics Institute, Inc.

STREET: 87 Cambridge Park Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/519,223

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2935 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 96..2352

US-09-519-223-1

Query Match 55.4%; Score 708; DB 3; Length 2935;

Best Local Similarity 87.6%; Pred. No. 2e-184;

Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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Job time : 131 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 12:10:46 ; Search time 728 Seconds

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Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 2 | 885.8 | 69.4 | 2112 | 9 | US-09-927-180-22 |
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| 5 | 876.2 | 68.6 | 3240 | 18 | US-10-476-991-10 |
| 6 | 708 | 55.4 | 2935 | 9 | US-09-927-180-1 |
| 7 | 472.2 | 37.0 | 70000 | 18 | US-10-476-991-3 |
| 8 | 268 | 21.0 | 411 | 10 | US-09-918-995-35047 |
| 9 | 60 | 4.7 | 60 | 10 | US-09-908-975-9474 |
| 10 | 50 | 3.9 | 3798 | 9 | US-09-908-975-31864 |
| 11 | 50 | 3.9 | 3798 | 9 | US-09-938-842A-1043 |
| 12 | 50 | 3.9 | 3798 | 11 | US-09-938-842A-1043 |

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| 36 | 42.4 | 3.3 | 154746 | 10 | US-09-827-688-8 | Sequence 8, Appl |
| 37 | 42.4 | 3.3 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appl |
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| 39 | 41.8 | 3.3 | 670 | 16 | US-10-239-134-29 | Sequence 29, Appl |
| 40 | 41.8 | 3.3 | 672 | 9 | US-09-965-703-30 | Sequence 30, Appl |
| 41 | 41.8 | 3.3 | 672 | 16 | US-10-239-134-30 | Sequence 30, Appl |
| 42 | 41.8 | 3.3 | 850 | 9 | US-09-965-703-28 | Sequence 28, Appl |
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ALIGNMENTS

RESULT 1
US-09-927-180-18
Sequence 18, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1277 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 396..1271
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-927-180-18

Query Match 100.0%; Score 1277; DB 9; Length 1277;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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US-09-927-180-22
Sequence 22, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 2112 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

```

MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 FEATURE: NAME/KEY: CDS
 LOCATION: 43..2106
 SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-09-927-180-22

Query Match 69.4%; Score 885.8; DB 9; Length 2112;
 Best Local Similarity 99.8%; Pred. No. 4e-243;
 Matches 887; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

389 CACAGAACTACAGATATCATGACATCTACAGGAGCCCGAAGCCGCTTACCTGAGG 448
 1224 CAGACAACTACAGATATCTATGACATCTACAGGAGCCCGAAGCCGCTTACCTGAGG 1283
 449 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 508
 1284 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1343
 509 GAAAGGCTCATATCATCTGCTCTCATGCTCATGAGAGGCTTGGGCTGCTGCTGCTGCT 568
 1344 GAAAGGCTCATATCATCTGCTCTCATGCTCATGAGAGGCTTGGGCTGCTGCTGCTGCT 1403
 569 CAAGACCTGTTGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 628
 1404 CAAGACCTGTTGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1463
 629 TCTGCACTGTTGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 688
 1464 TCTGCACTGTTGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1523
 689 GTTCCGGGAGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 748
 1524 GTTCCGGGAGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1583
 749 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 808
 1584 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1643
 809 GTCTGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 868
 1644 GTCTGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1703
 869 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 928
 1704 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1763
 929 GCTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 988
 1764 GCTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1823
 989 GCGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1048
 1824 GCGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1883
 1049 CCAATGAGTAAATCAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1108
 1884 CCAATGAGTAAATCAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1943
 1109 CATGCTGTTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1168
 1944 CATGCTGTTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1203
 1169 CTTCCGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1228
 2004 CTTCCGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1283
 1229 CAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1277
 2064 CAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2112

RESULT 3
 US-09-927-180-20
 ; Sequence 20, Application US/09927180
 ; Patent No. US20020106364A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/927,180
 ; FILING DATE: 09-Aug-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/519,223
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2109 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..2103
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 US-09-927-180-20

Query Match 69.4%; Score 885.6; DB 9; Length 2109;
 Best Local Similarity 97.9%; Pred. No. 4.6e-243;
 Matches 897; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

362 GACACAGAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
 1194 GACTCTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
 422 GGGCCGGAAGCCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
 1254 GGGCCGGAAGCCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1313
 482 CCGCT 541
 1314 CCGCT 1373
 542 CATGGAAGGAGGCTCGGAGTGTGGCCACCAAGACCTGTTGACTGGGTGGGCGGACCAAG 601
 1374 CATGGAAGGAGGCTCGGAGTGTGGCCACCAAGACCTGTTGACTGGGTGGGCGGACCAAG 1433
 602 CATGGAAGGAGTCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 661
 1434 CATGGAAGGAGTCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 1493
 662 CATGTACTTGGCATGAAGATGAGGTGTTCCGGGAGCTCAAGGCTTACGAGTGGGGGCC 721

Db 1494 CATGACTTTCGATGAAGATGAGTGTTCGGGGGCTCCAGGCCCTCAAGTCGGGGCC 1553
Qy 722 CCTGGAGGAATTCCTGAGAGGGAGGATTTGGGGAGCAACCAAGATGACGAGCGAGGAA 781
Db 1554 CTTGGAGGAATTCCTGAGAGGGAGGATTTGGGGAGCAACCAAGATGACGAGCGAGGAA 1613
Qy 782 ACCCAAGATGATCTGACAGGAGCACTGTCTGACCGGACCGGCTGAACTCCACTCTT 841
Db 1614 ACCCAAGATGATCTGACAGGAGCACTGTCTGACCGGACCGGCTGAACTCCACTCTT 1673
Qy 842 CCGGAATCAAGATGCTCCAGAACTGTCCGGAGCCTTGTTTCAACAGAACTGTTAACT 901
Db 1674 CCGGAATCAAGATGCTCCAGAACTGTCCGGAGCCTTGTTTCAACAGAACTGTTAACT 1733
Qy 902 CAGGCGCTCCAGCTCAAGCCCTCAGACGATGTGTGTGGCGGGCGGGCCGGAAGCAGCGGGC 961
Db 1734 CAGGCGCTCCAGCTCAAGCCCTCAGACGATGTGTGTGGCGGGCGGGCCGGAAGCAGCGGGC 1793
Qy 962 AGCTCTCACTTACTTCCGACCCCAATGAGGCGCTTCTCTGAGCGTGGGCTGTTGGCCAA 1021
Db 1794 AGCTCTCACTTACTTCCGACCCCAATGAGGCGCTTCTCTGAGCGTGGGCTGTTGGCCAA 1053
Qy 1022 CCCCAGCTGATGATCCATGACCGAGATCCATGATACATCAGAGCTGATTCGCAAGGG 1081
Db 1854 CCCCAGCTGATGATCCATGACCGAGATCCATGATACATCAGAGCTGATTCGCAAGGG 1913
Qy 1082 TCAGGCGCAAGAGTGAAGAACTCTCATGTTGTCTCCCTGGGGGACAGGGAGTCTCC 1141
Db 1914 TCAGGCGCAAGAGTGAAGAACTCTCATGTTGTCTCCCTGGGGGACAGGGAGTCTCC 1973
Qy 1142 ACAAGTCCCTGTGACCTGTGTGTGATCTTCCGTCCAGCAACCCCTGGAGCTGGCCAA 1201
Db 1974 ACAAGTCCCTGTGACCTGTGTGTGATCTTCCGTCCAGCAACCCCTGGAGCTGGCCAA 2033
Qy 1202 GACTGTTTTTGGGGCCAGAGAACTGGGCAAGATGTGTGTGACTGTTGACCGATCCAGA 1261
Db 2034 GACTGTTTTTGGGGCCAGAGAACTGGGCAAGATGTGTGTGACTGTTGACCGATCCAGA 2093
Qy 1262 CGGGCGGCGGGAATTC 1277
Db 2094 CGGGCGGCGGGAATTC 2109

RESULT 4

US-10-108-260A-1335
; Sequence 1335, Application US/10108260A
; Publication No. US2004005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US2004005560A1el full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1335
; LENGTH: 2755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1335

Query Match 68.6%; Score 876.2; DB 16; Length 2755;
Best Local Similarity 99.7%; Pred. No. 2,3e-240;
Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 392 AGAAGTACAGAGATCTCATGACATCTACGCGGCCCGGAAGCCAGCTTCACTCTGGGCTC 451
Db 1016 AGAAGTACAGAGATCTCATGACATCTACGCGGCCCGGAAGCCAGCTTCACTCTGGGCTC 1075
Qy 452 CATGAGGAGAGAGAGAGGAGCCCAAGCAACCTGCTGTGCTGATGAGAGAGAGTGA 511
Db 1076 CATGAGGAGAGAGAGAGGAGCCCAAGCAACCTGCTGTGCTGATGAGAGAGAGTGA 1135

Qy 512 AGGCTCATCATCATCCAGCTCTCTCATCCCATCGAAGAGGCTCGGTGTGGCCACCA 571
Db 1136 AGGCTCATCATCATCCAGCTCTCTCATCCCATCGAAGAGGCTCGGTGTGGCCACCA 1195
Qy 572 GGAAGCTGTTGACTGGGTGGCGGGACACAGACTGAGAGGATCTCTGGCCATTCT 631
Db 1196 GGAAGCTGTTGACTGGGTGGCGGGACACAGACTGAGAGGATCTCTGGCCATTCT 1255
Qy 632 GCACAGTATGATGATGAGGCTCAATGCGCGGCAATGATCTTTCGATAGAGATGAGTGT 691
Db 1256 GCACAGTATGATGATGAGGCTCAATGCGCGGCAATGATCTTTCGATAGAGATGAGTGT 1315
Qy 692 CCGGGGCTCCAGGCGCTTACAGAGTGGGGCCCTTGAGAGATTCTTGAAGCGGAGTTTG 751
Db 1316 CCGGGGCTCCAGGCGCTTACAGAGTGGGGCCCTTGAGAGATTCTTGAAGCGGAGTTTG 1375
Qy 752 GAGACACACCAAGATGACGAGCTCAGAAACCCAAAGTGTGTCTACAGGACACTGT 811
Db 1376 GAGACACACCAAGATGACGAGCTCAGAAACCCAAAGTGTGTCTACAGGACACTGT 1435
Qy 812 TGACCGGAGCGGGCTGAATCTCCACTCTTCCGGAATGATGCTCAAGAACTGTCCG 871
Db 1436 TGACCGGAGCGGGCTGAATCTCCACTCTTCCGGAATGATGCTCAAGAACTGTCCG 1495
Qy 872 GAGAGCTGTTTCAACAGAACGTTAACTCAGAGCTTCAGCTCAGCCCTCAGACGAGT 931
Db 1496 GAGAGCTGTTTCAACAGAACGTTAACTCAGAGCTTCAGCTCAGCCCTCAGACGAGT 1555
Qy 932 GGTGTGGCGGGCGGGCCCGGAAGAGCGGGGAGCTCTTACTTACTTCCGACCCAA 991
Db 1556 GGTGTGGCGGGCGGGCCCGGAAGAGCGGGGAGCTCTTACTTACTTCCGACCCAA 1615
Qy 992 CTTCCTGAGACGAGTGGGCTGTGTGSCCAACAACCCAGCTGATGCCATACAGATCCA 1051
Db 1616 CTTCCTGAGACGAGTGGGCTGTGTGSCCAACAACCCAGCTGATGCCATACAGATCCA 1675
Qy 1052 TGAATCAATCAGAGACTGATCCGCAAGGGTCAAGGCCAAMAGTGAAGAACTTCAT 1111
Db 1676 TGAATCAATCAGAGACTGATCCGCAAGGGTCAAGGCCAAMAGTGAAGAACTTCAT 1735
Qy 1112 CGTGTCTCTCTGGGAGACAGAGAGTCCCAACAAGTCTGTGATCTGTGTGATCTT 1171
Db 1736 CGTGTCTCTCTGGGAGACAGAGAGTCCCAACAAGTCTGTGATCTGTGTGATCTT 1795
Qy 1172 CCGTCCAGCAACCCCTGGGAGCTGGCAAGACTGTTTGGGAGCAAGAACTGGGCAA 1231
Db 1796 CCGTCCAGCAACCCCTGGGAGCTGGCAAGACTGTTTGGGAGCAAGAACTGGGCAA 1855
Qy 1232 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272
Db 1856 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1896

RESULT 5

US-10-476-991-10
; Sequence 10, Application US/10476991
; Publication No. US20040248297A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; APPLICANT: Andrew T. Walt
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI
; FILE REFERENCE: ISPh-0781
; CURRENT APPLICATION NUMBER: US/10/476,991
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 09/851,896
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 3240

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TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: unsure
LOCATION: 2770
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: CDS
LOCATION: (137)...(2557)
US-10-476-991-10

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Query Match      68.6%; Score 876.2; DB 18; Length 3240;
Best Local Similarity 99.7%; Pred. No. 2.4e-240;
Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 392 AGAAGTACAGAGATCTCATGACATCTTCAGCGGCGCCGGAAGCCAGCGTTACTCTGGGCTC 451
DB 1483 AGAAGTACAGAGATCTCATGACATCTTCAGCGGCGCCGGAAGCCAGCGTTACTCTGGGCTC 1542
QY 452 CATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511
DB 1543 CATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1602
QY 512 AGGAGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 571
DB 1603 AGGAGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1662
QY 572 GAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 631
DB 1663 GAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1722
QY 632 GCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAG 691
DB 1723 GCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAG 1782
QY 692 CCGGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCT 751
DB 1783 CCGGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCT 1842
QY 752 GAGACACACCAAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGAC 811
DB 1843 GAGACACACCAAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGAC 1902
QY 812 TGACCGGACACCGGCTGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGAC 871
DB 1903 TGACCGGACACCGGCTGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGAC 1962
QY 872 GAGAGCTCGTTTCAACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGAC 931
DB 1963 GAGAGCTCGTTTCAACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGAC 2022
QY 932 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 991
DB 2023 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2082
QY 992 CTTTCTTGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
DB 2083 CTTTCTTGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2142
QY 1052 TGAGTACATCAGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGAC 1111
DB 2143 TGAGTACATCAGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGAC 2202
QY 1112 CGTTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1171
DB 2203 CGTTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1262
QY 1172 CCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1231
DB 2263 CCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2232
QY 1232 GATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1272

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DB 2323 GATGT 2363

RESULT 6
US-09-927-180-1
Sequence 1, Application US/09927180
Patent No. US20020106364A1

GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridge Park Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 96..2352
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-927-180-1

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Query Match      55.4%; Score 708; DB 9; Length 2935;
Best Local Similarity 87.6%; Pred. No. 3.2e-192;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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QY 389 CACAGAACTACAGAGATCTCATGACATCTTCAGCGGCGCCGGAAGCCAGCGTTACTCTGGG 448
DB 1277 CAAACAGCTTACAGAGATCTCATGACATCTTCAGCGGCGCCGGAAGCCAGCGTTACTCTGGG 1336
QY 449 CTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 508
DB 1337 CTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1396
QY 509 GAAAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 568
DB 1397 GAAAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1456
QY 569 CAAAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 628
DB 1457 CAAAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1516
QY 629 TCTGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAGTAAATGCAAG 688

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Db 1517 TCGCAGTAAGTCCATGCGCTTATATGCTGTGTACTCCGTATGAAATGAGT 1576
 Qy GTTCCGGGGCTCCAGGCGCTACGAGTGGGGCCCTGGAGAGTCTCTGAAGGGGATT 748
 Db 1577 GTTCCGGGGCTCCAGGCGCTTATGAGTGAAGCCCTGAGAGTCTCTGAAGGGGATT 1636
 Qy TGGGAGACACCAAGATGACGAGCTCAGAAAACCCAGATGATGTGACAGGAGACT 808
 Db 1637 TGGGAGACACCAAGATGACGAGTCAAAAAACCAAGATGATGTGACAGGAGACT 1696
 Qy GTTGCACCGGACCGGCTGAACTCCACCTCTTCGGAACTGAGTCTCAAGAACTGT 868
 Db 1697 GTTGCACCGGACCGGCTGAACTCCACCTCTTCGGAACTGAGTCTCAAGAGTCT 1756
 Qy CCGGAGCGCTGTTTCAACGAAACGTTAACTCAGGCGCTCAGCTCAGGCGCTCAGCA 928
 Db 1757 TCGGAAACCTGCTTCAACCAAAACATTAACTGAAACCGCCCACTCAGCTGACACA 1816
 Qy GCTGTGTGGCGGCGCGCCGAAAGCAGCGGCGCAGCTCTTACTTCCGACCCATGG 988
 Db 1817 ACTGTATGCGAGCAGCGCGGAGCAGTGGGGCAGCCCAACTCTCCGGCCCAATGG 1876
 Qy GCGCTTCTTGAAGGCTGTGGCTGTGGCAACACCCCAAGCTGATCCATGACAGAT 1048
 Db 1877 ACTGTATGCGAGTGTGGGCTGTGGCAACACCCCAACTGATCCATGACTGAAAT 1936
 Qy CCATGATACATACAGGACCTGATCCGCAAGGGTCAAGGCCAAGGTTGAAGAACTCTC 1108
 Db 1937 CCATGATACATACAGGACCTGATCCGCAAGGGTCAAGGCCAAGGTTGAAGAACTCTC 1996
 Qy CATCTGTCTCCTCTGGGAGCAGGAGGTCCCAACAGTCCCTGTGACTGTGTGATGT 1168
 Db 1997 CATAGTGTCTCTGTGGGAGCAGGAGGTCCCAACAGTCCCTGTGACTGTGTGATGT 2056
 Qy CTTCCTGCTCCAGCAACCTCTGGGAGTGTGGCAAGACTTTTGGGGCCCAAGAACTGG 1228
 Db 2057 CTTCCTGCTCCAGCAACCTCTGGGAGTGTGGCAAGACTTTTGGGGCCCAAGAACTGG 2116
 Qy 1229 CAGAGTGTGTGAGTGTGACAGGATCCAGAGCGGCGGCGG 1272
 Db 2117 CAGAGTGTGTGAGTGTGACAGGATCCAGAGTGTGTGGGCTG 2160
 RESULT 7
 US-10-476-991-3
 ; Sequence 3, Application US/10476991
 ; Publication No. US20040248297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Andrew T. Walt
 ; APPLICANT: Isis Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI
 ; FILE REFERENCE: ISPH-0781
 ; CURRENT APPLICATION NUMBER: US/10/476,991
 ; CURRENT FILING DATE: 2003-11-05
 ; PRIOR APPLICATION NUMBER: 09/851,896
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 89
 ; SEQ ID NO 3
 ; LENGTH: 70000
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-476-991-3

Query Match 37.0%; Score 472.2; DB 18; Length 70000;
 Best Local Similarity 99.4%; Pred. No. 1.6e-124;
 Matches 474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GAATTTTACGGCCAGGTGTTATTCAGCATGCTCCGATGCAAGAAAGCACTTT 60

Db 53878 GAATTTTACGGCCAGGTGTTATTCAGCATGCTCCGATGCAAGAAAGCACTTT 53937
 Qy GTCTGAAGAGACACCGAAGGATTCATGCTTGGGGTTTCAAGAGAAAGATTTAGG 120
 Db 53938 GTCTGAAGAGACACCGAAGGATTCATGCTTGGGGTTTCAAGAGAAAGATTTAGG 53997
 Qy 121 GAAACCTGGAGCTGCTGGGAGGCTGGGAGCCCTTCCAGAGCAGTGGGCCCCCTT 180
 Db 53998 GAAACCTGGAGCTGCTGGGAGGCTGGGAGCCCTTCCAGAGCAGTGGGCCCCCTT 54057
 Qy 181 TCACCTCCAGCCCATTTCTCTGTGGGCTGTGGGCTGTGGGCTTCTCTGGGACAGATC 240
 Db 54058 TCACCTCCAGCCCATTTCTCTGTGGGCTGTGGGCTGTGGGCTTCTCTGGGACAGATC 54117
 Qy 241 CTTCCTGTGGGAGGAGACAGATGACAGGAGGAGTGGGGGATGAGGGGCTGTGGG 300
 Db 54118 CTTCCTGTGGGAGGAGACAGATGACAGGAGGAGTGGGGGATGAGGGGCTGTGGG 54177
 Qy 301 CGAGGACAGCCAGGTTGATCTAGGAGCTTGTGGGTTAGCAGGCTTGGGAGCCACC 360
 Db 54178 CGAGGACAGCCAGGTTGATCTAGGAGCTTGTGGGTTAGCAGGCTTGGGAGCCACC 54237
 Qy 361 TGACCAAGATGCTGCTGTGCTGTGCTGCTGACAGAACTACAGATCTCATGCACTCAC 420
 Db 54238 TGACCAAGATGCTGCTGTGCTGTGCTGCTGACAGAACTACAGATCTCATGCACTCAC 54297
 Qy 421 GGGCCCGGAAGCCAGGCTTCATCTGGGCTCCATGAGGAGCGAAGCCGACG 477
 Db 54298 GGGCCCGGAAGCCAGGCTTCATCTGGGCTCCATGAGGAGCGAAGCCGACGTAAG 54354

RESULT 8
 US-09-918-995-35047
 ; Sequence 35047, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: FROM VARIOUS CDNA LIBRARIES
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/918,995
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 35047
 ; LENGTH: 411
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-918-995-35047

Query Match 21.0%; Score 268; DB 10; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1.9e-66;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 392 AGAAGTACAGGATCTCATGACATCTCAGGCGCCCGAAGCCAGCTTCACTCTGGGCTC 451
 Db 144 AGAAGTACAGGATCTCATGACATCTCAGGCGCCCGAAGCCAGCTTCACTCTGGGCTC 203
 Qy 452 CATGAGGAGCAGAAAGCGGACCAAGCAACCACTGCTGTGCTCTGATGAGAGAGATGAA 511
 Db 204 CATGAGGAGCAGAAAGCGGACCAAGCAACCACTGCTGTGCTGATGAGAGAGATGAA 263
 Qy 512 AGGCTCATCATCATCAGTCTCTCATGCGCATGCAAGAGGCTCGGGGTGTGGCCAA 571
 Db 264 AGGCTCATCATCATCAGTCTCTCATGCGCATGCAAGAGGCTCGGGGTGTGGCCAA 323
 Qy 572 GGAAGCTTTTGAAGTGGGTGGCGGACACAGCACTGAGAGGATCTGCGCTTGGCACTTCT 631
 Db 324 GGAAGCTTTTGAAGTGGGTGGCGGACACAGCACTGAGAGGATCTGCGCTTGGCACTTCT 383
 Qy 632 GCAAGTAAAGTCAAGGCTTCAATGCGC 659

DB 384 GCACAGTACTGATGCTTCGCCGACCAACCCCTGGAGCTGGCCAAAGACTGTTT 411

RESULT 9

US-09-908-975-9474
; Sequence 9474, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: PAIGER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9474
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-9474

Query Match 4.7%; Score 60; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1153 TGACCTGTGTGATGCTTCCTCCGACCAACCCCTGGAGCTGGCCAAAGACTGTTT 1212
DB 1 TGACCTGTGTGATGCTTCCTCCGACCAACCCCTGGAGCTGGCCAAAGACTGTTT 60

RESULT 10

US-09-908-975-31864
; Sequence 31864, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: PAIGER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31864
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-31864

Query Match 4.7%; Score 60; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 TGTGACCTGTGTGATGCTTCCTCCGACCAACCCCTGGAGCTGGCCAAAGACTGTTT 1210
DB 1 TGTGACCTGTGTGATGCTTCCTCCGACCAACCCCTGGAGCTGGCCAAAGACTGTTT 60

DB 1 TGTGACCTGTGTGATGCTTCCTCCGACCAACCCCTGGAGCTGGCCAAAGACTGTTT 60

RESULT 11

US-09-938-842A-1043
; Sequence 1043, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1043
; LENGTH: 3798
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1043

Query Match 3.9%; Score 50; DB 9; Length 3798;
Best Local Similarity 58.9%; Pred. No. 0.00066;
Matches 86; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 484 TGCTGTGCTGTGATGAGGAGGAGTGAAGGCTCATCATTCAGCTTCATGCCA 543
DB 1364 TACTCAGCATGATGAGGAGGAGATGAAGGCTTCGCAACGGTGCAGATTTAAAGAGA 1423

QY 544 TCGAAGAGCTTCGGGTGGCCACCAAGGACTGTTTACTGGGTGGCGGACCA 603
DB 1424 TTGAGAGGAGAGTGGCAAGCCTATTCATGACTATTCACCTATATGTGGACATCAA 1483

QY 604 CTGGAGGATCTCGGCTGGCCATT 629
DB 1484 CAGGAGGAATGCTAGCTATTGCCCTT 1509

RESULT 12

US-09-938-842A-1043
; Sequence 1043, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1043
; LENGTH: 3798
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1043

```

Query Match      3.9%; Score 50; DB 11; Length 3798;
Best Local Similarity 58.9%; Pred. No. 0.00066;
Matches 86; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY      484 TGCTGTGCTTGATGTGAGAGAGATGAAGAGCCTCATCATCATCCAGCTCTCATATGCCA 543
DB      1364 TACTCACCATGATGTAGAGAGAGATGAAGATGAAGTCTTGCAACGGGTGAGATTCTTAAGAGAA 1423

QY      544 TCGAAGAGGCTCGGGGTGTGTGGCCACCAAGAACTGTTTGACTGTGGGTGGGGGCAACAGA 603
DB      1424 TTGGAAGGGAGAGGTGGAGAACCTTATTCATGTAACCTATTGCACTTATATGTGGCAATCAA 1483

QY      604 CTGAGAGCATCTCTGCGCCCTGGCCATT 629
DB      1484 CAGAGGAATGCTAGCTATTGCCCCCTT 1509

RESULT 13
US-10-369-493-42988
; Sequence 42988, Application US/10369493
; Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 42988
LENGTH: 1065
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-10-369-493-42988

Query Match      3.8%; Score 48.8; DB 15; Length 1065;
Best Local Similarity 55.2%; Pred. No. 0.0012;
Matches 95; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY      374 CCCTGCTCTGTGCTCACAAGACTCAAGATCTCATGACATCTCAACGGGCCCGGAAGCC 433
DB      663 CCGGATCTGTCCCCGAGGCAGTGACGAGGTGTGATGTGCGCGGAGCCAGAAAGCT 722

QY      434 AGCGTTTCATCTGGGCTCTCATGTAGGGACGAGAGCGAGAACCCAGCAACCACTCTGTGCT 493
DB      723 CGCGGCGCTCATGTGCCACCAACACACCGGTGGGCGCCCTTGAGCATTCCTCTGGCGAA 782

QY      494 GGATGAGAGAGAGATGAAGAGCCTCATCATCATTCACGCTCTCATGCCATC 545
DB      783 GGAAGCGGCGGCGCTGTCCGGCGCGCCGCTCCGCGAGCCCGCAAGCGCGCT 834

RESULT 14
US-10-411-910A-276
; Sequence 276, Application US/10411910A
; Publication No. US20040209256A1
GENERAL INFORMATION:
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
FILE REFERENCE: H2041203-P
CURRENT APPLICATION NUMBER: US/10/411,910A
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn version 3.2
SEQ ID NO 276
LENGTH: 1515

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/ TYPE: DNA
/ ORGANISM: Entamoeba histolytica
US-10-411-910A-276

Query Match      3.8%; Score 48.4; DB 18; Length 1515;
Best Local Similarity 46.2%; Pred. No. 0.0016;
Matches 160; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

OY TCATGCAATCTCAACGGGCGCCGGAAGCCAGCCTGTCATCTCTGGGCTTCATGAGGACGAGA 465
   |||||
DB  TCATCGGCCCCCTTCAACGCCAGCCGTGGGAACCTTGAAGACAGCACACCGACTACT 1078
   |||||

OY AGCGGACCCACGACCACTGTGTGCTTGGATGAGAGAGAGTAAGGCTCATATCA 525
   |||||
DB  GCGTGACCTTCGACGAGATCTTGGGCTTGTGAGGGCGAGCGCATCACTGACCAAG 1138
   |||||

OY TTCAGCTCCCTATCGGCATCGAAGAGCCCTGGGTGTGGCCACCAAGACCTGTTGACT 585
   |||||
DB  TGACGCCCTTACACTTCTGTGTGAAGAGCCCAAGAGAGGCGAAGATCTTGGCCGTGACG 1198
   |||||

OY GGGTGGCGGACCAACGACCTGAGGACATCTGACCCTTGCCATTTCTGCAAGTAAGTCA 645
   |||||
DB  GCGGCGGTGGCCAGCGCGCGGTGGCCAGCCTGCTGCCCAAGAGAGGTGCGCGCGGTGATCA 1258
   |||||

OY TGGCTTACATGCGCGGCAATGTAATTTTGCATGAAGATGAGTGTTCGGGGCTTCAGGC 705
   |||||
DB  AGCCCAACATCATGACGGCTTACGCAAGAACTTCAAGGCGCTGAAGAACTTCAAGA 1318
   |||||

OY CTTACGAGTGGGGGCCCTTGAGAGATTCTGAAGCGGAGATTGG 751
   |||||
DB  AGAACATACCGGCAACTGTGTGAGGTGATGTGTGCGAGGGCGG 1364
   |||||

RESULT 15
US-10-369-493-32157
/ Sequence 32157, Application US//10369493
/ Publication No. US20030233675A1
GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ PRIOR FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 32157
/ LENGTH: 1009
/ TYPE: DNA
/ ORGANISM: Ralstonia metallidurans
US-10-369-493-32157

Query Match      3.6%; Score 46.6; DB 15; Length 1009;
Best Local Similarity 46.5%; Pred. No. 0.005;
Matches 151; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

OY TCATCATCCAGCTCTCATATCGGCATGAGAGGCTCGGGTGTGCGCAACCAAGACTGT 579
   |||||
DB  TCAGTTTCGTCTACTCTCGCAGAGAAAGGGGCGCCCGGTGCGCATCAAGGAATACC 121
   |||||

OY TTGACTGGGTGGCGGGGACCAAGCACTGAGAGCATCTGTGCCCTTGCCAAATTCTGCAAGTA 639
   |||||
DB  TGGCGGTGTCACTGAGCCCGCGCAGTCCCGGAGACTGATCCGGGTCTTCGAGCGAGA 181
   |||||

OY AGTGCATGGCTTACATGCGGCGCATGTACTTTGCGATGAAGATAGGTGTTCGGGGCT 699
   |||||
DB  ACGTGGCCTCATTTTCGCTCGGCTGTAAATATTTCTTGAAGGAAGACGCTGCTGGCCC 241
   |||||

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QY      700  CCAGGCCCTACGAGTCGGGGCCCTGAGAGATTCTGAAGCGGAGATTGGGAGCACA 759
Db      242  GTATTTCGCACCCCAGCGTGTCCGCGTGTGAATTTCTTCCCGAGAAATTCACGCTCT 301
QY      760  CCAAGATGACGAGCGTCAAGGAAACCAAGGTGATGCTGACAGGAGACATGTCTGACCGGC 819
Db      302  ACATGGTCATGAACTAGAGCTGGGCAAGACGCTGCGAGAGCATATCTCTGACAGGCCCGGC 361
QY      820  AGCCGGCTGAACCTCCACCTTCTCCG 844
Db      362  AGCAGGGCAAGGCCAAAGTCTCTCCG 386

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Search completed: December 16, 2004, 15:22:16
 Job time : 739 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:55 / Search time 13.1857 Seconds
(Without alignments)
2130.736 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLMHISRRARXKPAFLIGSM.....GAKELGKVVDCCTDPDGR 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 1524 | 99.5 | 851 | 2 | T12503 |
| 2 | 456.5 | 29.8 | 1071 | 2 | T22327 |
| 3 | 419 | 27.4 | 1023 | 2 | T26261 |
| 4 | 261 | 17.0 | 468 | 2 | T33857 |
| 5 | 255 | 16.7 | 1265 | 2 | T02131 |
| 6 | 253.5 | 16.6 | 456 | 2 | T24442 |
| 7 | 235.5 | 15.4 | 355 | 2 | E82354 |
| 8 | 213.5 | 13.9 | 679 | 2 | G71615 |
| 9 | 211.5 | 13.8 | 782 | 2 | UC7284 |
| 10 | 201 | 13.1 | 382 | 2 | T48109 |
| 11 | 198 | 12.9 | 390 | 2 | AG2093 |
| 12 | 182 | 11.9 | 414 | 2 | G85437 |
| 13 | 179 | 11.7 | 428 | 2 | F85437 |
| 14 | 176 | 11.5 | 410 | 2 | T52234 |
| 15 | 176 | 11.5 | 414 | 2 | H85437 |
| 16 | 174.5 | 11.4 | 390 | 2 | T03841 |
| 17 | 164 | 10.7 | 499 | 2 | T02580 |
| 18 | 163 | 10.6 | 405 | 2 | T10260 |
| 19 | 161 | 10.5 | 407 | 2 | T00989 |
| 20 | 158.5 | 10.4 | 388 | 2 | T10770 |
| 21 | 158.5 | 10.4 | 490 | 2 | B97815 |
| 22 | 151.5 | 9.9 | 388 | 2 | T10765 |
| 23 | 151.5 | 9.9 | 388 | 2 | T10763 |
| 24 | 150.5 | 9.8 | 494 | 2 | T16655 |
| 25 | 147 | 9.6 | 526 | 2 | T08541 |
| 26 | 146 | 9.5 | 386 | 2 | T07532 |
| 27 | 140 | 9.1 | 386 | 2 | A29810 |
| 28 | 139 | 9.1 | 386 | 2 | A26017 |
| 29 | 138 | 9.0 | 377 | 2 | S05593 |

| | | | | | | |
|----|-------|-----|-----|---|--------|--------------------|
| 30 | 138 | 9.0 | 386 | 2 | S51596 | patatin precursor, |
| 31 | 137 | 8.9 | 320 | 2 | F70034 | conserved hypothe |
| 32 | 137 | 8.9 | 384 | 2 | A24142 | patatin precursor |
| 33 | 134 | 8.8 | 386 | 2 | S05592 | patatin precursor |
| 34 | 134 | 8.8 | 386 | 2 | B26017 | patatin T58 precu |
| 35 | 129.5 | 8.5 | 488 | 2 | T06725 | hypotheical prote |
| 36 | 124 | 8.1 | 318 | 2 | S24923 | TEG protein - Bac |
| 37 | 116 | 7.6 | 324 | 2 | D70943 | hypotheical prote |
| 38 | 112 | 7.3 | 473 | 2 | T28118 | hypotheical prote |
| 39 | 108 | 7.1 | 329 | 2 | A87087 | conserved hypothe |
| 40 | 103 | 6.7 | 610 | 2 | B87518 | conserved hypothe |
| 41 | 96.5 | 6.3 | 296 | 2 | E84000 | hypotheical prote |
| 42 | 95 | 6.2 | 598 | 2 | E71657 | hypotheical prote |
| 43 | 94 | 6.1 | 314 | 2 | AF3365 | serine proteinase |
| 44 | 91 | 5.9 | 260 | 2 | H69874 | conserved hypothe |
| 45 | 90.5 | 5.9 | 254 | 2 | G72343 | conserved hypothe |

ALIGNMENTS

RESULT 1

T12503

hypotheical protein DKFZp434A102.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C/Accession: T12503

R/Annotate, W. J. Kirkner, U. J. Mewes, H. W. J. Gaasenhuber, J. J. Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A/Reference number: Z17527

A/Accession: T12503

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-851 <ANS>

A/Cross-references: EMBL:AL080187

A/Experimental source: adult testis; clone DKFZp434A102

C/Genetics:

A/Note: DKFZp434A102.1

Query Match 99.5%; Score 1524; DB 2; Length 851;

Best Local Similarity 100.0%; Pred. No. 7.8e-130;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | | |
|----|-----|--|--|-----|--|
| QY | 1 | LQDLMHISRRARXKPAFLIGSM.....GAKELGKVVDCCTDPDGR 291 | | 1 | LQDLMHISRRARXKPAFLIGSM.....GAKELGKVVDCCTDPDGR 291 |
| DB | 496 | LQDLMHISRRARXKPAFLIGSM.....GAKELGKVVDCCTDPDGR 291 | | 496 | LQDLMHISRRARXKPAFLIGSM.....GAKELGKVVDCCTDPDGR 291 |
| QY | 61 | LFDWVAGTSTGILALALILHSKSMAYWQYFPMKDEVFPRGSRPYSGPLEBFLKGEFGE 120 | | 61 | LFDWVAGTSTGILALALILHSKSMAYWQYFPMKDEVFPRGSRPYSGPLEBFLKGEFGE 120 |
| DB | 556 | LFDWVAGTSTGILALALILHSKSMAYWQYFPMKDEVFPRGSRPYSGPLEBFLKGEFGE 615 | | 556 | LFDWVAGTSTGILALALILHSKSMAYWQYFPMKDEVFPRGSRPYSGPLEBFLKGEFGE 615 |
| QY | 121 | HTKQTDVRRKRWMLTGLTSRQPAELHLPFNRYAPETVPRPNQVNLPRPQSPQOLV 180 | | 121 | HTKQTDVRRKRWMLTGLTSRQPAELHLPFNRYAPETVPRPNQVNLPRPQSPQOLV 180 |
| DB | 616 | HTKQTDVRRKRWMLTGLTSRQPAELHLPFNRYAPETVPRPNQVNLPRPQSPQOLV 675 | | 616 | HTKQTDVRRKRWMLTGLTSRQPAELHLPFNRYAPETVPRPNQVNLPRPQSPQOLV 675 |
| QY | 181 | WRARSSGAAPYFRPFGRLDGLLANNPTLDMTEIHEYNODLIRKQGANVKKLSIV 240 | | 181 | WRARSSGAAPYFRPFGRLDGLLANNPTLDMTEIHEYNODLIRKQGANVKKLSIV 240 |
| DB | 676 | WRARSSGAAPYFRPFGRLDGLLANNPTLDMTEIHEYNODLIRKQGANVKKLSIV 735 | | 676 | WRARSSGAAPYFRPFGRLDGLLANNPTLDMTEIHEYNODLIRKQGANVKKLSIV 735 |
| QY | 241 | VSLGTGSPQVPVTCVDFPRSPNFWELAKTVFGAKELGKVVDCCTDPDGR 291 | | 241 | VSLGTGSPQVPVTCVDFPRSPNFWELAKTVFGAKELGKVVDCCTDPDGR 291 |
| DB | 736 | VSLGTGSPQVPVTCVDFPRSPNFWELAKTVFGAKELGKVVDCCTDPDGR 786 | | 736 | VSLGTGSPQVPVTCVDFPRSPNFWELAKTVFGAKELGKVVDCCTDPDGR 786 |

RESULT 2

T22327

hypotheical protein F47A4.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T22327

R/Kortimort, B.

submitted to the EMBL Data Library, June 1995

A/Reference number: Z19549

A:Accession: T22237
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1071 <MIL>
 A:Cross-references: UNIPROT:Q20500; EMBL:Z49888; PIDN:CAA90061.1; GSPDB:GN00028; CESP:F4
 A:Experimental source: clone F47A4
 C:Genetics:
 A:Gene: CESP:F47A4.5
 A:Map position: X
 A:Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 29.8%; Score 456.5; DB 2; Length 1071;
 Best Local Similarity 34.8%; Pred. No. 7.4e-33;
 Matches 102; Conservative 62; Mismatches 97; Indels 35; Gaps 8;

Qy 1 LODMHSRKARAFILGSRDEKRTDHLCLDGGVKGIIITQLIAIEKSGVATKD 60
 Db 730 IQDTLDGSRGKAKV-----NLISMDGGIRGLVITQLIAIEKLGDDIFK 777
 Qy 61 LFDVAGTSTGCLLALALHKSMAVNRGMYFRMKDVEFRG-SRPYSGLEELKKEFG 119
 Db 778 YFDMAGTSTGSLMGLATGKSLREMQYTLKORVFGIMPEYDTVGLKFTQDQFG 837
 Qy 120 EHTKMTDVRKPKWLTSTLSDROPALHLFRNYDAETVAREPRNQVNLPPAQPSDQL 179
 Db 838 TGT-VWEIPIPRMISAVNSEKLPVRLEMARNYKPAQV-----AETPREMP 884
 Qy 180 VMAARSSGAPTYFRPN-GRFLDGLANPTLDAMTEIHEYNQDLIRKQANKVKLS 238
 Db 885 LMAALRSTAAIPVLFKSEBRITDGGIISNNPALDMSVHAHYRELQLSGRSADVQNM 944
 Qy 239 IVVSLGTGRSPQVPTCVDFR--PSNPWEIAKTVFGAKELGKVVDDCTPDGRP 292
 Db 945 VLVSFGTG--QIPSTVIERLSTIDSNSPLQSIKTI--KULAMFIDQATASEGAP 994

RESULT 3

T26261
 hypothetical protein W07A8.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T26261; T26892

R:hasham, V.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z20184
 A:Accession: T26261
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1023 <MIL>
 A:Cross-references: UNIPROT:O62398; EMBL:Z82075; PIDN:CA804932.1; GSPDB:GN00023; CESP:W0
 A:Experimental source: clone W07A8
 R:hasham, V.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z20281
 A:Accession: T26892
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1023 <MIL>
 A:Cross-references: EMBL:AL021489; PIDN:CAAL6371.1; GSPDB:GN00023; CESP:W07A8.2
 A:Experimental source: clone Y44AC
 C:Genetics:
 A:Gene: CESP:W07A8.2
 A:Map position: 5
 A:Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/1; 331/2; 411/1; 479/3; 534/3; 571/2; 70

Query Match 27.4%; Score 419; DB 2; Length 1023;
 Best Local Similarity 33.9%; Pred. No. 1.8e-29;
 Matches 95; Conservative 61; Mismatches 110; Indels 14; Gaps 7;

Qy 17 LGSMDKERTHD--HLCLDGGVKGIIITQLIAIEKSGVATKDLFPVWAGTSGIL 74
 Db 678 LKELVEKKSINVINVLGDDGGIRGLVTVQMLICLAFDRLPIDVFDWIGATISGCIY 737

Qy 75 ALALHSKMAVNRGMYFRMKDVEFRG-SRPYSGLEELKKEFEHTKMTDVRKPKV 133
 Db 738 MSTMTGSLRKQRYYLWFKDQLFDSMTRPYDTKTLFTIQRFAFDRLMGDIKYPREF 797
 Qy 134 LTGTLSDROPALHLFRNYDAETVAREPRNQVNLPPAQPSDQLVMAARSSGAPTY 193
 Db 798 CTTVRADTFPPVQLELRNRLPISEKE--NNDLGF--TDPELTIWKATRRESSAPTY 851
 Qy 194 FRPN-GRFLDGLANPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQV 252
 Db 852 FSASBEKFTDGMISNNPVLDMSDIGFNTTCQKRIREKRVDMGCVLSVGTGIRPICP 911
 Qy 253 VTCVDVFRPNPWEIAKTVFGAKELGKVVDDCTPDGRP 292
 Db 912 VD-PSVFEMNDLFGMLR---GMKSLVAVDQATATEGAP 947

RESULT 4

T33857
 hypothetical protein D1037.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33857

R:Jedwith, J.; Biewald, T.
 submitted to the EMBL Data Library, November 1998
 A:Description: The sequence of C. elegans cosmid D1037.
 A:Reference number: Z21424
 A:Accession: T33857
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-468 <LED>
 A:Cross-references: EMBL:AF106592; PIDN:AC78490.1; GSPDB:GN00019; CESP:D1037.5
 A:Experimental source: strain Bristol N2; clone D1037
 C:Genetics:
 A:Gene: CESP:D1037.5
 A:Map position: 1
 A:Introns: 66/3; 89/3; 113/3; 151/2; 247/1; 354/2

Query Match 17.0%; Score 261; DB 2; Length 468;
 Best Local Similarity 29.8%; Pred. No. 1.3e-15;
 Matches 78; Conservative 54; Mismatches 100; Indels 30; Gaps 10;

Qy 16 ILGSMDEKRTHDH-LLCLDGGVKGIIITQLIAIEKSGVATKDLFPVWAGTSGIL 74
 Db 180 VLASEKQWKPBERVLLADGGIRAVITQMLIHIDYLLGKLVKLDIADTSGGVI 239
 Qy 75 ALAI-LHSKMAVNRGMYFRMKDVEFRG-SRPYSGLEELKKEFEHTKMTDVR 127
 Db 240 TLLSTNNRNIETRKLLDMRVRIRGADKAVPKYSNGMEYIARHYTTWEDSKMSI 299
 Qy 128 RKEKWLGTSLSDROPALHLFRNY--DAETVAREPRNQVNLPPAQPSDQLVWRAA 184
 Db 300 KRRRAIVTVADTMVPPQLLFRSYRPEMDEACEHYKF-----LDPTVVELMKTL 350
 Qy 185 RSSGAAPTYFRPNPWEIAKTVFGAKELGKVVDDCTPDGRP 292
 Db 351 RCTTAAPYFESEFNGSLDGLANPTLDAMTEIHEYNQDLIRKQANKVK-----K 236
 Qy 237 LSVSLGTGRSPQVPTCVDF 258
 Db 409 IGCVISLGTGVFTEKIDGIDL 430

RESULT 5

T02131
 hypothetical protein F8K4.6 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T02131

R:Vysotskaya, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Becker, J.R.; Federspiel, N.
 submitted to the EMBL Data Library, August 1998
 A:Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.

| | | | | | | | | | |
|---------|-----|--|-----|------------|-----|--------|-----|------|----|
| Matches | 86; | Conservative | 41; | Mismatches | 76; | Indels | 63; | Gaps | 14 |
| QY | 5 | MHISRAKPAFLGSMRDEKRTDHLCLDGGVKGII-IIQLLAIEKASGVAT-XDLF | 62 | | | | | | |

RESULT 8
G71615
phospholipase A2-like a/b fold hydrolase PF00410C - malaria parasite (Plasmodium falciparum)

C:Species: *Plasmodium falciparum*
C:Date: 13-Nov-1998 #sequence_rev: 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: G71615

A:Cross-references: UNIPROT:O8YUN7; GB:BA000019; PIDN:BA874001.1; PID:G17L31394; GSPDB:C
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: at12302
C:Superfamily: patatin

Query Match 12.9%; Score 198; DB 2; Length 390;
Best Local Similarity 24.3%; Pred. No. 5.1e-10;

Matches 68; Conservative 40; Mismatches 78; Indels 94; Gaps 10;

QY 30 LCLDGGGVKGLIIQLIAIEK---ASGVATKDLFDWVAGTSGILALAILHSKMA 85
DB 5 ILSDGGGIRGIVTARILQGEVERQIQQQQKSLHEVYDLAIGTSGILPAGIAAKNNS 64
QY 86 YNKGATFRMKDEVFRGSRP---YESGP-----LEEF-----LKREGEHTKM 124
DB 65 ELVOLQOEQKQIFPIERKERYKKIPSFLOPLIEAFSLPKYSHQGLINVLKYNLGD-TRI 123
QY 125 TDVKKPKVMTG-----TSDROPALHLFRNYDAPEVREPRFNQNVN 168
DB 124 KDVESPIMLIAYDTLYRNTTPTFNCHPDGDRMYDDCHL----- 163
QY 169 LRPPAPSDQLVWRARSSGAAPTYFRP-----NGRP--LDGGLANPTLDA 214
DB 164 -----WEICTAATAPFPFPYKLEPVNKEKYNWVFPHIDGVAAANNPALAA 211
QY 215 MTEIHYNQDLIRKQANKYKLSI-----VSLGTRGS 248
DB 212 LSLVRLSSSVSSAIKQKYNLDGINDIADIAIISIGGT 251

RESULT 12

patatin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85437
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <STO>
A:Cross-references: UNIPROT:O23180; GB:NC_001268; NID:G7270655; PIDN:CA80372.1; GSPDB:C
C:Genetics:
A:Gene: AT4G37060
A:Map position: 4
C:Superfamily: patatin

Query Match 11.9%; Score 182; DB 2; Length 414;
Best Local Similarity 27.3%; Pred. No. 1.6e-08;

Matches 73; Conservative 34; Mismatches 84; Indels 76; Gaps 13;

QY 30 LCLDGGGVKGLIIQLIAIEK---ASGVATKDLFDWVAGTSGILALAILHSK 83
DB 21 ILSDGGGIRGIVTARILQGEVERQIQQQQKSLHEVYDLAIGTSGILPAGIAAKNNS 80
QY 84 MAYMR-----GMVFRMKDEVFRGSRPYESGPLE-----EFLKREGE 120
DB 81 NGRPRPAKRIIVFPYLEHCKRIF---PQRTGVALLPKPKLSGPKSGNYRTLLGK 136
QY 121 --HTTKTVDRKPKVMTGLTSLDROPAELHLFRNYDAPEVREPRFNQNVNLRPPAPSD 177
DB 137 ILGETKLRQTLTNVNIPTFPIKLPF---IFSSYQA---LTDPSLDVKY-----SD 182
QY 178 QLVWRARSSGAAPTYFRP-----NGRFDGGLANPTLDMT-----RIHE 220
DB 183 ICI-----GISAATYPPPYFNSNDSQKTRHFNILVDGVANPTLVAMTAVTAKIYN 237
QY 221 YNODLIRKQANKY-KKLSIVSLGTTG 246

DB 238 NNPDW---GTINLPLAGYDQFLVISIGTG 261

RESULT 13

patatin-like protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: F85437

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: F85437

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-428 <STO>

A:Cross-references: UNIPROT:O23181; GB:NC_001268; NID:G7270654; PIDN:CA80371.1; GSPDB:G

C:Genetics:

A:Gene: AT4G37050

A:Map position: 4

C:Superfamily: patatin

Query Match 11.7%; Score 179; DB 2; Length 428;
Best Local Similarity 26.5%; Pred. No. 3.1e-08;
Matches 72; Conservative 41; Mismatches 81; Indels 78; Gaps 14;

QY 30 LCLDGGGVKGL---IIQLIAIEKASGVATK--DLFDWVAGTSGG-ILALAILHSK 82
DB 37 ILSDGGGIRGIIIPGTLAVLESQLOLDEBEARLVDPVIGTSGILVAMLTAAOQ 96
QY 83 SMAYMRG-----MYFRMKDEVFRGSR-----PYSSGPLEEF 113
DB 97 SGGSHSNRPLFEAKIYPIYKHSPKIFPQPRGIFCGKGETIYNLVGPKRNGKYLHD 156
QY 114 LKKEFEHTKMTDVRKPKYMLTGLSDROPALHLFRNYDAPEVREPRFNQNVNLRPPA 173
DB 157 LVGFGIDGKTLNGLNINVIIPCDIKKLPV---IFSSYQAVN-----NQAMN-----A 202
QY 174 QPSDQLVWRARSSGAAPTYFRPNRPF-----LDGGLANPTLDANTEH 219
DB 203 KLSIDICI-----STSAAPTFP--PAHRFTMEDSRGIRHFNILIDGIAANNPTLCAIAEV- 255
QY 220 EYNQDLIRKQGA-NKVKLS-----IYVSLGTTG 246
DB 256 --TKQIIKKNPVWGDSPIDFTFRFLVISIGTG 285

RESULT 14

patatin-like protein [imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C:Accession: T52294

R:Terryn, N.; Heijnen, L.; De Keyser, A.; Van Asseldonck, M.; De Clercq, R.; Verbaekel, H

Weller, C.; Meyer, K.; Dehais, P.; Rombaut, S.; Van Montagu, M.; Rouse, P.

FEBS Lett. 445, 237-245, 1999

A>Title: Evidence for an ancient chromosomal duplication in Arabidopsis thaliana by seq

A:Reference number: Z26022; MUID:99192287; PMID:10094464

A:Accession: T52294

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-410 <TR>

A:Cross-references: UNIPROT:O23148; EMBL:AJ002596; PIDN:CA05628.1

C:Genetics:

A:Map position: 4

C:Superfamily: patatin

Query Match 11.5%; Score 176; DB 2; Length 410;
Best Local Similarity 26.6%; Pred. No. 5.4e-08;
Matches 74; Conservative 36; Mismatches 70; Indels 98; Gaps 15;

QY 30 LCLDGGGVKGLIIQLIAIEK-----ASGVATKDLFDWVAGTSGILALAILHSK 83

```
Db      17 ILSDGGGVAGIAGVLAFLFKQLQELDGEARLADYFDVIAGTGTGGLVTAMLTVPDE 76
QY      84 MAYMRGMYFRMKDEVFRGSRPYE-----SGP-----LEE 112
Db      77 TG---RPHFAKDIY-----PFYLEHCPKIFPOPTGVALLPKLPSGPKYSGKYL RN 128
QY      113 FLKRERGE---HTKMTDVRRPKYMLTGLTSDRQPAELHLFRNYDAPETVREPRFNQVNL 169
Db      129 LLSKLTGETRLHQTLTNI-----VLPFDIKKLOPT---IFSSY---QLVDPSLDVKV-- 176
QY      170 RPPAQPSSDQLVMPRAASSGAPTYFRPN-----GRFLDGLLANNPTLDAMT 216
Db      177 -----SDICI-----GTSAPPTFFPPHYFSNEDSQGNKTEFNLVDGAVTANNPTLVAMT 225
QY      217 ---EIHEVYNQDLIRKQANKVKKS---IVVSLGTG 246
Db      226 AVSKQIVKNNPDM-----GKLKPLGPRFLVISIGTG 257
```

RESULT 15

```
H85437
patatin-like protein (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: H85437
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A/Reference number: A85001; MUID:20083486; PMID:10617198
A/Accession: H85437
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-414 <STO>
A/Cross-references: UNIPROT:O23179; GB:NC_001268; NID:g7270656; PIDN:CA80373.1; GSPDB:G
C/Genetics:
A/Gene: AT4g37070
A/Map position: 4
C/Superfamily: patatin
```

```
Query Match      11.54; Score 176; DB 2; Length 414;
Best Local Similarity 26.64; Pred. No. 5.5e-08;
Matches 74; Conservative 36; Mismatches 70; Indels 98; Gaps 15;

QY      30 ILCLDGGGVAGIAGVLAFLFKQLQELDGEARLADYFDVIAGTGTGGLVTAMLTVPDE 83
Db      21 ILSDGGGVAGIAGVLAFLFKQLQELDGEARLADYFDVIAGTGTGGLVTAMLTVPDE 80
QY      84 MAYMRGMYFRMKDEVFRGSRPYE-----SGP-----LEE 112
Db      81 TG---RPHFAKDIY-----PFYLEHCPKIFPOPTGVALLPKLPSGPKYSGKYL RN 132
QY      113 FLKRERGE---HTKMTDVRRPKYMLTGLTSDRQPAELHLFRNYDAPETVREPRFNQVNL 169
Db      133 LLSKLTGETRLHQTLTNI-----VLPFDIKKLOPT---IFSSY---QLVDPSLDVKV-- 180
QY      170 RPPAQPSSDQLVMPRAASSGAPTYFRPN-----GRFLDGLLANNPTLDAMT 216
Db      181 -----SDICI-----GTSAPPTFFPPHYFSNEDSQGNKTEFNLVDGAVTANNPTLVAMT 229
QY      217 ---EIHEVYNQDLIRKQANKVKKS---IVVSLGTG 246
Db      230 AVSKQIVKNNPDM-----GKLKPLGPRFLVISIGTG 261
```

Search completed: December 15, 2004, 13:14:17
Job time : 15.1857 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:25 ; Search time 63.5892 Seconds
(without alignments)
2642.105 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LODMHSRKRKPAFLISM.....GAKELKRVVDCCTDPDGR 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 57537466 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1524 | 99.5 | 806 | 1 | PA26 HUMAN |
| 2 | 1524 | 99.5 | 806 | 1 | CAG30429 |
| 3 | 1463 | 95.6 | 752 | 1 | PA26 MOUSE |
| 4 | 1463 | 95.6 | 752 | 2 | Q7TPX2 |
| 5 | 1463 | 95.6 | 807 | 2 | Q9JKE1 |
| 6 | 1463 | 95.6 | 807 | 2 | AAH57209 |
| 7 | 1454 | 95.0 | 751 | 1 | PA26 RAT |
| 8 | 1042 | 68.1 | 756 | 2 | Q6DDX0 |
| 9 | 966.5 | 63.1 | 818 | 2 | Q6NMV0 |
| 10 | 966.5 | 63.1 | 818 | 2 | AAH67375 |
| 11 | 736 | 48.1 | 877 | 2 | Q9VTE0 |
| 12 | 736 | 48.1 | 877 | 2 | AAFS0194 |
| 13 | 736 | 48.1 | 887 | 2 | Q7KUD4 |
| 14 | 736 | 48.1 | 887 | 2 | Q7KUD4 |
| 15 | 736 | 48.1 | 887 | 2 | AAH11936 |
| 16 | 720 | 47.0 | 879 | 2 | Q7QZ01 |
| 17 | 456.5 | 29.8 | 1071 | 2 | Q20500 |
| 18 | 419 | 27.4 | 1021 | 2 | Q81006 |
| 19 | 419 | 27.4 | 1021 | 2 | Q62398 |
| 20 | 376 | 24.6 | 762 | 2 | Q95YD2 |
| 21 | 287 | 18.7 | 501 | 2 | Q9NSU3 |
| 22 | 270.5 | 17.7 | 546 | 2 | Q9TYSO |
| 23 | 266 | 17.4 | 546 | 2 | Q8MKR3 |
| 24 | 260 | 17.0 | 433 | 2 | Q7O1S8 |
| 25 | 255 | 16.7 | 1265 | 2 | Q80693 |
| 26 | 253.5 | 16.6 | 456 | 2 | Q22152 |
| 27 | 235.5 | 15.4 | 355 | 2 | Q9KVG8 |
| 28 | 222 | 14.5 | 361 | 2 | Q6XGD7 |
| 29 | 222 | 14.5 | 361 | 2 | AAH70299 |
| 30 | 213.5 | 13.9 | 679 | 2 | Q96176 |
| 31 | 211.5 | 13.8 | 380 | 2 | Q95035 |

ALIGNMENTS

| | | | | | | |
|----|-------|------|------|---|----------|---------------------|
| 32 | 211.5 | 13.8 | 639 | 2 | Q9H7T5 | Q9H7E5 homo sapien |
| 33 | 211.5 | 13.8 | 782 | 2 | Q9NP80 | Q9NP80 homo sapien |
| 34 | 210.5 | 13.7 | 776 | 2 | Q8K1N1 | Q8K1N1 mus musculus |
| 35 | 210.5 | 13.7 | 803 | 2 | Q9DC20 | Q9DC20 mus musculus |
| 36 | 204.5 | 13.4 | 577 | 2 | Q9KSM3 | Q9KSM3 anabaena ci |
| 37 | 202.5 | 13.2 | 346 | 2 | Q6JBI3 | Q6JBI3 dictyocaulu |
| 38 | 202.5 | 13.2 | 346 | 2 | AAT06310 | AAT06310 dictyocau |
| 39 | 202 | 13.2 | 253 | 2 | Q6JBI2 | Q6JBI2 dictyocaulu |
| 40 | 202 | 13.2 | 253 | 2 | AAT06311 | AAT06311 dictyocau |
| 41 | 201 | 13.1 | 382 | 2 | Q9M1W9 | Q9M1W9 arabidopsis |
| 42 | 201 | 13.1 | 382 | 2 | Q93ZQ3 | Q93ZQ3 arabidopsis |
| 43 | 199.5 | 13.0 | 671 | 2 | Q7RKE1 | Q7RKE1 plasmodium |
| 44 | 198 | 12.9 | 390 | 2 | Q8YUN7 | Q8YUN7 anabaena sp |
| 45 | 190.5 | 12.4 | 1294 | 2 | Q7SF66 | Q7SF66 neurospora |

RESULT 1
PA26 HUMAN STANDARD; PRT; 806 AA.
AC Q60733; Q75645; Q8N452; Q9UG29; Q9UI70; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cat-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6; Synonyms=IPLA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SOURCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2).
RC TISSUE=B-cell, and Testis;
RX MEDLINE=98079046; PubMed=9417066;
RA Larsson P.K.A., Claesson H.E., Kennedy B.P.;
RT Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity.";
RL J. Biol. Chem. 273:207-214(1998).
RN [2]
RP SOURCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Pancratic Islets;
RX MEDLINE=99194813; PubMed=10092647;
RA Ma Z., Wang X., Nowatke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1.";
RL J. Biol. Chem. 274:9607-9616(1999).
RN [3]
RP SOURCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=99269033; PubMed=10336645;
RA Larsson Forell P.K.A., Kennedy B.P., Claesson H.-E.;
RT The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene.";
RL Eur. J. Biochem. 262:575-585(1999).
RN [4]
RP SOURCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RX Ansoyge W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SOURCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leitauer B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://esp.gs.washington.edu).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

[6]
 RA SEQUENCE FROM N.A.
 RA MEDLINE=20057265; PubMed=10591208; DOI=10.1038/990031;
 RX Dunham I., Hunt A.R., Collins J.E., Brunkewich R., Beare D.M.,
 RA Clamp M., Smitk L.J., Alnecough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corry N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dham P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.M.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McEann O.T.,
 RA McClellan J., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.J.C.T.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Rose M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sultson J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mituyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malat J.E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisose S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bams G., Bentley J., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinde K., Kemp K., Latreille P., Layman D., Ozerky P., Rottling T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
 RA Budarf M.L., McDevmid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanek J.P.,
 RA Peyrard M., Kedra D., Setouei E., Fransson I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tlilahun Y., Wright H.,
 RT "The DNA sequence of human chromosome 22.";
 RT Nature 402:489-495(1999).
 RL [7]
 RN SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
 RP TISSUE=Brain;
 RC MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
 RA Dlatshenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Cantucci P., Prange C.,
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmeiz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smallie D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maier M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and

CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -!- FUNCTION: Isoform ankyrin-1PLA2-1 and isoform ankyrin-1PLA2-2,
 CC which lack the catalytic domain, are probably involved in the
 CC negative regulation of IP2A2 activity.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC -!- SUBUNIT: Forms large oligomeric 270-350 kDa structures.
 CC -!- SUBCELLULAR LOCATION: Isoform LH-1PLA2 was found to be membrane
 CC bound. Isoform SH-1PLA2 is cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=LH-1PLA2;
 CC IsoId=O60733-1; Sequence=VSP_000278;
 CC Name=SH-1PLA2;
 CC IsoId=O60733-2; Sequence=VSP_000281; VSP_000282;
 CC Name=Ankyrin-1PLA2-1;
 CC IsoId=O60733-3; Sequence=VSP_000281; VSP_000282;
 CC Name=Ankyrin-1PLA2-2;
 CC IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
 CC -!- TISSUE SPECIFICITY: Four different transcripts were found to be
 CC expressed in a distinct tissue distribution.
 CC -!- SIMILARITY: Contains 7 ANK repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
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DR HSSP; Q60778; 10Y3.
DR Genew; HGNC:9039; PLA2G6.

Query Match 99.5%; Score 1524; DB 1; Length 806;
Best Local Similarity 100.0%; Pred. No. 1.7e-128;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 451 LODLMHSRARKPAFIIGSRDEKRTDHLCLDGGVKGIIITQLIAIEKASGVATKD 510
QY 61 LFDWVAGTGTGILALAILHSKSMAYVRGMYFRMKDEVFPGSRPYESGPLEEFLKREFG 120
DB 511 LFDWVAGTGTGILALAILHSKSMAYVRGMYFRMKDEVFPGSRPYESGPLEEFLKREFG 570
QY 121 HTKMTDVRKRWMLTGLSDROPALHLFRNYDAPEVREBRFQNVNLRPPAPSPQIV 180
DB 571 HTKMTDVRKRWMLTGLSDROPALHLFRNYDAPEVREBRFQNVNLRPPAPSPQIV 630
QY 181 WRARSSGAAPTYFRPGRFLDGLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 240
DB 631 WRARSSGAAPTYFRPGRFLDGLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 690
QY 241 VSLGTGRSPQVPTCVDFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 291
DB 691 VSLGTGRSPQVPTCVDFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 741

RESULT 2

CAG30429 PRELIMINARY; PRT; 806 AA.
ID CAG30429
AC CAG30429
DT 01-JUN-2004 (TEMBUREL 27, Created)
DT 01-JUN-2004 (TEMBUREL 27, Last sequence update)
DT 01-JUN-2004 (TEMBUREL 27, Last annotation update)
DE PLA2G6 protein.
GN PLA2G6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,
RA Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J.,
RA Beare D.M., Dunham I.,
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456543; CAG30429.1; -
SQ SEQUENCE 806 AA; 89902 MW; 8E55CD4EB9ACAD8B CRC64;

Query Match 99.5%; Score 1524; DB 2; Length 806;
Best Local Similarity 100.0%; Pred. No. 1.7e-128;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMHSRARKPAFIIGSRDEKRTDHLCLDGGVKGIIITQLIAIEKASGVATKD 60
DB 451 LODLMHSRARKPAFIIGSRDEKRTDHLCLDGGVKGIIITQLIAIEKASGVATKD 510
QY 61 LFDWVAGTGTGILALAILHSKSMAYVRGMYFRMKDEVFPGSRPYESGPLEEFLKREFG 120
DB 511 LFDWVAGTGTGILALAILHSKSMAYVRGMYFRMKDEVFPGSRPYESGPLEEFLKREFG 570
QY 121 HTKMTDVRKRWMLTGLSDROPALHLFRNYDAPEVREBRFQNVNLRPPAPSPQIV 180
DB 571 HTKMTDVRKRWMLTGLSDROPALHLFRNYDAPEVREBRFQNVNLRPPAPSPQIV 630
QY 181 WRARSSGAAPTYFRPGRFLDGLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 240
DB 631 WRARSSGAAPTYFRPGRFLDGLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 690
QY 241 VSLGTGRSPQVPTCVDFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 291
DB 691 VSLGTGRSPQVPTCVDFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 741

RESULT 3

PA26_MOUSE STANDARD; PRT; 752 AA.
ID PA26_MOUSE
AC P97819; Q99LA9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cat-
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=iPLA2G6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=97236816; Pubmed=9079688;
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RT "Identity between the Ca2+-independent phospholipase A2 enzymes from
RT P388D1 macrophages and Chinese hamster ovary cells.";
RL J. Biol. Chem. 272:8576-8580(1997).
RN [2]
RP REVISIONS TO 2-3; 9; 11 AND 211.
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toehlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H2O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U88624; AAB48511.2; -
DR EMBL; BC003487; AAB03487.1; -
DR HSSP; Q60778; 10Y3.
DR MGD; MGI:1859152; PLA2G6.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ANK; 6.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PSS0088; ANK_REPEAT; 4.

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat; Hydrophobic; Lipid degradation; Repeat.
 FT REPEAT 151 181 ANK 1.
 FT REPEAT 185 215 ANK 2.
 FT REPEAT 219 248 ANK 3.
 FT REPEAT 251 281 ANK 4.
 FT REPEAT 286 312 ANK 5.
 FT REPEAT 316 345 ANK 6.
 FT REPEAT 349 378 ANK 7.
 FT ACT SITE 465 465 Potential.
 SQ SEQUENCE 752 AA; 83702 MW; AAC347B0E1292E9 CRC64;
 Query Match 95.6%; Score 1463; DB 1; Length 752;
 Best Local Similarity 94.8%; Pred. No. 5.1e-123;
 Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LODMHSRARKRAFLGSRWDEKTRHDHLLCLDGGGVGLIITOLLIAEKASGVATND 60
 DB 397 LODMHSRARKRAFLGSRWDEKTRHDHLLCLDGGGVGLIITOLLIAEKASGVATND 456
 QY 61 LFDWVAGTGTGILALAIHLSKSMAYMRGVFRMKDEVRGSRPYSGPLEEFLKEEFG 120
 DB 457 LFDWVAGTGTGILALAIHLSKSMAYMRGVFRMKDEVRGSRPYSGPLEEFLKEEFG 516
 QY 121 HTKMTDVRKPKWLTGTLSDRQPAELHFRNYDAPETVREPRNQNVLPPAQPSDQIV 180
 DB 517 HTKMTDVRKPKWLTGTLSDRQPAELHFRNYDAPETVREPRNQNVLPPAQPSDQIV 576
 QY 181 WRAARSSGAAPYFRNGRFLDGGILLANPTLDAMTEIHEYNDLIRKQGANVKKLSTV 240
 DB 577 WRAARSSGAAPYFRNGRFLDGGILLANPTLDAMTEIHEYNDLIRKQGANVKKLSTV 636
 QY 241 VSLGTGRSPQVPYTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 291
 DB 637 VSLGTGRSPQVPYTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 687
 RESULT 4
 Q7PFX2 PRELIMINARY; PRT; 752 AA.
 AC 07PFX2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2004 (TrEMBLrel. 25, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Phospholipase A2, group VI.
 GN Name=Pla2g6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He; TISSUE=Osteoblast;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin C.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Maan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Skraml U., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywicki M.I., Skalka U., Small D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He; TISSUE=Osteoblast;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC052845; AAH52845.1; -
 DR GO; GO:0003824; F:cathecolytic activity; IEA.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF000023; ANK; 6.
 DR Pfam; PF01734; Patatin; 1.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.
 SQ SEQUENCE 752 AA; 83717 MW; DAC347B0E14AFC CRC64;
 Query Match 95.6%; Score 1463; DB 2; Length 752;
 Best Local Similarity 94.8%; Pred. No. 5.1e-123;
 Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LODMHSRARKRAFLGSRWDEKTRHDHLLCLDGGGVGLIITOLLIAEKASGVATND 60
 DB 397 LODMHSRARKRAFLGSRWDEKTRHDHLLCLDGGGVGLIITOLLIAEKASGVATND 456
 QY 61 LFDWVAGTGTGILALAIHLSKSMAYMRGVFRMKDEVRGSRPYSGPLEEFLKEEFG 120
 DB 457 LFDWVAGTGTGILALAIHLSKSMAYMRGVFRMKDEVRGSRPYSGPLEEFLKEEFG 516
 QY 121 HTKMTDVRKPKWLTGTLSDRQPAELHFRNYDAPETVREPRNQNVLPPAQPSDQIV 180
 DB 517 HTKMTDVRKPKWLTGTLSDRQPAELHFRNYDAPETVREPRNQNVLPPAQPSDQIV 576
 QY 181 WRAARSSGAAPYFRNGRFLDGGILLANPTLDAMTEIHEYNDLIRKQGANVKKLSTV 240
 DB 577 WRAARSSGAAPYFRNGRFLDGGILLANPTLDAMTEIHEYNDLIRKQGANVKKLSTV 636
 QY 241 VSLGTGRSPQVPYTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 291
 DB 637 VSLGTGRSPQVPYTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 687
 RESULT 5
 Q9JUK61 PRELIMINARY; PRT; 807 AA.
 AC Q9JUK61;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ca2+-independent phospholipase A2 long form (Pla2g6 protein).
 GN Name=Pla2g6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH/3T3;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin C.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RA Strainsberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF259401; AAF72651.1; -;
 DR EMBL; BC057209; AAH57209.1; -;
 DR HSSP; Q60778; 10Y3
 DR MGD; MG11859152; PLA2g6.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patactin.
 DR Pfam; PF000023; Ank_6.
 DR Pfam; PF01734; Patactin_1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PROSITE; PSS0088; ANK_REPEAT; 4.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.
 SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 95.6%; Score 1463; DB 2; Length 807;
 Best Local Similarity 94.8%; Pred. No. 5.6e-123;
 Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVKGKLIITQLIAIEKASGATKD 60
 DB 452 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVKGKLIITQLIAIEKASGATKD 511
 QY 61 LFDVAVGTSVGGILALAILHSKSMAYMRGVYFPMKDEVFVSGSPYSGPLEEFLKKEFGE 120
 DB 512 LFDVAVGTSVGGILALAILHSKSMAYMRGVYFPMKDEVFVSGSPYSGPLEEFLKKEFGE 571
 QY 121 HTXMTDVRRKPKWLTGTLSDROPABEHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 180
 DB 572 HTXMTDVRRKPKWLTGTLSDROPABEHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 631
 QY 181 WRAARSSGAAPTYFRPGRFLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
 DB 632 WRAARSSGAAPTYFRPGRFLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 691
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVNDCCTDPDGR 291
 DB 692 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVNDCCTDPDGR 742
 RESULT 6
 AAH57209 PRELIMINARY; PRT; 807 AA.
 AC AAH57209;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE PLA2g6 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strainsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RA Strainsberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057209; AAH57209.1; -;
 DR HSSP; Q60778; 10Y3
 DR MGD; MG11859152; PLA2g6.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patactin.
 DR Pfam; PF000023; Ank_6.
 DR Pfam; PF01734; Patactin_1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PROSITE; PSS0088; ANK_REPEAT; 4.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.
 SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 95.6%; Score 1463; DB 2; Length 807;
 Best Local Similarity 94.8%; Pred. No. 5.6e-123;
 Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVKGKLIITQLIAIEKASGATKD 60
 DB 452 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVKGKLIITQLIAIEKASGATKD 511
 QY 61 LFDVAVGTSVGGILALAILHSKSMAYMRGVYFPMKDEVFVSGSPYSGPLEEFLKKEFGE 120
 DB 512 LFDVAVGTSVGGILALAILHSKSMAYMRGVYFPMKDEVFVSGSPYSGPLEEFLKKEFGE 571
 QY 121 HTXMTDVRRKPKWLTGTLSDROPABEHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 180
 DB 572 HTXMTDVRRKPKWLTGTLSDROPABEHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 631
 QY 181 WRAARSSGAAPTYFRPGRFLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
 DB 632 WRAARSSGAAPTYFRPGRFLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 691
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVNDCCTDPDGR 291
 DB 692 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVNDCCTDPDGR 742
 RESULT 7
 PA26_RAT STANDARD; PRT; 751 AA.
 ID PA26_RAT;
 AC P97570;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE 85 kDa calcium-independent phospholipase A2 (BC 3.1.1.4) (iPLA2) (Cat-
 DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
 OS Rattus norvegicus (Rat).
 GN Name=PLA2g6;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=pancreatic islets;
 RX MEDLINE=97269008; PubMed=9111008;

RA Ma Z., Ramanadham S., Kempe K., Chi X.S., Ladenson J., Turk J.,
 RT "pancreatic islets express a Ca²⁺-independent phospholipase A2 enzyme
 RT that contains a repeated structural homologue to the integral
 RT membrane protein binding domain of ankyrin";
 RL J. Biol. Chem. 272:11118-11127(1997).
 CC -1- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and
 CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver,
 CC heart and skeletal muscle.
 CC -1- SIMILARITY: Contains 7 ANK repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U51898; AAC53136.1; -.
 CC HSSP: Q60778; 10Y3.
 CC RGD: 6288677; P1A295.
 CC InterPro: IPR002110; ANK.
 CC Pfam: PF00023; ANK; 6.
 CC PRINTS: PR01415; ANKYRIN.
 CC SMART: SM00248; ANK; 6.
 CC PROSITE: PSS0088; ANK_REPEAT: 4.
 CC PROSITE: PSS0297; ANK_REPEAT_REGION: 1.
 CC ANK repeat; Hydrophobic; Lipid degradation; Repeat.
 KM ANK repeat; Hydrophobic; Lipid degradation; Repeat.
 FT REPEAT 150 180 ANK 1.
 FT REPEAT 184 214 ANK 2.
 FT REPEAT 218 247 ANK 3.
 FT REPEAT 250 280 ANK 4.
 FT REPEAT 285 311 ANK 5.
 FT REPEAT 315 344 ANK 6.
 FT REPEAT 348 377 ANK 7.
 FT ACT SITE 464 464 Potential.
 SQ SEQUENCE 751 AA; 83582 MW; 393BBADA7FCC99B CRC64;
 Query Match 95.0%; Score 1454; DB 1; Length 751;
 Best Local Similarity 94.2%; Pred. No. 3.3e-122;
 Matches 274; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 1 LQDLMIHSRRKPAFILGSRDEKRTDHLCLDGGGVKGLIIQLIAIEKASGVATKD 60
 Db 396 LQDLMPVSRARKAFILSSMRDEKRTDHLCLDGGGVKGLVITQLIAIEKASGVATKD 455
 QY 61 LEPWVAGTSGGIIAIALIHSKSMAYNRGMVFRMKDEVFGRSRYESGPLEEFLKRE 120
 Db 456 LEPWVAGTSGGIIAIALIHSKSMAYNRGMVFRMKDEVFGRSRYESGPLEEFLKRE 515
 QY 121 HTWTDVRRKRWMLTGLSDRPAELHLFNNYDAPEVVRPRFQNNNLPPQPSQV 180
 Db 516 HTWTDVRRKRWMLTGLSDRPAELHLFNNYDAPEVVRPRFQNNNLPPQPSQV 575
 QY 181 WRARSSGAAPTYFRPGRFLDGLANPLDAMTEIHENODLIRKQANVKYKLSIV 240
 Db 576 WRARSSGAAPTYFRPGRFLDGLANPLDAMTEIHENODMIRKQGNKYKLSIV 635
 QY 241 VSLGTGRSPQVPTCVDFRPSNWEIAKTVFGAKELGKRVVDCCTDPGR 291
 Db 636 VSLGTGRSPQVPTCVDFRPSNWEIAKTVFGAKELGKRVVDCCTDPGR 686
 RESULT 8
 Q6DDKO

ID Q6DDKO PRELIMINARY; PRT; 756 AA.
 AC Q6DDKO;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin A.A., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Huijck S.W.,
 RA Vallion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Klein S., Strausberg R.,
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC077558; AA077558.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 756 AA; 84303 MW; C0278741CA52A71 CRC64;
 Query Match 68.1%; Score 1042; DB 2; Length 756;
 Best Local Similarity 67.9%; Pred. No. 5.5e-85;
 Matches 199; Conservative 34; Mismatches 56; Indels 4; Gaps 1;
 QY 2 QDLMIHSRRKPAFILGSRDEKRTDHLCLDGGGVKGLIIQLIAIEKASGVA 57
 Db 398 RDEYVSTALSGMLVPODYDPRDGLRVKDRLLCLDGGVIRGLVLMQLIAIEKASGR 457
 QY 58 TKDLFDWVAGTSGGIIAIALIHSKSMAYNRGMVFRMKDEVFGRSRYESGPLEEFLKRE 117
 Db 458 IRELFDWVAGTSGGIIAIALIHSKSMAYNRGMVFRMKDEVFGRSRYESGPLEEFLKRE 517
 QY 118 FGEHTKTDVRRKRWMLTGLSDRPAELHLFNNYDAPEVVRPRFQNNNLPPQPSD 177
 Db 518 FGEHTKTDVRRKRWMLTGLSDRPAELHLFNNYDAPEVVRPRFQNNNLPPQPSD 577
 QY 178 QLVWRARSSGAAPTYFRPGRFLDGLANPLDAMTEIHENODLIRKQANVKYK 237
 Db 578 QLVWRARSSGAAPTYFRPGRFLDGLANPLDAMTEIHENODLIRKQANVKYK 637

QY 238 SIIVSLCTGRSPQVPTCVDFRPSNPMLAKTVFGAKELGKGVVDCCTDPDG 290
 DB 638 GIVVSLCTGRSPQVPTCVDFRPSNPMLAKTVFGAKELGKGVVDCCTDPDG 690

RESULT 9

06NMWY0 PRELIMINARY; PRT; 818 AA.
 ID 06NMWY0
 AC 06NMWY0
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE ZGC:77476.
 GN Name=ZGC:77476;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.L., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnski M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC067375; AA67375.1; -
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002641; Patacin.
 DR Pfam: PF00023; Ank_6.
 DR Pfam: PF01734; Patacin.1.
 DR PRINTS: PRO1415; ANKYRIN.
 DR SMART: SM00248; ANK_6.
 DR PROSITE: PSS0088; ANK_REPEAT.4.
 DR PROSITE: PSS0297; ANK_REPEAT_REGION.1.
 KW ANK repeat.
 SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8BA9 CRC64;
 Query Match 63.1%; Score 966.5; DB 2; Length 818;
 Best Local Similarity 63.9%; Pred. No. 4e-78;
 Matches 184; Conservative 31; Mismatches 48; Indels 25; Gaps 1;
 QY 28 DHHLCDDGGGVKGLIIITQLIAIEKASGAVTKDLFDWVAGTSTGGIILALILHSKSNAYM 87
 DB 465 DHHLCDDGGGVKGLIIITQLIAIEKASGAVTKDLFDWVAGTSTGGIILALILHSKSNAYM 524
 QY 88 RGMVFRKMDVFRGSRPYESGPLEEFLKRGEGHTTKTDRKPKVMULTGLTSLDRPAELH 147
 DB 525 RCLYFRKKEGVFRGSRPYESGPLEEFLKRGEGHTTKTDRKPKVMULTGLTSLDRPAELH 584
 QY 148 LFRNYADPAPETVREPRFRQNVNLRPPAP-----SDQLVWR 182

DB 585 LFRNYADPAPETVREPRFRQNVNLRPPAP-----SDQLVWR 644
 QY 183 AARSSGAAPTYFRPNRPFLLDGLLANNPTIDANTEIHEYNODIRKQANKVKKSLIVS 242
 DB 645 AARSSGAAPTYFRPNRPFLLDGLLANNPTIDANTEIHEYNODIRKQANKVKKSLIVS 704
 QY 243 LGTGRSPQVPTCVDFRPSNPMLAKTVFGAKELGKGVVDCCTDPDG 290
 DB 705 LGTGRSPQVPTCVDFRPSNPMLAKTVFGAKELGKGVVDCCTDPDG 752

RESULT 10

AAH67375 PRELIMINARY; PRT; 818 AA.
 ID AAH67375
 AC AAH67375;
 DT 24-MAY-2004 (TREMBlrel. 27, Created)
 DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)
 DT 24-MAY-2004 (TREMBlrel. 27, Last annotation update)
 DE ZGC:77476.
 GN ZGC:77476.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.L., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnski M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC067375; AA67375.1; -
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002641; Patacin.
 DR Pfam: PF00023; Ank_6.
 DR Pfam: PF01734; Patacin.1.
 DR PRINTS: PRO1415; ANKYRIN.
 DR SMART: SM00248; ANK_6.
 DR PROSITE: PSS0088; ANK_REPEAT.4.
 DR PROSITE: PSS0297; ANK_REPEAT_REGION.1.
 KW ANK repeat.
 SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8BA9 CRC64;
 Query Match 63.1%; Score 966.5; DB 2; Length 818;
 Best Local Similarity 63.9%; Pred. No. 4e-78;
 Matches 184; Conservative 31; Mismatches 48; Indels 25; Gaps 1;
 QY 28 DHHLCDDGGGVKGLIIITQLIAIEKASGAVTKDLFDWVAGTSTGGIILALILHSKSNAYM 87
 DB 465 DHHLCDDGGGVKGLIIITQLIAIEKASGAVTKDLFDWVAGTSTGGIILALILHSKSNAYM 524
 QY 88 RGMVFRKMDVFRGSRPYESGPLEEFLKRGEGHTTKTDRKPKVMULTGLTSLDRPAELH 147
 DB 525 RCLYFRKKEGVFRGSRPYESGPLEEFLKRGEGHTTKTDRKPKVMULTGLTSLDRPAELH 584
 QY 148 LFRNYADPAPETVREPRFRQNVNLRPPAP-----SDQLVWR 182
 DB 585 LFRNYADPAPETVREPRFRQNVNLRPPAP-----SDQLVWR 644

QY 183 AARSGAAPTYPNPNRFLDGLIANNPTLDANTEIHEYNODLIRKQANKVKLSIVS 242
 DB 645 AARSGAAPTYPNPNRFLDGLIANNPTLDANTEIHEYNODLIRKQANKVKLSIVS 704
 QY 243 LGTGRSPQVAVTCDVFRPSNPWELAKTVFGAKELGKVVDDCTDPDG 290
 DB 705 LGTGRSPQVAVTCDVFRPSNPWELAKTVFGAKELGKVVDDCTDPDG 752

RESULT 11
 Q8MR13 PRELIMINARY; PRT; 386 AA.
 AC 08MR13;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE LD44515P.
 GN ORFNames=C66718;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Chavez M., Chavez C., Dorsett V., Dreesen D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munoz J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY122192; AAMS2704.1; -
 DR FlyBase; FBgn0036053; C66718.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro; IPR002641; Patactin.
 DR Pfam; PF01734; Patactin; 1.
 SQ SEQUENCE 386 AA; 42693 MW; B32B7BCFC36541DD CRC64;

Query Match 48.1%; Score 736; DB 2; Length 386;
 Best Local Similarity 50.3%; P-Id. No. 9,7e-58;
 Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;

QY 16 ILGSMDEKRTHTHLLCLDGGGVKGLIIQLLAIKASAVATKQD.FDMVAGTSGIILA 75
 DB 48 IAAEIDKPYGRRLCLDGGGIRGLVLQVLMLEIKLSTRPIIHMDWAGTSGIILA 107
 QY 76 LAILHGSMAVNRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVKRKYMLT 135
 DB 108 LALGCGKTRKQCGVIRKMEQCFVSGRPINSEFESILNDNGEPVMTDIGHPKIMVT 167
 QY 136 GTLSROPALHLFRNYDAPEYR--EPFNQNVNLRPPAOPSDDQVWPAARSSGAAPT 192
 DB 168 GWADBRKPYDLHLFRNYTASADILGIYTPINNRI--PPQSEQQLVMAAATGAAPS 224
 QY 193 YFPPNRPFLDGLIANNPTLDANTEIHEYNODLIRKQANKVKLSIVS LGTGRSPQV 252
 DB 225 YFPAFGFPLDGLIANNPTLDANTEIHEYNMALARSAERSEALPVSVMVSLGTHLIVTE 284
 QY 253 VTCVDVFRPSNPWELAKTVFGAKELGKVVDDCTDPDG 291
 DB 285 LKQIDVFRPSNPWELAKTVFGAKELGKVVDDCTDPDG 323

RESULT 12
 Q9VT60 PRELIMINARY; PRT; 877 AA.
 AC 09VT60;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-MAY-2004 (T-EMBLrel. 26, Last annotation update)
 GN C66718-PA.
 DE ORFNames=C66718;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Agbayani A., An H.U., Andrews-Pfankoch C., Baldwin D.,
 RA Bailow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster G., Gabrielian A.E., Garcia N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,
 RA Uetani M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mouton S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Palniet K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:1215-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodegren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers S.E., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Celniker S.E., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminke J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A.,
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RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.B.,
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
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RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
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RP SEQUENCE FROM N.A.
RG FLYBASE;
RL [6]
SEQUENCE FROM N.A.
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RG FLYBASE;
RL EMBL: AEO03550; AAF50194.3; -
DR HSSP: Q60778; 10Y3
DR FlyBase; FBgn0036053; CG6718.
DR GO: GO:0003824; F: catalytic activity; IEA.
DR GO: GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002641; Patatin.
DR Pfam: PF000023; ANK_5.
DR Pfam: PF01734; Patatin_1.
DR PRINTS: PR01415; ANKRYRN.
DR SMART: SM00248; ANK_6.
DR PROSITE: PSS0088; ANK_REPEAT; 3.
DR PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
DR ANK repeat.
SQ SEQUENCE 877 AA; 96862 MW; C9DCACD6C282868B CRC64;

Query Match 48.1%; Score 736; DB 2; Length 877;
Best Local Similarity 50.9%; Pred. No. 2.9e-57;
Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;

QY 16 ILSSMRDEKTHDHLCLDGGVKGGLIIQLILIEKASGVATDLPDWAGSTGGLA 75
DB 539 IAAEIGCKPYGRGLLCLDGGIRGLVQMLLEIKLSRTPPIIHMPDMAGSTGGLA 598
QY 76 LAILHSMSAMVYMGMYRMKDEVRGSRPYSEGLPEEFKREGEHTKMTDVRKPKMLT 135
DB 599 LALGCGKTKMQCKMGLYRMEQGVSRPINSSEFBSILKDNLEFVNMVDIKPKIMVT 658
QY 136 GTLSDRPAELHLFRNYDAETVR---EPRFNQVNLPPAOPSDQLVMPAASSGAAPT 192
DB 659 GWADNRKPVLDHLFRNVTASDILGITYPIINRRI---PPQPEQGLVMPAAATGAAPS 715
QY 193 YFPNNGRFLDGLIANNPTIDAMTEIHEYNODLIRKQANVKKLSTIVSLGTRSPQVP 252
DB 716 YFPAFGFLGLGGIANNPTIDAMTEIHEYNMALRSARRESBALFVSVMISLGTHIVTE 775
QY 253 VTCVDVFRSPNPMELATVFGAKELGKVVNDCCDDPPDR 291
DB 776 LKDIIVFRPSIMDTAKLAVGISITGLVLDQATCSQGR 814

RESULT 13
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DT 01-APR-2004 (TREMBlrel. 27, Last annotation update)
DE CG6718-PA.
GN CG6718.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxId=7227;

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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA Brandon R.C., Rogers J.R., Blazek R.G., Chame M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
RA Adair J.F., Agbayani A., An H.U., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,
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RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrefi A.,
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RA Palazzolo M., Peltan G.S., Pan S., Pollard J., Puri V., Reame M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheibel F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svaykbae R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodagett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
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RL Science 287:2185-2195 (2000).
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RA Celniker S.E., Wheeler D.A., Kromoller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
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RX MEDLINE=22426070; PubMed=12537573;
RA Kaminke J.S., Bergman C.M., Kromoller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
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RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";
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 RP SEQUENCE FROM N.A.
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 RA FlyBase;
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 DR EMBL: AEO03550; AAF50194.3; -
 DR FLYBASE; FBgn0036053; CG6718.
 SQ SEQUENCE 877 AA; 96863 MW; C9DC2C6C282869B CRC64;
 Query Match 48.1%; Score 736; DB 2; Length 877;
 Best local similarity 50.9%; Pred. No. 2,9e-57;
 Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;
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 DB 539 IAAEIGDKPYGRGLCLDGGGIRGLVQLVQLLEIKLSRTPIIHMDWIASTGGILA 598
 QY 76 LALHSKSMAYMGVFRMDDEVFRGSRPFESGPLEFLRREGENTKMTDVKKKMLT 135
 DB 599 LALGCGKTMQCKGLYLRKEQCFVSGRPNSSEFESILKDNIGEFVMTDIGHKIMWT 658
 QY 136 GTLSDROPALHFRNYDAPEYR---EPFRNQVNLPPAPSDQLVPRASSGAAPT 192
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 QY 253 VTCVDVFRPNPWEAKTVGAKELGKMYDCCCTDPDGR 291
 DB 776 LKQIDVFRPESIPWDTAKLAVIGTIGLVLVQATCSGDR 814
 RESULT 14
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 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CG6718-BB (CG6718-PC).
 GN ORFNames=CG6718;
 OS Drosophila melanogaster (Fruit fly).
 OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC Ephydroidea; Drosophilidae; Drosophila.
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 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,
 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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 RL Science 287:2185-2195(2000).
 RN [2]
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 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgeson A.,
 RA George R.A., Hoskins R.A., Laverly T., Murry D.M., Nelson C.R.,
 RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodegren E.J.,
 RA Sytkas R., Taber P.E., Wan K., Stapleton M., Sutten G.G., Venter C.,
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 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
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 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
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 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
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SQ SEQUENCE 887 AA; 97778 MW; 1387084E7265BEE5 CRC64;
 Query Match 48.1%; Score 736; DB 2; Length 887;
 Best Local Similarity 50.9%; Pred. No. 3e-57;
 Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;
 16 ILAGMDEKRTDHLCLDGGVYKGLIIQTLAIKASGAVATKDLFDVWAGTSGGIIA 75
 549 IAAEIDKPGRGRLICLDGGIRGLVVMLEIEKLSRTPIIHMDWLAGTSGIIA 608
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 DB 609 LALGCKTKMQCGLVLRKMEQCFVSRPNSFEFESILKDNIGEFVMTDIDKHPKIMVT 668
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 RESULT 15
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 AC ANA11936;
 DT 01-APR-2004 (TEMBLrel. 27, Created)
 DT 01-APR-2004 (TEMBLrel. 27, Last sequence update)
 DE CG6718-PB.
 GN CG6718.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatic
 RT a genomics perspective."
 RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN
 [5]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN
 [6]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03550; ANA11936.2;
 SQ SEQUENCE 887 AA; 97778 MW; 1387084E7265BEE5 CRC64;
 Query Match 48.1%; Score 736; DB 2; Length 887;
 Best Local Similarity 50.9%; Pred. No. 3e-57;
 Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;
 16 ILAGMDEKRTDHLCLDGGVYKGLIIQTLAIKASGAVATKDLFDVWAGTSGGIIA 75
 549 IAAEIDKPGRGRLICLDGGIRGLVVMLEIEKLSRTPIIHMDWLAGTSGIIA 608
 DB
 QY 76 LALHKSNAVMKGMFRMKDEVRFSRPSGPLEBFLKREGEHTKMTDVKKVMT 135
 DB 609 LALGCKTKMQCGLVLRKMEQCFVSRPNSFEFESILKDNIGEFVMTDIDKHPKIMVT 668
 QY 136 GTLSDROPALHLFRNYDAPEYR---EPRFNQVNLRPAPGSDOLVMAAASGAAPT 192
 DB 669 GWADKRPVDLHFRNYTASDLIGVTPINNRI---PPQSEDLVMAAARATGAAPS 725
 QY 193 YFRPNGRFLDGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIVSLGTRSPQVP 252
 DB 726 YFPAFGFLDGLLANNPTLDAMTEIHEYNMALSAGRESEALPVSVMSLGTGHPVTE 785

Thu Dec 16 19:13:28 2004

us-10-612-668-19.rup

Page 12

Dy 253 VTCTDVFPSPNPELAKTVFGAKELGKMVVDCCDDPGR 291
 : : ||||| : : | : : |||
Db 786 LKQIDVFRESINDTAKLAYGIISTIGNLLVDAQATCSDR 824

Search completed: December 15, 2004, 13:13:10
Job time : 66.5892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:51:45 : Search time 59.1231 Seconds
(without alignments)
1771.710 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LQDLNHRISARRKAPILGSM.....GAKELGRVVDCTDGRDP 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 1531 | 100.0 | 292 | AAW17846 | AAW17846 Cytochrome |
| 2 | 1531 | 100.0 | 292 | ABB82230 | Abb82230 Cytochrome |
| 3 | 1531 | 100.0 | 687 | AAW17847 | AAW17847 Cytochrome |
| 4 | 1531 | 100.0 | 687 | ABB82231 | Abb82231 Human cpl |
| 5 | 1531 | 100.0 | 688 | AAW17848 | AAW17848 Cytochrome |
| 6 | 1531 | 100.0 | 688 | ABB82232 | Abb82232 Human cpl |
| 7 | 1524 | 99.5 | 667 | ADMO5093 | Admo5093 Human pro |
| 8 | 1524 | 99.5 | 784 | ADDP9407 | Addp9407 Human lip |
| 9 | 1524 | 99.5 | 806 | AAE25968 | AAE25968 Human PLA |
| 10 | 1524 | 99.5 | 806 | ADO19776 | ADO19776 Human PRO |
| 11 | 1471 | 96.1 | 752 | AAAR8018 | AAAR8018 Calcium-1 |
| 12 | 1471 | 96.1 | 752 | AAW01479 | AAW01479 Calcium-1 |
| 13 | 1471 | 96.1 | 752 | AAW13163 | AAW13163 Calcium-1 |
| 14 | 1471 | 96.1 | 752 | AAW17849 | AAW17849 Hamster c |
| 15 | 1471 | 96.1 | 752 | AAW81825 | AAW81825 Chinese h |
| 16 | 1471 | 96.1 | 752 | ABB82215 | Abb82215 Calcium 1 |
| 17 | 1454 | 95.0 | 751 | ADDA6244 | Addda6244 Rat Prote |
| 18 | 1454 | 95.0 | 751 | ADBE6032 | Adbe6032 Rat Prote |
| 19 | 1454 | 95.0 | 751 | ADBE5230 | Adbe5230 Rat Prote |
| 20 | 1454 | 95.0 | 751 | ADBE5036 | Adbe5036 Rat Prote |
| 21 | 890 | 58.1 | 401 | AAAB92811 | AAAB92811 Human pro |
| 22 | 736 | 48.1 | 877 | ABB62624 | Abb62624 Drosophila |
| 23 | 234 | 15.3 | 387 | ADG76683 | Adg76683 Phospholip |
| 24 | 213.5 | 13.9 | 679 | AAAB18224 | AAAB18224 Plasmodiu |
| 25 | 211.5 | 13.8 | 370 | AAAB56905 | AAAB56905 Human pro |

| | | | | | | |
|----|-------|------|-----|---|-----------|---------------------|
| 26 | 211.5 | 13.8 | 380 | 3 | AAAB42509 | AAAB42509 Human ORF |
| 27 | 211.5 | 13.8 | 445 | 4 | AAW41310 | AAW41310 Human pol |
| 28 | 211.5 | 13.8 | 562 | 4 | AAW39524 | AAW39524 Human pol |
| 29 | 211.5 | 13.8 | 639 | 4 | AAAB5818 | AAAB5818 Human pro |
| 30 | 211.5 | 13.8 | 682 | 4 | AAAG63224 | AAAG63224 Human pro |
| 31 | 208.5 | 13.6 | 350 | 8 | ADG76717 | Adg76717 Phospholip |
| 32 | 204.5 | 13.4 | 577 | 8 | ADMA8198 | Adma8198 Polypepti |
| 33 | 204.5 | 13.4 | 577 | 8 | ADMA8197 | Adma8197 Polypepti |
| 34 | 190 | 12.4 | 378 | 8 | ADG76635 | Adg76635 Phospholip |
| 35 | 183.5 | 12.0 | 411 | 5 | AAAB52551 | AAAB52551 Nicotiana |
| 36 | 182.5 | 11.9 | 410 | 4 | AAE02387 | AAE02387 Wheat 11p |
| 37 | 182 | 11.9 | 37 | 7 | ADD15928 | Add15928 Peptide r |
| 38 | 182 | 11.9 | 404 | 3 | AAAG30647 | AAAG30647 Arabidops |
| 39 | 182 | 11.9 | 414 | 3 | AAAG30646 | AAAG30646 Arabidops |
| 40 | 179 | 11.7 | 428 | 3 | AAAG29735 | AAAG29735 Arabidops |
| 41 | 177 | 11.6 | 410 | 4 | AAAG99331 | AAAG99331 Maize pat |
| 42 | 177 | 11.6 | 410 | 4 | AAAG99329 | AAAG99329 Maize pat |
| 43 | 177 | 11.6 | 410 | 8 | ADMG3049 | Admg3049 Corn pata |
| 44 | 177 | 11.6 | 410 | 8 | ADMG3051 | Admg3051 Corn pata |
| 45 | 176 | 11.5 | 383 | 3 | AAAG50026 | AAAG50026 Arabidops |

ALIGNMENTS

| | | |
|----------|---|----------------------------|
| RESULT 1 | AAW17846 | standard; protein; 292 AA. |
| ID | AAW17846 | |
| XX | AAW17846; | |
| AC | 07-AUG-1997 (first entry) | |
| XX | | |
| DE | Cytosolic phospholipase A2/B (clone 19b product). | |
| XX | | |
| KM | Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; | |
| XX | inflammation; inhibitor; antiinflammatory. | |
| OS | Homo sapiens. | |
| XX | | |
| PN | W09717448-A2. | |
| XX | | |
| PD | 15-MAY-1997. | |
| XX | | |
| PF | 07-NOV-1996; 96MO-US017794. | |
| XX | | |
| PR | 08-NOV-1995; 95US-00555568. | |
| XX | | |
| PA | (GENE) GENETICS INST INC. | |
| XX | | |
| XX | Jones S, Tang J; | |
| XX | WPI; 1997-281037/25. | |
| DR | N-PSDB; AAT68824. | |
| XX | | |
| PT | Calcium independent phospholipase A2/B - used to reduce inflammation in a | |
| PT | mammalian subject. | |
| XX | | |
| PS | Claim 12; Page 46-47; 74pp; English. | |
| XX | | |
| CC | A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17845) is | |
| CC | characterized by activity in the absence of calcium, by activity in a | |
| CC | mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl- | |
| CC | phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a | |
| CC | lack of stimulation by ATP, and by including in its sequence at least one | |
| CC | of the amino acid sequences given in AAW17839- 44). It is encoded by | |
| CC | partial cDNA clone 19b (AAT68824), derived from Burkitt's lymphoma Raji | |
| CC | (ATCC CRU86) cells. Other PLA2/B enzymes (AAW17845, AAW17847-48) have | |
| CC | also been identified. sPLA2/B enzymes are thought to be involved in the | |
| CC | release of arachidonic acid in specific tissues. Recombinant sPLA2/B | |
| CC | polypeptides produced in transformed host cells can be used to screen for | |
| CC | sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the | |
| CC | arachidonic acid cascade | |

XX Sequence 292 AA;
SQ

Query Match 100.0%; Score 1531; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.7e-163;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIISARKAPAFILGSRDEKRTDHLCLDGGVKGIIITQLIAIEKASGVATKD 60
DB 1 LQDLMIISARKAPAFILGSRDEKRTDHLCLDGGVKGIIITQLIAIEKASGVATKD 60

QY 61 LFDWVAGTGTGILALAILHSKSMAYRMGYFRMKDEVFRGSRPYSGPLEEFLKEEFG 120
DB 61 LFDWVAGTGTGILALAILHSKSMAYRMGYFRMKDEVFRGSRPYSGPLEEFLKEEFG 120

QY 121 HTKMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQLV 180
DB 121 HTKMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQLV 180

QY 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
DB 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240

QY 241 VSLGTGRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
DB 241 VSLGTGRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292

RESULT 2
ABB82230
ID ABB82230 standard; protein; 292 AA.
XX ABB82230;
XX

DT 08-JAN-2003 (first entry)
XX

DE Calcium independent phospholipase A2/B (cPLA2/B) (clone 19b).
XX

KM Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX antiinflammatory; antiarthritic; antipruritic; antirheumatic; cytosolic;
XX antiseptic; human.
XX

OS Homo sapiens.
XX

PN US2002106364-A1.
XX

PD 08-AUG-2002.
XX

PF 09-AUG-2001; 2001US-00927180.
XX

PR 27-JUL-1994; 94US-00281193.
XX

PR 14-APR-1995; 95US-00422106.
XX

PR 14-APR-1995; 95US-00422106.
XX

PR 26-JUN-1995; 95WO-US008069.
XX

PR 08-NOV-1995; 95US-0055568.
XX

PR 09-SEP-1998; 98US-00149988.
XX

PR 06-MAR-2000; 2000US-00519223.
XX

PA (GENY) GENETICS INST INC.
XX

PI Jones S, Tang J;
XX

DR WPI; 2002-739923/80.
XX

DR N-PSDB; ABV73009.
XX

XX Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
XX

PS Claim 6; Page 21-22; 41pp; English.
XX

CC The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is

CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kd on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (II),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme (clone 19b)
XX

SQ Sequence 292 AA;
Query Match 100.0%; Score 1531; DB 5; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.7e-163;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIISARKAPAFILGSRDEKRTDHLCLDGGVKGIIITQLIAIEKASGVATKD 60
DB 1 LQDLMIISARKAPAFILGSRDEKRTDHLCLDGGVKGIIITQLIAIEKASGVATKD 60

QY 61 LFDWVAGTGTGILALAILHSKSMAYRMGYFRMKDEVFRGSRPYSGPLEEFLKEEFG 120
DB 61 LFDWVAGTGTGILALAILHSKSMAYRMGYFRMKDEVFRGSRPYSGPLEEFLKEEFG 120

QY 121 HTKMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQLV 180
DB 121 HTKMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQLV 180

QY 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
DB 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240

QY 241 VSLGTGRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
DB 241 VSLGTGRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292

RESULT 3
AAW17847
ID AAW17847 standard; protein; 687 AA.
XX AAW17847;
XX

DT 07-AUG-1997 (first entry)
XX

DE Cytosolic phospholipase A2/B (alternatively spliced clone 19a).
XX

KM Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
XX inflammation; inhibitor; antiinflammatory.
XX

OS Homo sapiens.
XX

PN W09717448-A2.
XX

PD 15-MAY-1997.
XX

PF 07-NOV-1996; 96WO-US017794.
XX

PR 08-NOV-1995; 95US-0055568.
XX

PA (GENY) GENETICS INST INC.
XX

PI Jones S, Tang J;
XX

DR WPI; 1997-281037/25.
XX

DR N-PSDB; AAT68825.
XX

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PT mammalian subject.
 XX
 PS Claim 12; Page 49-51; 74pp; English.
 XX
 CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
 CC characterized by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
 CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAW17839-44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17845)
 CC and is encoded by an isolated cDNA (AAW68825). Other PLA2/B enzymes
 CC (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
 CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade
 CC
 XX
 SQ Sequence 687 AA:
 Query Match 100.0%; Score 1531; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1e-162;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LODLMIISRRKPAFLIGSRDEKRTDHLCLDGGGVKGLIIQLLAIKASGVATKD 60
 DB 396 LODLMIISRRKPAFLIGSRDEKRTDHLCLDGGGVKGLIIQLLAIKASGVATKD 455
 QY 61 LFDWVAGTGTGGILALAILHSKSMAYVRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
 DB 456 LFDWVAGTGTGGILALAILHSKSMAYVRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
 QY 121 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPRPQPSDQLV 180
 DB 516 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPRPQPSDQLV 575
 QY 181 WRAARSSGAAPTYFRPGRFLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
 DB 576 WRAARSSGAAPTYFRPGRFLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 635
 QY 241 VSLGTRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 292
 DB 636 VSLGTRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 687
 RESULT 4
 ABB82231
 ID ABB82231 standard; protein; 687 AA.
 XX
 XX ABB82231:
 DT 08-JAN-2003 (first entry)
 XX
 DE Human cPLA2/B splice variant (clone 19a).
 XX
 KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiatheritic; antiporiatic; antirheumatic; cytosolic;
 KW antiesthmetic; human.
 XX
 OS Homo sapiens.
 XX
 PN US2002106364-A1.
 PD 08-AUG-2002.
 XX
 PF 09-AUG-2001; 2001US-00927180.
 XX
 PR 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422420.
 PR 26-JUN-1995; 95WO-US008069.
 PR 08-NOV-1995; 95US-00555568.

PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GENEY) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 DR WPI; 2002-739923/80.
 DR N-PSDB; ABV73010.
 XX
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX
 PS Claim 6; Page 23-25; 41pp; English.
 XX
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19a)
 XX
 SQ Sequence 687 AA:
 Query Match 100.0%; Score 1531; DB 5; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1e-162;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LODLMIISRRKPAFLIGSRDEKRTDHLCLDGGGVKGLIIQLLAIKASGVATKD 60
 DB 396 LODLMIISRRKPAFLIGSRDEKRTDHLCLDGGGVKGLIIQLLAIKASGVATKD 455
 QY 61 LFDWVAGTGTGGILALAILHSKSMAYVRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
 DB 456 LFDWVAGTGTGGILALAILHSKSMAYVRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
 QY 121 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPRPQPSDQLV 180
 DB 516 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPRPQPSDQLV 575
 QY 181 WRAARSSGAAPTYFRPGRFLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
 DB 576 WRAARSSGAAPTYFRPGRFLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 635
 QY 241 VSLGTRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 292
 DB 636 VSLGTRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 687
 RESULT 5
 AAW17848
 ID AAW17848 standard; protein; 688 AA.
 XX
 AC AAW17848;
 XX
 DT 07-AUG-1997 (first entry)
 XX
 DE Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
 XX
 KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

KW Inflammation; inhibitor; antiinflammatory.
 XX Homo sapiens.
 OS
 XX MO9717448-A2.
 PN
 XX
 XX 15-MAY-1997.
 PD
 XX 07-NOV-1996; 96MO-US017794.
 PF
 XX 08-NOV-1995; 95US-00555568.
 PR
 XX (GENY) GENETICS INST INC.
 PA
 XX Jones S, Tang J;
 XX
 PI WPI; 1997-281037/25.
 DR N-PSDB; AAT68826.
 XX
 XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PT mammalian subject.
 PT
 XX
 PS Claim 12; Page 54-56; 74pp; English.
 XX
 CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is
 CC characterized by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
 CC phosphatidylcholine of about 1-20 nmol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAW17839-44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17846)
 CC and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes
 CC (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
 CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade
 CC
 XX
 SQ Sequence 688 AA;
 Query Match 100.0%; Score 1531; DB 2; Length 688;
 Best Local Similarity 100.0%; Pred. No. 1e-162;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQDLMIISRRARPAFLIGSRDEKRTDHLCLDGGVGKLIITQLLIAIEKASGVATKD 60
 DB 397 LQDLMIISRRARPAFLIGSRDEKRTDHLCLDGGVGKLIITQLLIAIEKASGVATKD 456
 QY 61 LFDWVAGTSTGGILALAILHSKSMAYVRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 120
 DB 457 LFDWVAGTSTGGILALAILHSKSMAYVRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 516
 QY 121 HTKMTDVRKPKWMLTGTLSRQPAELHLFRNYDAPETVREPRNQVNLRPAPQSDQLV 180
 DB 517 HTKMTDVRKPKWMLTGTLSRQPAELHLFRNYDAPETVREPRNQVNLRPAPQSDQLV 576
 QY 181 WRARSSGAAPTYFRPNRGFLDGGILANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 240
 DB 577 WRARSSGAAPTYFRPNRGFLDGGILANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 636
 QY 241 VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVFGAKELGKMWVDCCTDPGRP 292
 DB 637 VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVFGAKELGKMWVDCCTDPGRP 688
 RESULT 6
 ID ABB82232 standard; protein; 688 AA.
 XX
 AC ABB82232;
 XX
 DT 08-JAN-2003 (first entry)
 XX

DE Human cPLA2/B splice variant (clone 19b).
 XX
 XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiarthritic; antipsoaratic; antirheumatic; cytosolic;
 KW antiaesthetic; human.
 XX
 XX Homo sapiens.
 OS
 XX US2002106364-A1.
 PN
 XX 08-AUG-2002.
 PD
 XX 09-AUG-2001; 2001US-00927180.
 PF
 XX 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-004223420.
 PR 26-JUN-1995; 95MO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 XX Jones S, Tang J;
 PT
 XX WPI; 2002-739923/80.
 DR N-PSDB; ABV73011.
 XX
 XX Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 PS Claim 6; Page 28-30; 41pp; English.
 XX
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotrienes or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19b)
 CC
 XX
 SQ Sequence 688 AA;
 Query Match 100.0%; Score 1531; DB 5; Length 688;
 Best Local Similarity 100.0%; Pred. No. 1e-162;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQDLMIISRRARPAFLIGSRDEKRTDHLCLDGGVGKLIITQLLIAIEKASGVATKD 60
 DB 397 LQDLMIISRRARPAFLIGSRDEKRTDHLCLDGGVGKLIITQLLIAIEKASGVATKD 456
 QY 61 LFDWVAGTSTGGILALAILHSKSMAYVRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 120
 DB 457 LFDWVAGTSTGGILALAILHSKSMAYVRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 516
 QY 121 HTKMTDVRKPKWMLTGTLSRQPAELHLFRNYDAPETVREPRNQVNLRPAPQSDQLV 180
 DB 517 HTKMTDVRKPKWMLTGTLSRQPAELHLFRNYDAPETVREPRNQVNLRPAPQSDQLV 576
 QY 181 WRARSSGAAPTYFRPNRGFLDGGILANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 240

Db 577 WRAASSGAAPTFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 636
 Qy 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 292
 Db 637 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 688

RESULT 7

ADM05093
 ID ADM05093 standard; protein; 667 AA.

AC ADM05093;

DT 20-MAY-2004 (first entry)

DE Human protein of the invention SEQ ID NO:3778.

KW human; gene therapy; diagnostic marker; pharmaceutical.

OS Homo sapiens.

PN EP1347046-A1.

PD 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
 PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;

XX WPI; 2003-723558/69.

DR N-PDSB; ADM02650.

XX New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

XX Claim 1; SEQ ID NO 3778; 305pp; English.

CC The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents a

CC protein sequence of the invention.

XX Sequence 667 AA;

XX

XX Query Match 99.5%; Score 1524; DB 7; Length 667;

XX Best Local Similarity 100.0%; Pred. No. 6.1e-162;

XX Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LODLMIISRRKRAFLIGSWRDKRTDHLCLDGGGVKLLITQLLIAEKASGVATKD 60

Db 312 LODLMIISRRKRAFLIGSWRDKRTDHLCLDGGGVKLLITQLLIAEKASGVATKD 371

Qy 61 LFDPMVAGTSGGILALAILHKSMAVYRGMVFRPKDEVFGRSPYBSGPLEEPLKTEFGE 120

Db 372 LFDPMVAGTSGGILALAILHKSMAVYRGMVFRPKDEVFGRSPYBSGPLEEPLKTEFGE 431

Qy 121 HTKMTVVRKPKVMTGTLSDRQAPAEHLFRNYDAPETVREPRFNQVNLPPAQPSPQV 180

Db 432 HTKMTVVRKPKVMTGTLSDRQAPAEHLFRNYDAPETVREPRFNQVNLPPAQPSPQV 491

Qy 181 WRAASSGAAPTFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
 Db 492 WRAASSGAAPTFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 551

Qy 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 291

Db 552 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 602

RESULT 8

ADD93407
 ID ADD93407 standard; protein; 784 AA.

AC ADD93407;

DT 29-JAN-2004 (first entry)

DE Human lipid-associated molecule LIPAM-14 polypeptide.

KW Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;

KW antichyroid; antidiabetic; cytosolic; dermatological; immunosuppressive;

KW antiinflammatory; thyromimetic; antiallergic; cerebroprotective;

KW gastrointestinal; hepatotropic; nephrotoxic; anticonvulsant;

KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;

KW viroinhibitor; uteropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;

XX noctropic.

XX Homo sapiens.

XX WO2003083081-A2.

XX 09-OCT-2003.

XX 27-MAR-2003; 2003WO-UG009755.

XX 29-MAR-2002; 2002US-0368722P.

XX 03-MAY-2002; 2002US-0377576P.

XX 05-JUL-2002; 2002US-0393934P.

XX 27-SEP-2002; 2002US-0414269P.

XX (INCYTE) INCYTE CORP.

XX Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;

XX Baughn MR, Lee EA, Griffin JA, Kabie AE, Elliott VS, Chang H;

XX Lee S, Ramkumar J, Bulloch SA, Hafalia ADA, Khare R, Jiang X;

XX Jackson AA;

XX WPI; 2003-788347/74.

XX N-PDSB; ADD93426.

XX New LIPAM polypeptides, useful for diagnosing, preventing, and treating

XX disorders associated with abnormal expression or activity of LIPAM, e.g.

XX PT neuromuscular, immunological, cardiovascular disorders, cancer and/or

XX infections.

XX Claim 69; Page 206-207; 238pp; English.

XX The present sequence is the protein sequence of human lipid-associated

XX molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows

CC atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention
 CC also relates to the assessment of the effects of exogenous compounds on
 CC the expression of nucleic acids and lipids. The invention provides
 CC expression vectors, host cells, antibodies, agonists and antagonists,
 CC transgenic organisms, and arrays and microarrays of the polynucleotides.

XX Sequence 784 AA;

Query Match 99.5%; Score 1524; DB 7; Length 784;
 Best Local Similarity 100.0%; Pred. No. 7, 9e-162;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIISRRKPAFLIGSWRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 60
 DB LQDLMIISRRKPAFLIGSWRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 488
 QY 61 LFPWVAGTGTGGILALAIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFGE 120
 DB LFPWVAGTGTGGILALAIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFGE 548
 QY 121 HTKMTDVRKPKVMTLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQV 180
 DB HTKMTDVRKPKVMTLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQV 608
 QY 181 WRAARSSGAAPTYFRNGRFLDGGILLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
 DB WRAARSSGAAPTYFRNGRFLDGGILLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 668
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVNVDCCCTDPDGR 291
 DB VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVNVDCCCTDPDGR 719

RESULT 9

AAE25968
 ID AAE25968 standard; protein; 806 AA.

AC AAE25968;

DT 15-NOV-2002 (first entry)

XX Human PLA2 group VI (Ca2+-independent) protein.

KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
 KM antisense therapy; PLA2 protein.

OS Homo sapiens..

PN US6410325-B1.

XX 25-JUN-2002.

PF 09-MAY-2001; 2001US-00651896.

PR 09-MAY-2001; 2001US-00851896.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Freier SM, Watt AT;

DR WPI; 2002-616513/66.

DR N-PSDB; AAD42941.

PT Novel antisense compounds useful for inhibiting gene expression of human
 PT phospholipase A2, group VI and for treating diseases associated with
 PT expression of phospholipase A2, group VI.

PS Disclosure; Col 109-116; 72pp; English.

XX The present invention relates to novel antisense compounds which inhibit
 CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 CC (Ca2+-independent) in human cells or tissues and for treating an animal,

CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnostics, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) protein

XX Sequence 806 AA;

Query Match 99.5%; Score 1524; DB 5; Length 806;
 Best Local Similarity 100.0%; Pred. No. 8, 2e-162;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIISRRKPAFLIGSWRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 60
 DB LQDLMIISRRKPAFLIGSWRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 510
 QY 61 LFPWVAGTGTGGILALAIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFGE 120
 DB LFPWVAGTGTGGILALAIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFGE 570
 QY 121 HTKMTDVRKPKVMTLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQV 180
 DB HTKMTDVRKPKVMTLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQV 630
 QY 181 WRAARSSGAAPTYFRNGRFLDGGILLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
 DB WRAARSSGAAPTYFRNGRFLDGGILLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 690
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVNVDCCCTDPDGR 291
 DB VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVNVDCCCTDPDGR 741

RESULT 10

AD019776
 ID AD019776 standard; protein; 806 AA.

AC AD019776;

DT 12-AUG-2004 (first entry)

XX Human PRO polypeptide #350.

XX Human; PRO; immune related disorder; systemic lupus erythematosus;
 KM rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KM systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KM autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KM diabetes mellitus; renal disease; demyelinating disease;
 KM central nervous system; peripheral nervous system;
 KM demyelinating polyneuropathy; Guillain-Barre syndrome;
 KM chronic inflammatory demyelinating polyneuropathy.

XX Homo sapiens.

PN WO2004043361-A2.

XX 27-MAY-2004.

PF 06-NOV-2003; 2003WO-US035268.

PR 08-NOV-2002; 2002US-0425235P.

PA (GETH) GENENTECH INC.

PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PW;
 PI Wood WI, Wu TD;

DR WPI; 2004-42067/39.

DR N-PSDB; AD019775.

PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO6838 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,

PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.

XX Claim 7; SEQ ID NO 700; 1731pp; English.

XX The invention relates to human PRO polypeptides and the polynucleotides
XX encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC hemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.

XX Sequence 806 AA;

Query Match 99.5%; Score 1524; DB 8; Length 806;

Best Local Similarity 100.0%; Pred. No. 8.2e-162;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LQDLMISSARKKAPFLIGSMRDEKRTDHLCLDGGGVGLIITQLIAIEKASGVATKD 60
DB 451 LQDLMISSARKKAPFLIGSMRDEKRTDHLCLDGGGVGLIITQLIAIEKASGVATKD 510
QY 61 LFDWVAGTGTGILALAIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFG 120
DB 511 LFDWVAGTGTGILALAIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFG 570
QY 121 HTKMTDVRKKPKWMLTGTLSDRQPAELHLFRNYDAPEVIREPRFNQVINLKPPQADQLV 180
DB 571 HTKMTDVRKKPKWMLTGTLSDRQPAELHLFRNYDAPEVIREPRFNQVINLKPPQADQLV 630
QY 181 WRAARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNDLIRKQGANVKKLSTV 240
DB 631 WRAARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNDLIRKQGANVKKLSTV 690
QY 241 VSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 291
DB 691 VSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 741

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RESULT 11

AAR83018

ID AAR83018 standard; protein; 752 AA.

XX AAR83018;

XX 15-JUN-1996 (first entry)

XX Calcium-independent cytosolic phospholipase-A2/B enzyme.

XX CMO; calcium-independent cytosolic phospholipase-A2/B; enzyme;
XX phospholipase-A2; phospholipase-B; drug screening; antiinflammatory;
XX antibody.

XX Criceetus griseus.

XX US5466595-A.

XX 14-NOV-1995.

XX 27-JUL-1994; 94US-00281193.

XX 27-JUL-1994; 94US-00281193.

XX (GEMY) GENETICS INST INC.

XX Tang J, Jones S;

XX

DR WPI; 1996-009526/01.

DR N-FSDB; AAT05842.

XX Isolated polynucleotide encoding cytosolic phospholipase A2/8 - for
PT producing enzyme for use in screening anti-inflammatory agents and prodn.
PT of antibodies.

XX Claim 5; Col 15-22; 24pp; English.

XX The enzyme may be produced recombinantly in host cells such as animal
CC cells, insect cells, eukaryotes, prokaryotes, etc. The protein may also
CC be expressed in transgenic animals (e.g. milk of transgenic cow). The
CC protein is used to screen for agents which inhibit phospholipase activity
CC for use as anti-inflammatory agents. These agents can be used to treat
CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
CC and other disease mediated by increased levels of prostaglandins,
CC leukotriene or platelet activating factor. The enzyme can also be used
CC for the production of antibodies for use as research or diagnostic tools

XX Sequence 752 AA;

Query Match 96.1%; Score 1471; DB 2; Length 752;

Best Local Similarity 95.2%; Pred. No. 7e-156;

Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

```

QY 1 LQDLMISSARKKAPFLIGSMRDEKRTDHLCLDGGGVGLIITQLIAIEKASGVATKD 60
DB 397 LQDLMISSARKKAPFLIGSMRDEKRTDHLCLDGGGVGLIITQLIAIEKASGVATKD 456
QY 61 LFDWVAGTGTGILALAIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFG 120
DB 457 LFDWVAGTGTGILALAIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFG 516
QY 121 HTKMTDVRKKPKWMLTGTLSDRQPAELHLFRNYDAPEVIREPRFNQVINLKPPQADQLV 180
DB 517 HTKMTDVRKKPKWMLTGTLSDRQPAELHLFRNYDAPEVIREPRFNQVINLKPPQADQLV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNDLIRKQGANVKKLSTV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNDLIRKQGANVKKLSTV 636
QY 241 VSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 291
DB 637 VSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 687

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RESULT 12

AAW01479

ID AAW01479 standard; protein; 752 AA.

XX AAW01479;

XX 25-MAR-2003 (revised)

XX 12-FEB-1997 (first entry)

XX Calcium-independent cytosolic phospholipase A2/B.

XX cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
XX arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;
XX anti-inflammatory; screen; rheumatoid arthritis.

XX Synthetic.

XX US5554511-A.

XX 10-SEP-1996.

XX 14-APR-1995; 95US-00422420.

XX 27-JUL-1994; 94US-00281193.

XX (GEMY) GENETICS INST INC.

XX

PI Tang J, Jones S;
 XX WPI: 1996-424653/42.
 DR N-PSDB; AAT4578.
 XX
 PT Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing
 PT host cells contg. the phospholipase gene, useful for screening anti-
 PT inflammatory agents for treating e.g. rheumatoid arthritis.
 PS Claim 1; Col 15-22; 24pp; English.
 XX
 CC The present sequence is that of a calcium-independent cytosolic
 CC phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release
 CC of arachidonic acid in specific tissues characterised by unique membrane
 CC phospholipids. The invention provides a process for producing such an
 CC enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence
 CC of one or more amino acid sequences selected from AAM01480-92, cPLA2/B
 CC has activity in a mixed micelle assay with 1-palmitoyl-2-[14C]-
 CC arachidonyl- phosphatidylcholine. The enzyme is useful for screening anti-
 CC -inflammatory agents mediated by the arachidonic acid cascade, for
 CC treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF
 CC field.)
 CC
 XX Sequence 752 AA:
 SQ
 Query Match 96.1%; Score 1471; DB 2; Length 752;
 Best Local Similarity 95.2%; Pred. No. 7e-156;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY "1 LODLMHSRRKPAFLIGSMRDEKRTDHLCLDGGVGGLIITQLLIAEKSGVATKD 60
 DB 397 LODLMPSRRKPAFLIGSMRDEKRIHDHLCLDGGVGGLVITQLLIAEKSGVATKD 456
 QY 61 LFDWVAGTGTGILALAILHSKSMAYMRGMYFRMKDEVFRSGRPYSGPLEEFLEKPEGE 120
 DB 457 LFDWVAGTGTGILALAILHSKSMAYMRGMYFRMKDEVFRSGRPYSGPLEEFLEKPEGE 516
 QY 121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRPNQVNLPRPAQSPDQV 180
 DB 517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRPNQVNLPRPAQSPDQV 576
 QY 181 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHEYNDLIRKGOANVKKLSIV 240
 DB 577 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHEYNDLIRKGOANVKKLSIV 636
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
 DB 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 687
 DB
 RESULT 13
 AAM13163
 ID AAM13163 standard; protein; 752 AA.
 XX
 AC AAM13163;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 20-MAY-1997 (first entry)
 XX
 DE Ca-independent phospholipase A2/B protein.
 XX
 CC Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
 KM chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
 KM heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;
 KM CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.
 XX
 OS Cricetus griseus; ovary cells.
 XX
 PN US5589170-A.
 XX
 PD 31-DEC-1996.
 XX

PF 14-APR-1995; 95US-00422106.
 XX
 PR 27-JUL-1994; 94US-00281193.
 XX
 PA (GEM) GENETICS INST INC.
 XX
 PI Tang J, Jones S;
 XX WPI: 1997-076789/07.
 DR N-PSDB; AAT59199.
 XX
 PT Compn. comprising calcium-independent phospholipase enzyme - for
 PT screening for anti-inflammatory agents.
 PS Claim 5; Col 15-22; 24pp; English.
 XX
 CC This is the amino acid sequence of the Ca-independent phospholipase A2/B
 CC from Chinese hamster ovary cells. The protein was isolated from these
 CC cells by conventional chromatographic methods e.g. DEAE anion exchange,
 CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20
 CC chromatofocusing chromatography. The purified protein has mol. wt. of 86
 CC kD and an optimum pH 6. The protein was used for amino acid sequencing
 CC from which pools of degenerate probes were synthesised. The probes were
 CC used to screen a CHO cell cDNA library in lambda ZAPIT vector. Of 40000
 CC recombinant phages screened, 12 positive plaques were isolated. One of
 CC these, designated clone 9, contained this sequence. The phospholipase
 CC gene can be inserted into eukaryotic vectors for expression in COS or CHO
 CC cells. The protein, or peptides derived from it e.g. AAM13164-76, can be
 CC used to identify phospholipase inhibitors that can be used as anti-
 CC inflammatory agents, esp. against components of the arachidonic acid
 CC cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT
 CC -2003 to standardise OS field)
 CC
 XX Sequence 752 AA:
 SQ
 Query Match 96.1%; Score 1471; DB 2; Length 752;
 Best Local Similarity 95.2%; Pred. No. 7e-156;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LODLMHSRRKPAFLIGSMRDEKRTDHLCLDGGVGGLIITQLLIAEKSGVATKD 60
 DB 397 LODLMPSRRKPAFLIGSMRDEKRIHDHLCLDGGVGGLVITQLLIAEKSGVATKD 456
 QY 61 LFDWVAGTGTGILALAILHSKSMAYMRGMYFRMKDEVFRSGRPYSGPLEEFLEKPEGE 120
 DB 457 LFDWVAGTGTGILALAILHSKSMAYMRGMYFRMKDEVFRSGRPYSGPLEEFLEKPEGE 516
 QY 121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRPNQVNLPRPAQSPDQV 180
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 QY 181 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHEYNDLIRKGOANVKKLSIV 240
 DB 577 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHEYNDLIRKGOANVKKLSIV 636
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
 DB 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 687
 DB
 RESULT 14
 AAM17849
 ID AAM17849 standard; protein; 752 AA.
 XX
 AC AAM17849;
 XX
 DT 27-AUG-2003 (revised)
 DT 07-AUG-1997 (first entry)
 XX
 DE Hamster cytosolic phospholipase A2/B.
 XX
 CC Cytosolic phospholipase A2/B; aPLA2/B; arachidonic acid cascade;
 KM inflammation; inhibitor; antiinflammatory; CHO.
 XX

XX Cricetus.
 OS Key Location/Qualifiers
 PH Active-site 465
 FT /note= "mutagenesis of Ser-465 results in loss of
 FT activity"
 XX
 XX MO9717448-A2.
 XX PD 15-MAY-1997.
 XX PF 07-NOV-1996; 96MO-US017794.
 XX PR 08-NOV-1995; 95US-00555568.
 XX (GEMT) GENETICS INST INC.
 XX PA Jones S, Tang J;
 XX PI WPI; 1997-281037/25.
 XX DR N-PSDB; AAT68827.
 XX PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 XX mammalian subject.
 XX PS Example 4; Page 33-36; 74pp; English.
 XX CC A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is
 XX CC thought to be involved in the arachidonic acid cascade. Its amino acid
 XX CC sequence was deduced from a cDNA clone (AAT68827) obtd. from a CHO-DUX
 XX CC cDNA library. The recombinant enzyme has been expressed in CHO and COS
 XX CC host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also
 XX CC been isolated. These can be used to screen for inhibitors useful as
 XX CC antiinflammatory agents that block the arachidonic acid cascade in
 XX CC mammals. (Updated on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 752 AA;
 Query Match 96.1%; Score 1471; DB 2; Length 752;
 Best Local Similarity 95.2%; Pred. No. 76-156;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LODLMHSRARKPAFLISMRDEKRTDHLCLDGGGVGLIIQLLIAIKASGVATKD 60
 DB 397 LODLMPSRARKPAFLISSMRDEKRIHDLCLDGGGVGLVLIQLLIAIKASGVATKD 456
 QY 61 LFDWVAGSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFG 120
 DB 457 LFDWVAGSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFG 516
 QY 121 HTKMTDKRKPKVMTGTLSDROPALHLFRNTDAPETVREPRNQNVLPPAPQSDQV 180
 DB 517 HTKMTDKRKPKVMTGTLSDROPALHLFRNTDAPETVREPRNQNVLPPAPQSDQV 576
 QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKQGANVKKLSIV 240
 DB 577 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKQGANVKKLSIV 636
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKGVVDDCCTDPGR 291
 DB 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKGVVDDCCTDPGR 687
 RESULT 15
 AAW81825
 ID AAW81825 standard; protein; 752 AA.
 AC AAW81825;
 XX 02-FEB-1999 (first entry)
 XX Chinese hamster calcium independent cPLA2/B protein.
 DE

XX Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening;
 KW anti-inflammatory; arachidonic acid cascade; chinese hamster.
 XX Cricetus griseus.
 XX OS US5840511-A.
 XX PN 24-NOV-1998.
 XX PD 23-OCT-1996; 96US-00735716.
 XX PF 27-JUL-1994; 94US-00281193.
 XX PR 14-APR-1995; 95US-00422106.
 XX (GEMT) GENETICS INST INC.
 XX PA Tang J, Jones S;
 XX PI WPI; 1999-034032/03.
 XX DR N-PSDB; AAW64840.
 XX PT Screening assay for phospholipase inhibitors - using specified
 XX PT phospholipase polypeptide.
 XX PS Claim 1b; Col 21-24; 24pp; English.
 XX CC This sequence represents a novel calcium independent cytosolic
 XX CC phospholipase A2/B enzyme isolated from chinese hamster ovary cells. This
 XX CC protein can be used for screening unknown compounds for anti-inflammatory
 XX CC activity mediated by the arachidonic acid cascade
 XX SQ Sequence 753 AA;
 Query Match 96.1%; Score 1471; DB 2; Length 752;
 Best Local Similarity 95.2%; Pred. No. 76-156;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LODLMHSRARKPAFLISMRDEKRTDHLCLDGGGVGLIIQLLIAIKASGVATKD 60
 DB 397 LODLMPSRARKPAFLISSMRDEKRIHDLCLDGGGVGLVLIQLLIAIKASGVATKD 456
 QY 61 LFDWVAGSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFG 120
 DB 457 LFDWVAGSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKKEFG 516
 QY 121 HTKMTDKRKPKVMTGTLSDROPALHLFRNTDAPETVREPRNQNVLPPAPQSDQV 180
 DB 517 HTKMTDKRKPKVMTGTLSDROPALHLFRNTDAPETVREPRNQNVLPPAPQSDQV 576
 QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKQGANVKKLSIV 240
 DB 577 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKQGANVKKLSIV 636
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKGVVDDCCTDPGR 291
 DB 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKGVVDDCCTDPGR 687
 Search completed: December 15, 2004, 13:08:05
 Job time : 61.1231 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 13:01:00 ; Search time 14.8871 Seconds

(without alignments)
1300.780 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLMIHSRAKRAFLIGSM.....GAKELGMVVDCTDPDGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 1531 | 100.0 | 292 | 2 | US-08-555-568B-19 |
| 2 | 1531 | 100.0 | 292 | 3 | US-09-519-223-19 |
| 3 | 1531 | 100.0 | 292 | 4 | US-09-927-180-19 |
| 4 | 1531 | 100.0 | 687 | 2 | US-08-555-568B-21 |
| 5 | 1531 | 100.0 | 687 | 2 | US-09-519-223-21 |
| 6 | 1531 | 100.0 | 687 | 4 | US-09-927-180-21 |
| 7 | 1531 | 100.0 | 688 | 2 | US-08-555-568B-23 |
| 8 | 1531 | 100.0 | 688 | 3 | US-09-519-223-23 |
| 9 | 1531 | 100.0 | 688 | 4 | US-09-927-180-23 |
| 10 | 1471 | 96.1 | 752 | 1 | US-08-281-193-2 |
| 11 | 1471 | 96.1 | 752 | 1 | US-08-422-106-2 |
| 12 | 1471 | 96.1 | 752 | 2 | US-08-735-716-2 |
| 13 | 1471 | 96.1 | 752 | 2 | US-08-555-568B-2 |
| 14 | 1471 | 96.1 | 752 | 3 | US-09-519-223-2 |
| 15 | 1471 | 96.1 | 752 | 3 | US-09-927-180-2 |
| 16 | 1471 | 96.1 | 752 | 5 | PCT-US95-08069-2 |
| 17 | 736 | 48.1 | 896 | 4 | US-09-270-767-46130 |
| 18 | 610 | 39.8 | 545 | 4 | US-09-270-767-61684 |
| 19 | 371 | 24.2 | 143 | 4 | US-09-755-630B-290 |
| 20 | 177 | 11.6 | 410 | 4 | US-09-755-630B-292 |
| 21 | 177 | 11.6 | 410 | 4 | US-09-755-630B-292 |
| 22 | 177 | 11.6 | 410 | 4 | US-09-755-274-10 |
| 23 | 177 | 11.6 | 410 | 4 | US-09-755-274-12 |
| 24 | 175 | 11.4 | 337 | 4 | US-09-755-630B-293 |
| 25 | 175 | 11.4 | 337 | 4 | US-09-755-274-13 |
| 26 | 175 | 11.4 | 410 | 2 | US-08-449-986-2 |
| 27 | 175 | 11.4 | 410 | 2 | US-08-756-855-2 |

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| 28 | 175 | 11.4 | 410 | 4 | US-09-755-630B-288 | Sequence 288, App |
| 29 | 175 | 11.4 | 410 | 4 | US-09-755-630B-291 | Sequence 291, App |
| 30 | 175 | 11.4 | 410 | 4 | US-09-755-274-8 | Sequence 8, Appl |
| 31 | 175 | 11.4 | 410 | 4 | US-09-755-274-11 | Sequence 11, Appl |
| 32 | 175 | 11.4 | 508 | 4 | US-09-755-630B-289 | Sequence 289, App |
| 33 | 175 | 11.4 | 508 | 4 | US-09-755-630B-289 | Sequence 9, Appl |
| 34 | 142.5 | 9.3 | 383 | 1 | US-07-936-163-3 | Sequence 4, Appl |
| 35 | 140 | 9.1 | 381 | 1 | US-07-936-163-3 | Sequence 3, Appl |
| 36 | 140 | 9.1 | 386 | 4 | US-09-755-630B-278 | Sequence 278, App |
| 37 | 140 | 9.1 | 386 | 4 | US-09-755-274-5 | Sequence 5, Appl |
| 38 | 139 | 9.1 | 366 | 4 | US-09-755-630B-263 | Sequence 263, App |
| 39 | 139 | 9.1 | 366 | 4 | US-09-755-274-29 | Sequence 29, Appl |
| 40 | 138 | 9.0 | 367 | 4 | US-09-755-630B-7 | Sequence 7, Appl |
| 41 | 138 | 9.0 | 367 | 4 | US-09-755-274-41 | Sequence 41, Appl |
| 42 | 138 | 9.0 | 386 | 4 | US-09-755-630B-2 | Sequence 2, Appl |
| 43 | 138 | 9.0 | 386 | 4 | US-09-755-630B-265 | Sequence 265, App |
| 44 | 138 | 9.0 | 386 | 4 | US-09-755-630B-286 | Sequence 286, App |
| 45 | 138 | 9.0 | 386 | 4 | US-09-755-274-1 | Sequence 1, Appl |

ALIGNMENTS

```
RESULT 1
US-08-555-568B-19
Sequence 19, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Genetech Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-19
Query Match 100.0%; Score 1531; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 8.5e-168;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LQDLMIHSRAKRAFLIGSMRDEKRTDHLCDGGGKGLITIQLLIAIEKSGVATKD 60
Db 1 LQDLMIHSRAKRAFLIGSMRDEKRTDHLCDGGGKGLITIQLLIAIEKSGVATKD 60
Cy 61 LFDVAVAGTGTGILLALAILHSKSMAYVRGMYFRMKDEVFRSGRPYSGLPEFLKRFGE 120
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Db 121 HTKMTDYKKPKMLGTSDRQPAELHFRNYPDAETVBPBRNQVNLPRPQSDQLY 180

QY 181 WPAARSSGAFTYFRPNGRFLDGGLLANNPTLDAMEIHEYNDLIRKGOANKYKLSIV 240

Db 181 WPAARSSGAFTYFRPNGRFLDGGLLANNPTLDAMEIHEYNDLIRKGOANKYKLSIV 240

QY 241 VSLGTRSPQVAVTCDVFRPSNPMEIATVFGAKELGKVVDDCTDPDGRP 292

Db 241 VSLGTRSPQVAVTCDVFRPSNPMEIATVFGAKELGKVVDDCTDPDGRP 292

RESULT 2

US-09-519-223-19
: Sequence 19, Application US/09519223
: Patent No. 6274140
: GENERAL INFORMATION:
: APPLICANT: Jones, Simon
: APPLICANT: Tang, Jim
: TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/519,223
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/555,568
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 292 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-519-223-19

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| Query Match | 100.0% | Score 1531 | DB 3 | length 292 |
| Best Local Similarity | 100.0% | Pred. No. 8.5e+168 | | |
| Matches 292 | Conservative | 0 | Mismatches | 0 |
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| | | | Gaps | 0 |

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| QY | 61 | LFDWAGTSTGGIILALAIHLSKSMAYMRGMVPRMKQVFRGSRPYESGPLEEFLKREFGE | 120 |
| Db | 61 | LFDWAGTSTGGIILALAIHLSKSMAYMRGMVPRMKQVFRGSRPYESGPLEEFLKREFGE | 120 |
| QY | 121 | HTKMTDVARKPKYMLTGTLSDRQPAELHLFRNYDAPEIVBPRENQNVNLRPPAQPSDOLV | 180 |
| Db | 121 | HTKMTDVARKPKYMLTGTLSDRQPAELHLFRNYDAPEIVBPRENQNVNLRPPAQPSDOLV | 180 |
| QY | 181 | WRPAASGGAAPYFFPNRGRFLDGGGLIANNPTLDAMTEIIEHYNODLIRKQGANVKKLSIV | 240 |

Db 181 WRARSSGAFFYFRPNRGLDGGILANPLDAMTEHEHQDLIRKGAANKVKLSIV 240

QY 241 VSLGSRSPQVPEVTCVDVFRPSNPWELAKTVFGAKEIGKMWVDCCTDPDGRP 292

241 VSLGSRSPQVPEVTCVDVFRPSNPWELAKTVFGAKEIGKMWVDCCTDPDGRP 292

RESULT 3

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US-09-927-180-19
: Sequence 19, Application US/09927180
: Patent No. 6645736
: GENERAL INFORMATION:
: APPLICANT: Jones, Simon
: Tang, Jim
: TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/927,180
: FILING DATE: 09-Aug-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/519,223
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 292 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

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|-----------------------|--------|-------------|--------|------------|
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| Best Local Similarity | 100.0% | Pred. No. 8 | 5e-168 | |
| Matches 292 | 0 | Mismatches | 0 | Indels 0 |
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Db 1 LODMHIISARAPAFILGSMDEKRTTHLLCLDGGVKGIIITQLLAEKSGVATKD 60
QY 61 LFDPAVGISTGGILALAILHKSMAVYRGATFRMKDVFRCGRPYESGPLEEFLKEPGE 120
Db 61 LFDPAVGISTGGILALAILHKSMAVYMGATFRMKDVFRCGRPYESGPLEEFLKEPGE 120
QY 121 HTKMTDVRKPKWMLTGTSLSDROPALHLFRYVDAPETVRBEPRQNUNLRPPAPSDOLV 180
Db 121 HTKMTDVRKPKWMLTGTSLSDROPALHLFRYVDAPETVRBEPRQNUNLRPPAPSDOLV 180
QY 181 WPAARSSGAAPTYFRPNGRFLDGGILANPFLDAMTELHEXNOOLIRKGGANVKKLSIV 240
Db 181 WPAARSSGAAPTYFRPNGRFLDGGILANPFLDAMTELHEXNOOLIRKGGANVKKLSIV 240
QY 241 VSLGTGRSFQVPEVTCUDVFRPSNPWELAKTVFGAKEIGKMYVDCCTPDGAP 292

DB 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 292

RESULT 4

US-08-555-568B-21
 ; Sequence 21, Application US/08555568B
 ; Patent No. 5976854
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 21:
 ; LENGTH: 687 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-555-568B-21

Query Match 100.0%; Score 1531; DB 2; Length 687;

Best Local Similarity 100.0%; Pred. No. 3.3e-167; Mismatches 0; Indels 0; Gaps 0;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 LFDWVAGTSGGIIAIIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
 DB 456 LFDWVAGTSGGIIAIIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
 QY 121 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVNLRPPAQPSDQV 180
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 QY 181 WRAARSSGAAPTYFRPNRGLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
 DB 576 WRAARSSGAAPTYFRPNRGLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 635
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 292
 DB 636 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 687

RESULT 5

US-09-519-223-21
 ; Sequence 21, Application US/09519223
 ; Patent No. 6274140
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon

APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/519,223
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 21:
 ; LENGTH: 687 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-519-223-21

Query Match 100.0%; Score 1531; DB 3; Length 687;

Best Local Similarity 100.0%; Pred. No. 3.3e-167; Mismatches 0; Indels 0; Gaps 0;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 396 LQDLMIISRAKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 455
 QY 61 LFDWVAGTSGGIIAIIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
 DB 456 LFDWVAGTSGGIIAIIHLSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
 QY 121 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVNLRPPAQPSDQV 180
 DB 516 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVNLRPPAQPSDQV 575
 QY 181 WRAARSSGAAPTYFRPNRGLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
 DB 576 WRAARSSGAAPTYFRPNRGLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 635
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 292
 DB 636 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 687

RESULT 6

US-09-927-180-21
 ; Sequence 21, Application US/09927180
 ; Patent No. 6645736
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 1531; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMIISARKKPAFLIGSMRDEKRTDHLCLDGGVGLIIQLLIAIEKASGVATKD 60
DB 396 LQDLMIISARKKPAFLIGSMRDEKRTDHLCLDGGVGLIIQLLIAIEKASGVATKD 456
QY 61 LFPWVAGTSTGGILALAIILHSKSMAYRMGYFRMKDEVFRGSRPYSGPLEEFLKEEFG 120
DB 456 LFPWVAGTSTGGILALAIILHSKSMAYRMGYFRMKDEVFRGSRPYSGPLEEFLKEEFG 516
QY 121 HTKMTVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPPAPQSDQV 180
DB 516 HTKMTVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPPAPQSDQV 576
QY 181 WRARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
DB 576 WRARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 636
QY 241 VSLGTGRSPQVPYTCVDVFRPSPNWEIATVFGAKELGKMYVDCCTDPDGRP 292
DB 636 VSLGTGRSPQVPYTCVDVFRPSPNWEIATVFGAKELGKMYVDCCTDPDGRP 687

RESULT 7
US-08-555-568B-23
Sequence 23, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-23

Query Match 100.0%; Score 1531; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMIISARKKPAFLIGSMRDEKRTDHLCLDGGVGLIIQLLIAIEKASGVATKD 60
DB 397 LQDLMIISARKKPAFLIGSMRDEKRTDHLCLDGGVGLIIQLLIAIEKASGVATKD 456
QY 61 LFPWVAGTSTGGILALAIILHSKSMAYRMGYFRMKDEVFRGSRPYSGPLEEFLKEEFG 120
DB 457 LFPWVAGTSTGGILALAIILHSKSMAYRMGYFRMKDEVFRGSRPYSGPLEEFLKEEFG 516
QY 121 HTKMTVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPPAPQSDQV 180
DB 517 HTKMTVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPPAPQSDQV 576
QY 181 WRARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
DB 577 WRARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 636
QY 241 VSLGTGRSPQVPYTCVDVFRPSPNWEIATVFGAKELGKMYVDCCTDPDGRP 292
DB 637 VSLGTGRSPQVPYTCVDVFRPSPNWEIATVFGAKELGKMYVDCCTDPDGRP 688

RESULT 8
US-09-519-223-23
Sequence 23, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-519-223-23

Query Match 100.0%; Score 1531; DB 3; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 60
DB 397 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 456
QY 61 LFDWVAGTSGGILALAILHSKSMAYVRGVPFRMKDEVFRGSRPYESGPLEEFKKEFG 120
DB 457 LFDWVAGTSGGILALAILHSKSMAYVRGVPFRMKDEVFRGSRPYESGPLEEFKKEFG 516
QY 121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVREPRNQVNLPRPAQPSDOLV 180
DB 517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVREPRNQVNLPRPAQPSDOLV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 636
QY 241 VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVEGAKELGKVVVDCCTDPDGRP 292
DB 637 VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVEGAKELGKVVVDCCTDPDGRP 688

RESULT 9
US-09-927-180-23
Sequence 23, Application US/09927180
Patent No. 6645736
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 1531; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 60
DB 397 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 456
QY 61 LFDWVAGTSGGILALAILHSKSMAYVRGVPFRMKDEVFRGSRPYESGPLEEFKKEFG 120
DB 457 LFDWVAGTSGGILALAILHSKSMAYVRGVPFRMKDEVFRGSRPYESGPLEEFKKEFG 516
QY 121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVREPRNQVNLPRPAQPSDOLV 180
DB 517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVREPRNQVNLPRPAQPSDOLV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 636
QY 241 VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVEGAKELGKVVVDCCTDPDGRP 292
DB 637 VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVEGAKELGKVVVDCCTDPDGRP 688

RESULT 10
US-08-281-193-2
Sequence 2, Application US/08281193
Patent No. 546595
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-281-193-2

Query Match 96.1%; Score 1471; DB 1; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 60
DB 397 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 456
QY 61 LFDWVAGTSGGILALAILHSKSMAYVRGVPFRMKDEVFRGSRPYESGPLEEFKKEFG 120
DB 457 LFDWVAGTSGGILALAILHSKSMAYVRGVPFRMKDEVFRGSRPYESGPLEEFKKEFG 516

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QY      121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVREPRNQVNLPRPAQPSDQV 180
      517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVIRPRNQVNLPRPAQPSDQV 576
DB
QY      181 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 240
DB      577 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 636
QY      241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKXNVDDCTDPDGR 291
DB      637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKXNVDDCTDPDGR 687

RESULT 11
US-08-422-106-2
; Sequence 2, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-422-106-2

Query Match      96.1%; Score 1471; DB 1; Length 752;
Best Local Similarity 95.2%; Pred. No. 3,1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY      1 LODLMIISRRKRAFLIGSRDEKRTDHLCLDGGGVKGLIITQLLIAIEKSGVATKD 60
DB      397 LODLMIISRRKRAFLIGSRDEKRTDHLCLDGGGVKGLIITQLLIAIEKSGVATKD 456
QY      61 LFDWVAGSTGGILALAILHSKSMAYRWGYFRMKDEVRGSRPYESGPLEEFKKEFG 120
DB      457 LFDWVAGSTGGILALAILHSKSMAYRWGYFRMKDEVRGSRPYESGPLEEFKKEFG 516
QY      121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVREPRNQVNLPRPAQPSDQV 180
DB      517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVIRPRNQVNLPRPAQPSDQV 576
QY      181 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 240
DB      577 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 636
QY      241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKXNVDDCTDPDGR 291
DB      637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKXNVDDCTDPDGR 687

RESULT 12
US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:

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; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

Query Match      96.1%; Score 1471; DB 2; Length 752;
Best Local Similarity 95.2%; Pred. No. 3,1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY      1 LODLMIISRRKRAFLIGSRDEKRTDHLCLDGGGVKGLIITQLLIAIEKSGVATKD 60
DB      397 LODLMIISRRKRAFLIGSRDEKRTDHLCLDGGGVKGLIITQLLIAIEKSGVATKD 456
QY      61 LFDWVAGSTGGILALAILHSKSMAYRWGYFRMKDEVRGSRPYESGPLEEFKKEFG 120
DB      457 LFDWVAGSTGGILALAILHSKSMAYRWGYFRMKDEVRGSRPYESGPLEEFKKEFG 516
QY      121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVREPRNQVNLPRPAQPSDQV 180
DB      517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPEVIRPRNQVNLPRPAQPSDQV 576
QY      181 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 240
DB      577 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 636
QY      241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKXNVDDCTDPDGR 291
DB      637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKXNVDDCTDPDGR 687

RESULT 13
US-08-555-568B-2
; Sequence 2, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-2

Query Match 96.1%; Score 1471; DB 2; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLMHSRARKPAFLIGSMRDEKRTDHLCLDGGGVGLIIQLLAIERKASGVATKD 60
DB 397 LODLMHSRARKPAFLIGSMRDEKRTDHLCLDGGGVGLIIQLLAIERKASGVATKD 456
QY 61 LFDWVAGSTGGILALAIHLSKSMAYMRGVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
DB 457 LFDWVAGSTGGILALAIHLSKSMAYMRGVFRMKDEVFRGSRPYESGPLEEFLKREFGE 516
QY 121 HTKMTDVKKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLRRPAQPSDQV 180
DB 517 HTKMTDVKKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLRRPAQPSDQV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKKLSTV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKKLSTV 636
QY 241 VSLGTRSPQVPTCVDFRPSNPWEIATVFGAKELGKRVVDCCTDPDGR 291
DB 637 VSLGTRSPQVPTCVDFRPSNPWEIATVFGAKELGKRVVDCCTDPDGR 687

RESULT 14
US-09-519-223-2
Sequence 2, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-519-223-2

Query Match 96.1%; Score 1471; DB 3; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLMHSRARKPAFLIGSMRDEKRTDHLCLDGGGVGLIIQLLAIERKASGVATKD 60
DB 397 LODLMHSRARKPAFLIGSMRDEKRTDHLCLDGGGVGLIIQLLAIERKASGVATKD 456
QY 61 LFDWVAGSTGGILALAIHLSKSMAYMRGVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
DB 457 LFDWVAGSTGGILALAIHLSKSMAYMRGVFRMKDEVFRGSRPYESGPLEEFLKREFGE 516
QY 121 HTKMTDVKKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLRRPAQPSDQV 180
DB 517 HTKMTDVKKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLRRPAQPSDQV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKKLSTV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKKLSTV 636
QY 241 VSLGTRSPQVPTCVDFRPSNPWEIATVFGAKELGKRVVDCCTDPDGR 291
DB 637 VSLGTRSPQVPTCVDFRPSNPWEIATVFGAKELGKRVVDCCTDPDGR 687

RESULT 15
US-09-927-180-2
Sequence 2, Application US/09927180
Patent No. 6645736
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

Query Match 96.1%; Score 1471; DB 4; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

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QY 1 LODLMHISRARKPAFILGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 397 LODLMFISRRARKPAFILSSMRDEKRIHDHLCLDGGGVKGLVLIQLLIAIEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAIHSKSMAYRMGYFRMKDEVFRGSRPYESGPLKEEFLKREFGE 120
DB 457 LFDWVAGTSTGGILALAIHSKSMAYRMGYFRMKDEVFRGSRPYESGPLKEEFLKREFGE 516
QY 121 HTKMTDVRKPKWMLTGTLSRQPAELHLPNNYDAPETVRPPRPNQVNLRPAPQPSDQLV 180
DB 517 HTKMTDVRKPKWMLTGTLSRQPAELHLPNNYDAPEVIREPRPNQVNLKPPQPADQLV 576
QY 181 WRAARSSGAAPTVERPNGRFLDGGLLANNPTLDAMTEIHEYNODLIRKGOANKVKKLSIV 240
DB 577 WRAARSSGAAPTVERPNGRFLDGGLLANNPTLDAMTEIHEYNODMIRKGOANKVKKLSIV 636
QY 241 VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVFGAKELGKKNVVDCTDPDGR 291
DB 637 VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVFGAKELGKKNVVDCTDPDGR 687
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Search completed: December 15, 2004, 13:15:33
Job time : 16.8871 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 13:13:21 : Search time 51.2542 Seconds
(Without alignments)
2034.879 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LODMHISARKRPFILGSM.....GATELGKVVDCCTDDGR 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues
Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
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16: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
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20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|------------------------------|-------------------|
| 1 | 1531 | 100.0 | 292 9 US-09-927-180-19 | Sequence 19, Appl |
| 2 | 1531 | 100.0 | 687 9 US-09-927-180-21 | Sequence 21, Appl |
| 3 | 1531 | 100.0 | 688 9 US-09-927-180-23 | Sequence 23, Appl |
| 4 | 1524 | 99.5 | 667 15 US-10-108-260A-3778 | Sequence 3778, Ap |
| 5 | 1471 | 96.1 | 752 9 US-09-927-180-2 | Sequence 2, Appl1 |
| 6 | 456.5 | 29.8 | 1071 14 US-10-369-493-6865 | Sequence 6865, Ap |
| 7 | 419 | 27.4 | 1023 14 US-10-369-493-6689 | Sequence 6689, Ap |
| 8 | 419 | 27.4 | 1023 14 US-10-369-493-6680 | Sequence 6680, Ap |
| 9 | 261 | 17.0 | 468 14 US-10-369-493-4998 | Sequence 4998, Ap |
| 10 | 245 | 16.0 | 1053 17 US-10-425-115-196524 | Sequence 196524, |
| 11 | 235 | 15.3 | 1254 16 US-10-437-963-169583 | Sequence 169583, |
| 12 | 234 | 15.3 | 387 15 US-10-421-654-66 | Sequence 66, Appl |
| 13 | 211.5 | 13.8 | 370 9 US-09-925-300-1483 | Sequence 1483, Ap |

| | | | | |
|----|-------|------|-----------------------------|-------------------|
| 14 | 208.5 | 13.6 | 350 15 US-10-421-654-100 | Sequence 100, App |
| 15 | 204.5 | 13.4 | 577 14 US-10-310-154-616 | Sequence 616, App |
| 16 | 201 | 13.1 | 325 15 US-10-424-599-259117 | Sequence 259117, |
| 17 | 201 | 13.1 | 382 14 US-10-310-154-615 | Sequence 615, App |
| 18 | 195.5 | 12.8 | 382 15 US-10-424-599-258423 | Sequence 258423, |
| 19 | 193.5 | 12.6 | 387 16 US-10-437-963-177823 | Sequence 177823, |
| 20 | 190 | 12.4 | 378 15 US-10-421-654-18 | Sequence 18, Appl |
| 21 | 178 | 11.6 | 435 17 US-10-425-115-343159 | Sequence 343159 |
| 22 | 177 | 11.6 | 410 10 US-09-755-630A-290 | Sequence 290, App |
| 23 | 177 | 11.6 | 410 10 US-09-755-630A-292 | Sequence 292, App |
| 24 | 177 | 11.6 | 410 10 US-10-658-180-290 | Sequence 290, App |
| 25 | 177 | 11.6 | 410 17 US-10-658-180-292 | Sequence 292, App |
| 26 | 177 | 11.6 | 434 15 US-10-425-114-39447 | Sequence 39447, A |
| 27 | 177 | 11.6 | 437 15 US-10-425-114-39376 | Sequence 39376, A |
| 28 | 177 | 11.6 | 437 15 US-10-425-114-39375 | Sequence 39375, A |
| 29 | 177 | 11.6 | 441 15 US-10-425-114-57061 | Sequence 57061, A |
| 30 | 177 | 11.6 | 442 16 US-10-437-963-138254 | Sequence 138254, |
| 31 | 176 | 11.5 | 423 17 US-10-425-115-282153 | Sequence 282153, |
| 32 | 176 | 11.5 | 438 15 US-10-425-114-72032 | Sequence 72032, A |
| 33 | 176 | 11.5 | 438 15 US-10-425-114-72035 | Sequence 72035, A |
| 34 | 176 | 11.5 | 448 15 US-10-425-114-65072 | Sequence 65072, A |
| 35 | 175 | 11.4 | 337 10 US-09-755-630A-293 | Sequence 293, App |
| 36 | 175 | 11.4 | 337 17 US-10-658-180-293 | Sequence 293, App |
| 37 | 175 | 11.4 | 410 10 US-09-755-630A-288 | Sequence 288, App |
| 38 | 175 | 11.4 | 410 10 US-09-755-630A-291 | Sequence 288, App |
| 39 | 175 | 11.4 | 410 17 US-10-658-180-288 | Sequence 288, App |
| 40 | 175 | 11.4 | 410 17 US-10-658-180-291 | Sequence 291, App |
| 41 | 175 | 11.4 | 436 15 US-10-425-114-39450 | Sequence 39450, A |
| 42 | 175 | 11.4 | 436 15 US-10-425-114-47374 | Sequence 47374, A |
| 43 | 175 | 11.4 | 508 10 US-09-755-630A-289 | Sequence 289, App |
| 44 | 175 | 11.4 | 508 17 US-10-658-180-289 | Sequence 289, App |
| 45 | 174.5 | 11.4 | 405 16 US-10-437-963-129647 | Sequence 129647, |

ALIGNMENTS

RESULT 1
US-09-927-180-19
Sequence 19, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match 100.0%; Score 1531; DB 9; Length 292;
Best Local Similarity 100.0%; Pred. No. 4,2e-152;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMIISRRARPAFLIGSMRDEKRTDHLCLDGGVKGKLIITQLLIAIEKASGVATKD 60
DB 1 LODLMIISRRARPAFLIGSMRDEKRTDHLCLDGGVKGKLIITQLLIAIEKASGVATKD 60
QY 61 LFDWVAGTGTGGILALAIHLSKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKKEPGE 120
DB 61 LFDWVAGTGTGGILALAIHLSKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKKEPGE 120
QY 121 HTKMTVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 180
DB 121 HTKMTVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 180
QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDDCTDPDGRP 292
DB 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDDCTDPDGRP 292

RESULT 2

US-09-927-180-21
Sequence 21, Application US/09927180
Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-927-180-21

Query Match 100.0%; Score 1531; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMIISRRARPAFLIGSMRDEKRTDHLCLDGGVKGKLIITQLLIAIEKASGVATKD 60
DB 396 LODLMIISRRARPAFLIGSMRDEKRTDHLCLDGGVKGKLIITQLLIAIEKASGVATKD 455
QY 61 LFDWVAGTGTGGILALAIHLSKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKKEPGE 120
DB 456 LFDWVAGTGTGGILALAIHLSKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKKEPGE 515
QY 121 HTKMTVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 180
DB 516 HTKMTVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 575
QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 576 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 635
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDDCTDPDGRP 292
DB 636 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDDCTDPDGRP 687

RESULT 3

US-09-927-180-23
Sequence 23, Application US/09927180
Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-927-180-23

Query Match 100.0%; Score 1531; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LODLMHSRARKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 60
      397 LODLMHSRARKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 456
      61 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 120
      457 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 516
      121 HTKMTDVRRKRWMLTGLSDROPALHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180
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      181 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
      577 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 636
      241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 292
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RESULT 4
US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108, 260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

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Query Match          99.5%; Score 1524; DB 15; Length 667;
Best Local Similarity 100.0%; Pred. No. 7,7e-151;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      372 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 431
      121 HTKMTDVRRKRWMLTGLSDROPALHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180
      432 HTKMTDVRRKRWMLTGLSDROPALHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 491
      181 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
      492 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 551
      241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 291
      552 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 602

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RESULT 5
US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
;          Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

```

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; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

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Query Match          96.1%; Score 1471; DB 9; Length 752;
Best Local Similarity 95.2%; Pred. No. 3,5e-145;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

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QY      1 LODLMHSRARKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 60
      397 LODLMHSRARKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 456
      61 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 120
      457 LFDWVAGTSTGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 516
      121 HTKMTDVRRKRWMLTGLSDROPALHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180
      517 HTKMTDVRRKRWMLTGLSDROPALHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 576
      181 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
      577 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 636
      241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 291
      637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKNVVDCCCTDPDGR 687

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RESULT 6
US-10-369-493-6865
; Sequence 6865, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

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; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6865
 ; LENGTH: 1071
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-6665

Query Match 29.8%; Score 456.5; DB 14; Length 1071;
 Best Local Similarity 34.5%; Pred. No. 3,2e-38;
 Matches 102; Conservative 62; Mismatches 97; Indels 35; Gaps 8;

QY 1 LQDLNHSRARKAFPLGSRDEKTHDHLCLDGGGVKGLIIQLIAIEKASGVATKD 60
 DB 730 IQDTLDSGRGKAKY-----NLISMDGGGIRGLVLIQLIAIEKSLDDIFK 777
 QY 61 LEPVWAGTSGILALALHSHKSMAYRWGYFPMKDEVFRG-SRPYSGPLEEFLKREFG 119
 DB 778 YFDWMSGTSGSLIMGLATGKSLREMQOTYLLKQRFVGIMPPYDVQLKFIQDFG 837
 QY 120 EHTKMTDVKKPKMLTGTSLDROPAELHLFRNYDAETVAREPRFNQVNLPPAQSDDL 179
 DB 838 TGT-VWEIPYPLMIAVNSEKLVRLEMAKNYKPAKDV-----ABETPKEMP 864
 QY 180 VWRPAASSGAAPYFPRPN-GRFLDGLLANNPTLDANTEIHEYNODLIRKQANKYKLS 238
 DB 885 LMMALRRSTRAPVLFEPSEERYIDGGIISNNPALDMSVHAYNRELQSLGRSDAVQNM 944
 QY 239 IVVSLGTGRSPQVPTCVDFR--PSNPWEAKTVFGAKELGKVVDCCTDPDGRP 292
 DB 945 VLVSFGTG--QPSVTFIEFLSIDSNSPLQSIKTI---KYLAMFIDQATASEGAP 994

RESULT 7
 US-10-369-493-6689
 ; Sequence 6689, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6689
 ; LENGTH: 1023
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-6689

Query Match 27.4%; Score 419; DB 14; Length 1023;
 Best Local Similarity 33.9%; Pred. No. 2.6e-34;
 Matches 95; Conservative 61; Mismatches 110; Indels 14; Gaps 7;
 QY 17 LQSMREKRTHD--HLCLDGGGVKGLIIQLIAIEKASGVATKDLFPMVAGTSGIL 74
 DB 678 LKEIVKKTISNVINVLGDDGGIRGLVYQMLICAEALDRPLIDYFWMIGATSTGCIY 737
 QY 75 ALALHSHKSMAYRWGYFPMKDEVFRG-SRPYSGPLEEFLKREFGHTMTDVRRPKYM 133
 DB 738 MSMTMTGGSLRKQRYLMLFKDQLFDSWTRPYDTKLTLEFIQAFGADRLMGDIKYPREF 797
 QY 134 LTGTLSDROPAELHLFRNYDAETVAREPRFNQVNLPPAQSDDLWMAASSGAAPY 193

DB 798 CTIVRADTPEPVQLELRLNRLPISEKE---NNDLGF--TDPELTIWATRTRSSAAPT 851
 QY 194 FRPN-GRFLDGLLANNPTLDANTEIHEYNODLIRKQANKYKLSIVSLGTGRSPQV 252
 DB 852 FSASEKFLIDGMSISNNPVLDMSDIGFNTTCQKRIEKKVMDCMCVSLVGIGIPICP 911
 QY 253 VTCVDVFRPSNPWEAKTVFGAKELGKVVDCCTDPDGRP 292
 DB 912 VD-PSVFEWMDLFGMLR---GKKNLSLVVIDQATATEGAP 947

RESULT 8
 US-10-369-493-6690
 ; Sequence 6690, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6690
 ; LENGTH: 1023
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-6690

Query Match 27.4%; Score 419; DB 14; Length 1023;
 Best Local Similarity 33.9%; Pred. No. 2.6e-34;
 Matches 95; Conservative 61; Mismatches 110; Indels 14; Gaps 7;
 QY 17 LQSMREKRTHD--HLCLDGGGVKGLIIQLIAIEKASGVATKDLFPMVAGTSGIL 74
 DB 678 LKEIVKKTISNVINVLGDDGGIRGLVYQMLICAEALDRPLIDYFWMIGATSTGCIY 737
 QY 75 ALALHSHKSMAYRWGYFPMKDEVFRG-SRPYSGPLEEFLKREFGHTMTDVRRPKYM 133
 DB 738 MSMTMTGGSLRKQRYLMLFKDQLFDSWTRPYDTKLTLEFIQAFGADRLMGDIKYPREF 797
 QY 134 LTGTLSDROPAELHLFRNYDAETVAREPRFNQVNLPPAQSDDLWMAASSGAAPY 193
 DB 798 CTIVRADTPEPVQLELRLNRLPISEKE---NNDLGF--TDPELTIWATRTRSSAAPT 851
 QY 194 FRPN-GRFLDGLLANNPTLDANTEIHEYNODLIRKQANKYKLSIVSLGTGRSPQV 252
 DB 852 FSASEKFLIDGMSISNNPVLDMSDIGFNTTCQKRIEKKVMDCMCVSLVGIGIPICP 911
 QY 253 VTCVDVFRPSNPWEAKTVFGAKELGKVVDCCTDPDGRP 292
 DB 912 VD-PSVFEWMDLFGMLR---GKKNLSLVVIDQATATEGAP 947

RESULT 9
 US-10-369-493-4998
 ; Sequence 4998, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 4998
 ; LENGTH: 1023
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-4998

FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 4998
 LENGTH: 468
 TYPE: PRT
 ORGANISM: Caenorhabditis elegans
 US-10-369-493-4998

Query Match 17.0%; Score 261; DB 14; Length 468;
 Best Local Similarity 29.8%; Pred. No. 3.5e-18;
 Matches 78; Conservative 54; Mismatches 100; Indels 30; Gaps 10;

16 ILGSMDEKRTKTHD-LLCLDGGGVKGLIIQLIAIEKASGVATKDLFDWVAGTSTGGL 74
 180 VLASEKQWPEBEVILLADGGIRAVITQMLIHIDYLLGKLVKLDIDAGTSCGVI 239
 QY 75 ALAI-LHKSMAVMRGVFRMKDEV-RGSR--PYSSGLEFLKREF--GEHTKTTDV 127
 DB 240 TLLSTNNRIEETRKLLDMRDVRVFTGADKAVPKYSSNGMEYIAHVTTWEDSKMSI 299
 QY 128 RKPWMLTGLSDROPALHLFRNY--DABETVREP-RFQNVNLRPPAQSDQLVRAA 184
 DB 300 KRRRAVTVADTMVFPQILLFRSYRPEMBEACEHYK-----LDPTVYELMKTL 350
 QY 185 RSSGAAPYFRPGRFLDGLANPTLDMTEIHEYNODLIRKQANKYK-----K 236
 DB 351 RCTTAAPYFESFNGLSGGLINNPFLALISDFPLTK--LKSFSKSSSERENGNWK 408
 QY 237 LSTIVSLGTRSPQVPTCDV 258
 DB 409 IGCVISLGTGVFPEKIDGL 430

RESULT 10
 US-10-425-115-196524
 Sequence 196524, Application US/10425115
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO 196524
 LENGTH: 1053
 TYPE: PRT
 ORGANISM: Zea mays
 NAME/KEY: unsure
 LOCATION: (1).(1053)
 OTHER INFORMATION: unsure at all Xaa locations
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_110814C.1.pep
 US-10-425-115-196524

Query Match 16.0%; Score 245; DB 17; Length 1053;
 Best Local Similarity 25.7%; Pred. No. 5.5e-16;
 Matches 86; Conservative 46; Mismatches 98; Indels 104; Gaps 12;
 QY 1 LODM-----HISRAKPAFIIIGSMDEKRTHD-----HLCLDGGGVKGLI 42
 DB 220 LRDLRLRLTISQRRVSAARALAILGENENLRRAIRGRPAVKGLRIILSMGGGMKGLA 279
 QY 43 IIOILIAIEKASGVATKDLFDWVAGTSTGILALAI-LHKSMAVMRGVFRM----- 94

DB 280 TVQMLKIQIGSGKRIHEMFDLICGTSTGMLAMALGIQMTLDQCEBIYTKGLVPAE 339
 QY 95 ---KDR-----VFRGSRPIYSSGLEELK-----EFGEHTKMTD 126
 DB 340 PIPKDEAATWKEKIDQLFRSSSQSFVVVHGK--HSADQFERLLKMKCADEDDLLIESA 398
 QY 127 VRK-PRVMLTGLSDROPALHLFRNYDAPEYREPRFQNVNLRPPAQSDQL----- 179
 DB 399 VKGIRKVPVSTLVSVMPAQPIFRNYQYPPGTL-----VSGMAESPSISALGTA 450
 QY 180 -----VWRARSSGAAPTYR-----PNGRFLDGLANPTLDM 215
 DB 451 VSGAPVIGKGAFMGSCKRIVWEALIASAAPYLLDPSVDANRWQDGAIVANNPTIPAI 510
 QY 216 TEIHEYNODLIRKQANKYKLSIVSLGTGNSP 249
 DB 511 RBAQLMPD-----TRIDCLVISIGGSVP 534

RESULT 11
 US-10-437-963-169583
 Sequence 169583, Application US/10437963
 Publication No. US20040123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 169583
 LENGTH: 1254
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_67990C.1.pep
 US-10-437-963-169583

Query Match 15.3%; Score 235; DB 16; Length 1254;
 Best Local Similarity 25.9%; Pred. No. 8.1e-15;
 Matches 89; Conservative 48; Mismatches 101; Indels 106; Gaps 15;
 QY 1 LODM-----HISRAKPAF-IIGSMDEKRTHD-----HLCLDGGGVKGL 41
 DB 487 LRDLRLRLTISQRRVSAARALAILGENENLRRAIRGRPAVKGLRIILSMGGGMKGL 546
 QY 42 IIOILIAIEKASGVATKDLFDWVAGTSTGILALAI-LHKSMAVMRGVFRM----- 94
 DB 547 ATVOILKQIBQGGKRIHEMFDLICGTSTGMLAMALGVKQMTLDQCEBIYTKGLVPA 606
 QY 95 ---KDE-----VFRGSRPIYSSGLEELK-----EFGEHTKMTD 125
 DB 607 EPAFKDEAATWKEKIDQLFRSSSQSFVVVHGK--HSADQFERLLKMKCADEDDLLIES 665
 QY 126 DVAK-PRVMLTGLSDROPALHLFRNYDAPEYR-----PRFQNVN 168
 DB 666 AVGIRKVPVSTLVSVMPAQPIFRNYQYPPGTVSVSVMTESPSISAGTIPVSGAPVG 725
 QY 169 LRP-----PAQP-----SDQLVWRARSSGAAPTY-----FRPN-GRFLDGG 205
 DB 726 IKPINTVGAVSAPVIGIRGAFMGSCKRIVWEALIASAAPYLLDPSVDANRWQDGA 785
 QY 206 LANNPTLDMTEIHEYNODLIRKQANKYKLSIVSLGTGNSP 249

DB 786 VANNPTFAIREAQLMMPD-----TRIDLVSIGGSGVP 819

RESULT 12

US-10-421-654-66

Sequence 66, Application US/10421654
Publication No. US20040005604A1

GENERAL INFORMATION:

APPLICANT: Gramatikova, Svetlana

APPLICANT: Hazlewood, Geoff

APPLICANT: Lam, David B.

APPLICANT: Barton, Nelson R.

TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND

FILE REFERENCE: 09010-094001

CURRENT APPLICATION NUMBER: US/10/421,654

CURRENT FILING DATE: 2003-04-21

PRIOR FILING DATE: 2002-04-19

NUMBER OF SEQ ID NOS: 106

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 66

LENGTH: 387

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Obtained from an environmental sample

US-10-421-654-66

Query Match 15.3%; Score 234; DB 15; Length 387;

Best Local Similarity 27.8%; Pred. No. 1,8e-15;

Matches 89; Conservative 39; Mismatches 112; Indels 80; Gaps 13;

DB 30 LCLDGGVKGIIITOLLAIE-----KASGVA TKOLFVAVAGTSGGIALAIHS 81

DB 17 ILACDGGGILGLSVLEILAKIEADLTAKGDKONFVLADYFVCGTSTGATIAACTSSG 76

QY 82 KSNVAVRGVYFRMKDEVF-----RGSREYSGPLSEFLKREGEHTKQTDVRRKVM 134

DB 77 MSMAKIRQFLDGGKMFDAASLLKRLQVSYDDEPLARQLRAAFDQLKETAAGSAHL 136

QY 135 TGLSLRQPAELHLPYNY--DAPETRE--PRFN---QNVNLRPPAGSDQLVRRAR 185

DB 137 KTL-----WVVMNHSTDSPPVSNPNYAKYNNIARDCNLNP-----LWQLVR 182

QY 186 SSGAATFYRP-----NGRFLDGGLLA--NNPTLDAMTEIHEYNQDLIRKGA 231

DB 183 ASTAATFYRPPEYITRADGTPREYNYIFVDGVTYNNPAYLAFLAATAKPYALNPTGS 242

QY 232 NKVKLSIVSLGTGRSPQV--PVTQVD-----VFRSPNPELAKTVFGA- 274

DB 243 NQL-----LIVSVGTGSAANVRPMLDVMNLIHFAKNIPALMNAASAGDMTCRYLGGC 298

QY 275 -----KELGKRVVDCCTD 287

DB 299 RHGMLDRSFGDMVMPASRD 318

US-09-925-300-1483

Sequence 1483, Application US/09925300

GENERAL INFORMATION:

APPLICANT: Craig Rozen,

APPLICANT: Steve Ruben

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05988

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

US-10-421-654-100

Query Match 13.6%; Score 208.5; DB 15; Length 350;

Best Local Similarity 28.0%; Pred. No. 7,5e-13;

Matches 76; Conservative 29; Mismatches 65; Indels 101; Gaps 13;

DB 30 LCLDGGVKGIIITOLLAIEK--ASGVA TKOLFVAVAGTSGGIALA--LAILHSKMA 86

DB 6 ILISDGGIRGIIIPALIVELAKRLEGDLHKAFLMIACTSGIIMAGLTCRHP----- 60

QY 87 MEGWYFRMKDE-----VFRSGRPSGSP-----LEEF 113

DB 61 -----DDEEAACTPTDLKLYVDHGKLFKKPIGLINPGLANDPRYQDELNR 112

QY 114 LKREGEHTKMTDVRRPKMLTGLSDRQPAELHLPFRNDAPETVREPRFNQNVNLRPPA 173

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1483

LENGTH: 370

TYPE: PRT

ORGANISM: Homo sapiens

US-09-925-300-1483

Query Match 13.8%; Score 211.5; DB 9; Length 370;

Best Local Similarity 28.5%; Pred. No. 3,9e-13;

Matches 72; Conservative 33; Mismatches 107; Indels 41; Gaps 8;

QY 16 ILGSKDEKRTDHLCLDGGVKGIIITOLLAIEKASGVA TKOLFVAVAGTSGGIALA 75

DB 18 LIGYVDPVKGRIIRISIDGGGTRGVVALQTRKVELTQKRVHQFLFDYICGVTGATIA 77

QY 76 LAI--LHSKMAVYRGVYFRMKDEVF-----GSRPYSGPLSEFLKREGEHT 122

DB 78 FMGLFHPMLDCEBELYRKLSGVDSQVNYVGTVMKMSHAFYDSQTWENILKDRKGSAL 137

QY 123 KMTDVK--PKVMTGLTSDRQ--PAELHLPFRNYDAPETVREPRFNQNVNLRPPAQPSDQ 178

DB 138 MIETANPTCPKVAANSTIVNGITPKAFVFNNG-----HPPGINSY-----LGGCY 187

QY 179 LVWRAARSSGAAPTYRP---NGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANV 234

DB 188 KMWQAIRASSAABGYEAYALGNDLHQDGGLLNNPSALAMHECKCLMPDV----- 238

QY 235 KKLIVSVSLGTGR 247

DB 239 -PLECTIVSLGTGR 250

US-10-421-654-100

Sequence 100, Application US/10421654

Publication No. US20040005604A1

GENERAL INFORMATION:

APPLICANT: Gramatikova, Svetlana

APPLICANT: Hazlewood, Geoff

APPLICANT: Lam, David B.

APPLICANT: Barton, Nelson R.

TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND

FILE REFERENCE: 09010-094001

CURRENT APPLICATION NUMBER: US/10/421,654

CURRENT FILING DATE: 2003-04-21

PRIOR APPLICATION NUMBER: US 60/374,313

PRIOR FILING DATE: 2002-04-19

NUMBER OF SEQ ID NOS: 106

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 100

LENGTH: 350

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Obtained from an environmental sample

US-10-421-654-100

Query Match 13.6%; Score 208.5; DB 15; Length 350;

Best Local Similarity 28.0%; Pred. No. 7,5e-13;

Matches 76; Conservative 29; Mismatches 65; Indels 101; Gaps 13;

DB 30 LCLDGGVKGIIITOLLAIEK--ASGVA TKOLFVAVAGTSGGIALA--LAILHSKMA 86

DB 6 ILISDGGIRGIIIPALIVELAKRLEGDLHKAFLMIACTSGIIMAGLTCRHP----- 60

QY 87 MEGWYFRMKDE-----VFRSGRPSGSP-----LEEF 113

DB 61 -----DDEEAACTPTDLKLYVDHGKLFKKPIGLINPGLANDPRYQDELNR 112

QY 114 LKREGEHTKMTDVRRPKMLTGLSDRQPAELHLPFRNDAPETVREPRFNQNVNLRPPA 173

Db 113 LKAQIG-LTATLBDKGLTKVLITA--YDIQOQALFMANTD-----NENSNFR--- 156
 Qy 174 QPSDQLVWRARSSGAAPTYFRP-----NGRF---LGGCLANNPTLDAMTEIH 219
 Db 157 -----YMEARARATSAAPTYFRPALIERVEKXNDKRFVPLIDGVFANDPILAAAYEAR 210
 Qy 220 EY---NODLIRKGOANKVKLSIVSLGTGR 247
 Db 211 KKKKGNDEL-----VFLSLGTGQ 228

RESULT 15

US-10-310-154-616
 ; Sequence 616, Application US/10310154
 ; Publication No. US20030233670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; APPLICANT: Chomet, Paul S.
 ; APPLICANT: Adams, Thomas H
 ; APPLICANT: Ruff, Thomas G.
 ; APPLICANT: Agarwal, Ameeta K.
 ; APPLICANT: Ahrens, Jeffrey E.
 ; APPLICANT: Ball, James A.
 ; APPLICANT: Banu, G.
 ; APPLICANT: Bell, Erin
 ; APPLICANT: Boddupalli, Raghava
 ; APPLICANT: Deikman, Jill
 ; APPLICANT: Deng, Molian
 ; APPLICANT: Dong, Jinhua
 ; APPLICANT: Duff, Stephen M.
 ; APPLICANT: Galligan, Meghan M.
 ; APPLICANT: Hinchey, Brenda S.
 ; APPLICANT: Huang, Shihshien
 ; APPLICANT: Johnson, G. Richard
 ; APPLICANT: Jung, Vincent
 ; APPLICANT: Kretzmer, Keith A.
 ; APPLICANT: Laccetti, Lucille B.
 ; APPLICANT: Lai, Chao-Qiang
 ; APPLICANT: Lee, Gary
 ; APPLICANT: Lin, Jie-Yi
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Lu, Bin
 ; APPLICANT: Luethy, Michael M.
 ; APPLICANT: Lund, Adrian
 ; APPLICANT: Madson, Linda L.
 ; APPLICANT: Malloy, Kathleen A.
 ; APPLICANT: McKiel, Christine L.
 ; APPLICANT: Miller, Philip W.
 ; APPLICANT: Padmavathi, Manohikanti
 ; APPLICANT: Parnell, Laurence D.
 ; APPLICANT: Scart, William G.
 ; APPLICANT: Tennessee, Dan
 ; APPLICANT: Vidya, K.R.
 ; APPLICANT: Wang, Haiyun
 ; APPLICANT: Xin, Zhanguo
 ; APPLICANT: Xu, Nanfei
 ; APPLICANT: Yang, Chunzhi
 ; APPLICANT: Zeng, Xiaoping
 ; APPLICANT: Zhang, Qiang
 ; APPLICANT: Zhao, Yajuan
 ; APPLICANT: Zhou, Li
 ; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
 ; FILE REFERENCE: 38-15(52796)B
 ; CURRENT APPLICATION NUMBER: US/10/310,154
 ; CURRENT FILING DATE: 2002-12-04
 ; PRIOR APPLICATION NUMBER: 60/337,358
 ; PRIOR FILING DATE: 2001-12-04
 ; NUMBER OF SEQ ID NOS: 736
 ; SEQ ID NO 616
 ; LENGTH: 577
 ; TYPE: PRT
 ; ORGANISM: Anabaena
 ; US-10-310-154-616

Query Match 13.4%; Score 204.5; DB 14; Length 577;
 Best Local Similarity 26.7%; Pred. No. 4.1e-12;
 Matches 86; Conservative 47; Mismatches 98; Indels 91; Gaps 14;
 Qy 19 SMDEKRTDHD-----LLCLDGGGVKGLIILQLLALAEKASGVATKOLFVWAGTSTG 71
 Db 216 SDESQKTNNTNTPKPKKLALIDGGIRGIRPAILITEIEKTKQKQIFSLFDLIAGSSSG 275
 Qy 72 GILALAILSK-----SMAYRGMYFFMKDVEFRG-----S 102
 Db 276 GILALGILTKPRDLADSDSPVQAYSABEILQYIEYGAEIFYEPPEWEOILGLEDIFVQ 335
 Qy 103 RPYESGPLEEFLKREGEHTTKTDVAKPKYMLTGITSDQPAELHLFRNYDADETYREPR 162
 Db 336 PKYSSGREGREITKQYGDSPLENNLK--EVFVY-----STDLEQ--RIP 376
 Qy 163 FNQNVMLRPPAOPSDQLVWR-----AARSSGAAPTYFRP-----NGRF--L 201
 Db 377 FFTN---KLEKQOTKSKKPKKLCGLFTLIDALATATPTYPFAPYVSSSHNTNGFYTLV 433
 Qy 202 DGGCLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTGRSPQVPTCVDFRFP 261
 Db 434 DGGLVANNPANIALLAQAISRQ---NQOALNMEDI-LVSLGTG-----SLTSVYPTDQ 484
 Qy 262 SNPWELAKTVFGAKKEGKRVVD 283
 Db 485 VKXWGLIQ---WTKPILNNVLD 503

Search completed: December 15, 2004, 13:34:54
 Job time : 53.2542 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:55 ; Search time 31.0226 Seconds
(without alignments)
2130.736 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
Sequence: 1 MOPFGRLVNTFSQVTLFNSN.....GAKELGKMYVDCTDPR 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 79:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------|--------------------|
| 1 | 3566.5 | 98.5 | 851 | T12503 | hypothetical prote |
| 2 | 647.5 | 17.9 | 1071 | T22327 | hypothetical prote |
| 3 | 634.5 | 17.5 | 1023 | T26261 | hypothetical prote |
| 4 | 332 | 9.2 | 3924 | S37431 | ankyrin 2, neuona |
| 5 | 324.5 | 9.0 | 468 | T33857 | hypothetical prote |
| 6 | 324.5 | 9.0 | 2039 | T15347 | ankyrin-related un |
| 7 | 320 | 8.8 | 1549 | T13940 | ankyrin - fruit fl |
| 8 | 296 | 8.2 | 4377 | A55575 | ankyrin 3, long sp |
| 9 | 294.5 | 8.1 | 1765 | T42714 | ankyrin 3, splice |
| 10 | 294.5 | 8.1 | 1940 | T42715 | ankyrin 3, splice |
| 11 | 294.5 | 8.1 | 1943 | T42713 | ankyrin 3, splice |
| 12 | 294.5 | 8.1 | 1961 | T42716 | ankyrin 3, splice |
| 13 | 294 | 8.1 | 1856 | B35049 | ankyrin 1, erythro |
| 14 | 294 | 8.1 | 1880 | A35049 | ankyrin 1, erythro |
| 15 | 285 | 7.9 | 1848 | S37771 | ankyrin 1, erythro |
| 16 | 285 | 7.9 | 1848 | S37771 | ankyrin 1, erythro |
| 17 | 285 | 7.9 | 1848 | S37771 | ankyrin 1, erythro |
| 18 | 282.5 | 7.8 | 397 | T46445 | hypothetical prote |
| 19 | 278.5 | 7.7 | 1411 | S30355 | alpha-lactoferrin |
| 20 | 269.5 | 7.4 | 1265 | T02131 | hypothetical prote |
| 21 | 268 | 7.3 | 456 | T24442 | death-associated p |
| 22 | 264 | 7.3 | 1423 | T3275 | hypothetical prote |
| 23 | 250.5 | 6.9 | 1435 | T32930 | hypothetical prote |
| 24 | 249 | 6.9 | 791 | T42691 | hypothetical prote |
| 25 | 244 | 6.7 | 247 | D84448 | probable ankyrin l |
| 26 | 242.5 | 6.7 | 1401 | S11527 | transmembrane prot |
| 27 | 242 | 6.7 | 2437 | S42612 | hypothetical prote |
| 28 | 239.5 | 6.6 | 426 | A82149 | hypothetical prote |
| 29 | 235.5 | 6.5 | 355 | B82354 | patatin-related pr |

| | | | | | | |
|----|-------|-----|------|---|--------|--------------------|
| 30 | 234.5 | 6.5 | 633 | 2 | T27499 | hypothetical prote |
| 31 | 231 | 6.4 | 934 | 1 | H71274 | probable ankyrin - |
| 32 | 229.5 | 6.3 | 368 | 2 | T18184 | ankyrin repeat pro |
| 33 | 225 | 6.2 | 2524 | 2 | A35844 | notch protein - Af |
| 34 | 221.5 | 6.1 | 907 | 2 | I50404 | p508/p97 (Lyt-10) |
| 35 | 221.5 | 6.1 | 1062 | 2 | T14151 | inv protein - mous |
| 36 | 220.5 | 6.1 | 1062 | 2 | T30255 | inversin - mouse |
| 37 | 220 | 6.1 | 1184 | 2 | T00253 | gene Ankhzn protel |
| 38 | 219 | 6.0 | 2531 | 2 | A46019 | notch-1 protein - |
| 39 | 215 | 5.9 | 2531 | 2 | A40043 | notch protein homo |
| 40 | 214.5 | 5.9 | 2531 | 2 | S18188 | notch protein homo |
| 41 | 213.5 | 5.9 | 679 | 2 | G71615 | phospholipase A2-1 |
| 42 | 213.5 | 5.9 | 782 | 2 | JC7284 | phospholipase A2 (|
| 43 | 213.5 | 5.9 | 933 | 2 | S17233 | transcription fact |
| 44 | 208.5 | 5.8 | 606 | 2 | AC2508 | hypothetical prote |
| 45 | 207 | 5.7 | 2352 | 2 | T30201 | Notch homolog prot |

ALIGNMENTS

RESULT 1

T12503
hypothetical protein DKFZp434A102.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C/Accession: T12503
R:Ansoerge, W.; Whitner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: 217527
A:Accession: T12503
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <AMS>
A:Cross-references: EMBL:AL080187
A:Experimental source: adult testis; clone DKFZp434A102
C:Genetics:
A>Note: DKFZp434A102.1

| | | | | |
|-----------------------|-----------------|--|------------|-------------|
| Query Match | 98.5% | Score 3566.5; | DB 2; | Length 851; |
| Best Local Similarity | 92.3% | Pred. No. 1.5e-273; | | |
| Matches 684; | Conservative 1; | Mismatches 1; | Indels 55; | Gaps 1; |
| QY | 1 | MOPFGRLVNTFSQVTLFNSNPFVKAVAVADYSSDRVRESGQLIFONTPNTMDCVLV | 60 | |
| DB | 46 | MOPFGRLVNTFSQVTLFNSNPFVKAVAVADYSSDRVRESGQLIFONTPNTMDCVLV | 105 | |
| QY | 61 | NPNRSQGFRLPQLEADALVNFHOYSSQLPFYESSPQVLTTEVLQHLTDLIRNHPW | 120 | |
| DB | 106 | NPNRSQGFRLPQLEADALVNFHOYSSQLPFYESSPQVLTTEVLQHLTDLIRNHPW | 165 | |
| QY | 121 | SVHLAVELGIRCFPHSRIRISCANCAENEGCTPLHLACKDGEIIVLVQYCHTOMD | 180 | |
| DB | 166 | SVHLAVELGIRCFPHSRIRISCANCAENEGCTPLHLACKDGEIIVLVQYCHTOMD | 225 | |
| QY | 181 | VTPYKGETVHVAVQDNGSVQLLGRNAVAGLNVNNGSLTPLHLACOLGKQEMRVLL | 240 | |
| DB | 226 | VTPYKGETVHVAVQDNGSVQLLGRNAVAGLNVNNGSLTPLHLACOLGKQEMRVLL | 285 | |
| QY | 241 | LCNARCINMGPNVPIHSANKFQKCAEMTISMSQSQHSKDPKRYGASPLHAKNAEMA | 300 | |
| DB | 286 | LCNARCINMGPNVPIHSANKFQKCAEMTISMSQSQHSKDPKRYGASPLHAKNAEMA | 345 | |
| QY | 301 | RMILKGCNVNSTSSAGNTALHVGVMNRPFDCAILVLTTHGANDARGEHNTPLHLAMSK | 360 | |
| DB | 346 | RMILKGCNVNSTSSAGNTALHVGVMNRPFDCAILVLTTHGANDARGEHNTPLHLAMSK | 405 | |
| QY | 361 | DNVEIMKALIVPAGAVDTPNDPGETPLFLASKIGK----- | 395 | |
| DB | 406 | DNVEIMKALIVPAGAVDTPNDPGETPLFLASKIGRLVTRKAILTLRTVGAECPPPIHG | 465 | |
| QY | 396 | -----LQDLMIHSRAKRDPAFLGSRNDEKRTDHL | 425 | |

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Db      466 VPABOQSAAHHBPSLERAQPPISLNLELODLMHISRARKPAFLGSMRDEKRTDHL 525
Qy      426 LCGDGGGVKLIITIIQLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMYRM 485
Db      526 LCGDGGGVKLIITIIQLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMYRM 585
Qy      486 YFMKQEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDROPALHLFR 545
Db      586 YFMKQEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDROPALHLFR 645
Qy      546 NYAPAEVFRPRPNQNNLAPPAQPSQIYWRAPARSSGAAPTYRPRNGRFLDGLLANNP 605
Db      646 NYAPAEVFRPRPNQNNLAPPAQPSQIYWRAPARSSGAAPTYRPRNGRFLDGLLANNP 705
Qy      606 TLDAATEIHEYNODLIRKGOANKVKLSIVSLGTGSRSPQVPTCVVFRPSPNWEI LAKT 665
Db      706 TLDAATEIHEYNODLIRKGOANKVKLSIVSLGTGSRSPQVPTCVVFRPSPNWEI LAKT 765
Qy      666 VFQAKELGKRVVDCCTDPDGR 686
Db      766 VFQAKELGKRVVDCCTDPDGR 786

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RESULT 2

T22327

hypothetical protein F47A4.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T22327

R:Wormmore, B.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z19549

A:Accession: T22327

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1071 <M1>

A:Cross-references: UNIPROT:Q20500; EMBL:Z49888; PIDD:CAA90061.1; GSPDB:GN00028; CESP:F4

A:Experimental source: clone F47A4

C:Genetics:

A:Gene: CESP:F47A4.5

A:Map position: X

A:Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 17.9%; Score 647.5; DB 2; Length 1071;

Best Local Similarity 27.0%; Pred. No. 1.5e-42;

Matches 194; Conservative 126; Mismatches 260; Indels 139; Gaps 20;

```

Qy      69 FRFQLELELDALVNFHQYSQLLPFYESSPOVLHTEVL-----QHLTDLIRNHPMSVAH 124
Db      315 FSLFRATDKKMDLMLHLCDKESFLFLSLDMSTMRADILRSKIEELVQIRLKPHTYMIH 374
Qy      125 LAVELGREGCFHHSRI-----ISCANCAENEGCTPLHLACKGDEILVELVOY 174
Db      375 VALATRLDLFFSOGMITKTNMETLEPEFSSQRLCHTENCYVHLALTMDRQKIVERLLEL 434
Qy      175 CHTQMDVTYKGEVFFHYAVQGDSQVQLQILGRNAVAG--LQVNNQGLTPLHLACOLG 231
Db      435 DPLFLFCETDKAGNNVMHV---NSSPCAQIIMDRCPASQHFIDERNNDGSPLEINASTA 491
Qy      232 KQEMNVRVLLICNARCINMGNGYPIHSAMKFSQKCAEMTISM-----DSS 277
Db      492 KPLVAVTFL-----IGKAKFTGRDRNELFVAMTSKNAQSVVEVAVLTDKP 535
Qy      278 QHSKSDPRYGASPLHMAKNAMAMLLK-----GCNNSTSSAGNTALHYGVWRNRPDCA 333
Db      536 EIANERDALNSAIVHLYESLALNLRKVEGLDIDVKNAGETLLLPITTRKPDLL 595
Qy      334 IYLLT---HGANDARGEHGTPLHLAMS-----KDVNEMI KALIYGAEVDPNDGET 385
Db      596 PLVLTLYAHGANNATPDRHNTALHKSALVDAKKISLECVKPLISAGSNPNKINLARGS 655
Qy      386 PTLASTKGLKQDLMHSRA---RKPAFLIG-----SMRDE----- 418

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Db      656 PRHLAASL-QNDEMIALNKAAGATRCPKYKGRSNCRRDCCSADEYEBETLOKIRIGNE 714
Qy      419 -----KRTDHLICDGGGVKLIITIIQLIAIEKASGVA 452
Db      715 SDYEKTEFTASEKNTQDPLDGRSGRKAKVNNISMDGGIRLVIITIIAIEEELGDD 774
Qy      453 TKDLFDWVAGTSTGGILALAILHKSMAVMYRMGYFMKQEVFRG-SRPYSGPLEEFLK 511
Db      775 IFKYPFMSAGTSGSLIMAGLATGKSLREMOQYTLCLKRVDFGIMPPDYVQLERKFIOD 834
Qy      512 EFGEHKMTDVRKPKVMTGTLSDROPALHLFRNYDADETVRPRFNQNNLAPPAQGS 571
Db      835 QFGTGT-VWEIPYRLMISVNSEKLPVRELMARKKPAVDV-----ABETPK 881
Qy      572 DQVWRAPARSSGAAPTYRPRN-GRFLDGLLANNPTLDAATEIHEYNODLIRKGOANKVK 630
Db      882 EMPLMMLAKRSTAPLPLFKPSBDRYIDGILSNPPLDMSVHAHNLRELQSGRSADV 941
Qy      631 KLSIVSLGTGSRSPQVPTCVVFR--PSNWEIATVFGAKELGKRVVDCCTDPDGRP 687
Db      942 QMNVLSFGTG--QIPSTVIEFLSIDSNSPLQSIKTI--KDLAMFIDQATASEGAP 994

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RESULT 3

T26261

hypothetical protein W07A8.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26261; T26892

R:Baslam, V.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z20184

A:Accession: T26261

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1023 <M1>

A:Cross-references: UNIPROT:O62338; EMBL:Z62075; PIDD:CAE04932.1; GSPDB:GN00023; CESP:W0

A:Experimental source: clone W07A8

R:Ainscough, R.

submitted to the EMBL Data Library, January 1998

A:Reference number: Z20281

A:Accession: T26892

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1023 <M1>

A:Cross-references: UNIPROT:A021489; PIDD:CAA16371.1; GSPDB:GN00023; CESP:W07A8.2

A:Experimental source: clone Y44A6C

C:Genetics:

A:Gene: CESP:W07A8.2

A:Map position: 5

A:Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/1; 331/2; 411/1; 479/3; 534/3; 571/2; 706

Query Match 17.5%; Score 634.5; DB 2; Length 1023;

Best Local Similarity 24.2%; Pred. No. 1.5e-41;

Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

```

Qy      37 RVEEGQLILFQNTPRMTDCLVLPNRSQSGRFLQLELELD--ALVNFHQYSQLLPF 94
Db      204 RAKEEBEL---KKRPLHLAIIITLYNENKYYVLSLRSHKLDVVALCGRCRNPBLFVY 260
Qy      95 YESSPOV---LHTEVLQHLTDLIRNHPMSVAH LAVELGREGCFH---SRISCANCAE 148
Db      261 FRGNVNIKQVLT-----IFHELRDNMTWKSVAHISKIGLIEFFENMKHKLKYVNLIV 315
Qy      149 NEEGCTPLHLACKGDEILVELVOYCHTQMDVTYKGEVFFHYAVQGDSQVQLQIL--G 206
Db      316 QPBGSLPLMIAVONTQIETVSMWLDH-GADINILSSEGQVHLVAATAASGDILKILMET 374
Qy      207 RNAVAGLQVNNQGLTPLHLACOLGQKQEMNVRVLLICNARCINMGNG-----Y 254
Db      375 KCEETMINQDSDSGYTPAYVA-----LINALSNQGLTRGRGGGIGSSDSTQMAN 424
Qy      255 PIHSAMKFSQ--KCAEMTISMDSQIHSKDPRYGASPLHMAKNAMAMLLK---GCN 309

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Db 425 PIGAMKRGGLDVSRLKMLEKQDGLTERPTGTVHICANKKLLIMKEFRQTD 484
Qy 310 VNSTSSAGNTALHVGVRNRFPDCAIVLLTGANADARGHGNTPLHLSKDVEMIKAL 369
Db 485 PEARNAIQOPLHTFVFKDELGLVMTLSAGVMDADQINDGNTPLHCAVTRGNTIARML 544
Qy 370 IYVGAEDVTNDGERTPTPLASKIGKQDLMHSRAR-----KAFI----- 411
Db 545 LCGAEPDINRKRKESPRHIAARLTERKAMDIVRALIICGAGACDDGFIGACFGCHKT 604
Qy 412 -----IGSM----- 421
Db 605 GLTSCKTQGLSSSDSGSMEDRVKDHSVSNASAPYEPVLDPTQVLEBAVARNETRA 664
Qy 422 HDH----- 456
Db 665 PPRBEALKRVKMLKELVEKKKTSNVINVLGLOGGGRGLVTVQMLCLFAFLDRPLDY 724
Qy 457 FDMVAGTSTGGLALALILHKSMAVYMGVFRMKDEVFRG-SRPRYSGPLEEFLKRRGE 515
Db 725 FDMVAGTSTGGLALALILHKSMAVYMGVFRMKDEVFRG-SRPRYSGPLEEFLKRRGE 515
Qy 516 HTGATDVREKRVMLTGLSDROPALHLPFRYDAPETVREPRFQNVNLRPPAQPSDQV 575
Db 785 DRLMGDIKVRFPCTVTRADTPVQVLELNNYRLPISEKE---NNDLGF---TDPNELTI 838
Qy 576 WRARSSGAAPTYFRPN-GPFLDGLIANNPTLDAMTEIHEYNODLIRKQANKVKKLSI 634
Db 839 WKATRRSSAAPTYFRPN-GPFLDGLIANNPTLDAMTEIHEYNODLIRKQANKVKKLSI 634
Qy 635 VVSLGCRSPQVPTCTCDVFRSPNPELAKTVREKELGKGVNDCCTDPGR 687
Db 899 VLSVGTITPTCPVD-PSVEFEMNDLFGMLR---GMKNLSLVVDQATVATGAP 947

RESULT 4
S37431
Ankyrin 2, neuronal long splice form - human
N/Alternate names: ankyrin B, 440K splice form; ankyrin-B, brain ankyrin; non-erythroid
N/Contains: ankyrin 2, short form
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
C/Accession: S37431; A39643; B39643; A40334; A49462; S14553; S14569
R/Chan. W.
Submitted to the EMBL Data Library, September 1993
A/Reference number: S37431
A/Accession: S37431
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-3924 <CHA>
A/Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:9406287; PIDN:CAA81387.1; PID:94062
R/Octo, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A/Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
A/Reference number: A39643; MUID:91302466; PMID:1830053
A/Accession: A39643
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-2077 <OT1>
A/Cross-references: GB:X56957
A/Accession: B39643
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1443, 3585-3924 <OTT>
A/Cross-references: EMBL:X56958
R/Tee, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
Genomics 10, 858-866, 1991
A/Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A/Reference number: A40334; MUID:92009921; PMID:1833308
A/Accession: A40334
A/Molecule type: DNA
A/Residues: 463-474, 'PB', 477-495 <TSE>

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A/Cross-references: GB:M37123; NID:9178647; PIDN:AA62828.1; PID:9178648
R/Chan. W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A/Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and se
A/Reference number: A49462; MUID:94075409; PMID:8253844
A/Accession: A49462
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-3924 <RES>
A/Cross-references: EMBL:Z26634; NID:9406287; PIDN:CAA81387.1; PID:9406288
C/Genetics:
A/Genes: GDB:ANK2
A/Map position: 4q25-4q27
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keywords: alternative splicing
F/2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F/2-1443, 3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
F/63-95/Domain: ankyrin repeat homology <AN01>
F/96-128/Domain: ankyrin repeat homology <AN02>
F/129-161/Domain: ankyrin repeat homology <AN03>
F/162-190/Domain: ankyrin repeat homology <AN04>
F/191-223/Domain: ankyrin repeat homology <AN05>
F/232-264/Domain: ankyrin repeat homology <AN06>
F/265-297/Domain: ankyrin repeat homology <AN07>
F/298-330/Domain: ankyrin repeat homology <AN08>
F/331-363/Domain: ankyrin repeat homology <AN09>
F/364-396/Domain: ankyrin repeat homology <AN10>
F/397-429/Domain: ankyrin repeat homology <AN11>
F/430-462/Domain: ankyrin repeat homology <AN12>
F/463-495/Domain: ankyrin repeat homology <AN13>
F/496-528/Domain: ankyrin repeat homology <AN14>
F/529-561/Domain: ankyrin repeat homology <AN15>
F/562-594/Domain: ankyrin repeat homology <AN16>
F/595-627/Domain: ankyrin repeat homology <AN17>
F/628-660/Domain: ankyrin repeat homology <AN18>
F/661-693/Domain: ankyrin repeat homology <AN19>
F/694-726/Domain: ankyrin repeat homology <AN20>
F/727-759/Domain: ankyrin repeat homology <AN21>
F/760-792/Domain: ankyrin repeat homology <AN22>
F/793-825/Domain: ankyrin repeat homology <AN23>

Query Match 9.2%; Score 332; DB 2; Length 3924;
Best Local Similarity 27.3%; Pred. No. 9.7e-17;
Matches 100; Conservative 62; Mismatches 127; Indels 77; Gaps 9;

Qy 103 HTEVLQHTLD-----LIRNHPMSVLAHLVGLIRECFHH-----SRIL 141
Db 311 HDQVELLERGAPFLAFTNGSLPLHMAAQGDHVECHGLLOHKAPEVDVDTLYLTALH 370
Qy 142 SCANC-----ANEBCGTPHLACKRGDELIVELYOY----- 174
Db 371 VAAHCGHYRVTKLLDKRANPNBALNGTPPLHIAKKRIKMWELLYRGASIOATTS 430
Qy 175 -----CH-----TQMDYDYGVETFPYAAVQGDNSOYLLOLGRANAAG 212
Db 431 GLTPHYAAMPGLINLVLLLONGASPDVTNIRGETALMAARAQGVYVRCILRRG-AL 489
Qy 213 LNOVNOGLTPPLHIAQOLQKQEMVRLDLCNRCNIMGNGY-PIHSANKFSQGAEMT 271
Db 490 VBARBEQTPPLHIAIRLGTETIVQLLQHMHPDAATNGYPLHISAREGQDVASVYL 549
Qy 272 ISMDSQHSKDRYQASPLHMAK---NEMAMMLKRCGNVNSTSAGNTALHGVNKN 328
Db 550 --LEAGAAHSLATKQFTPLHVAKYGSIDVAGLLQRRAAADSAGKNGITPLHVAHYD 607
Qy 329 RPDCAIVLLTHGANAARGHGNTPLHLSKDVEMIKALIVFGAEVDTPNDFGSETPTF 388
Db 608 NQVVALILLEKSGASPHATKNGITPLHIAKKQWQIASTLNAVGAETNIVTKQVTPPLH 667
Qy 389 LASKIG 394
Db 668 LASQEG 673

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RESULT 5

hypothetical protein D1037.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C/Accession: T33857

R/edwith: J.: Biewald, T.

submitted to the EMBL Data Library, November 1998

A/Description: The sequence of C. elegans cosmid D1037.

A/Reference number: Z21424

A/Accession: T33857

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-468 <LED>

A/Cross-references: EMBL:AF106992; PIDN:AACT8490.1; GSPDB:GN00019; CESP:D1037.5

A/Experimental source: strain Bristol N2; clone D1037

C/Genetic:

A/Map position: 1

A/Introns: 66/3; 89/3; 113/3; 151/2; 247/1; 354/2

Query Match 9.0%; Score 324.5; DB 2; Length 468;
 Best Local Similarity 27.0%; Pred. No. 1.4e-17;
 Matches 110; Conservative 74; Mismatches 164; Indels 59; Gaps 16;

```

QY 286 YGASPLHMAKNAEMARMLKRGCVNNTSGAGNTALHVGWRN----RFPCAIVLLTHG 340
DB 44 YDLSVITWLN---LRFILIRYCR-----SEVNCNHELEMLNARAGNTDLKLYIHH 94
QY 341 ANADAGEHGNTPHLHMSKDNVEMIKALVFGAEVD---TPNDFGETPTFLASKIGKLO 397
DB 95 IDLRMTDETGTAMHVAVMNQKIVMLVLCAPCQIWKIKONNGITSTELCTDKKISE 154
QY 398 DLMHISRAKRP---AF-----ILGSRDEKRTIHD-LLCLDGGGVKGLIITQLLA 444
DB 155 DFKSLNPPSPGAFVDVSEVNNVLAISKQWKPEERVLALDGGGIRAVITIQWLIH 214
QY 445 IEKASGATKDLFDWVAGTSGGILALAI-LHSKMAVMKGMVFRMKDEVF-RGSR---P 499
DB 215 IDVLGKLVKEDDLADIGTSCGVITILLSTNNRIETKLLIDMRDRFIFIGADKAVP 274
QY 500 YESGPLEEPLKREF--GEHTKMTDVKRPKMYLTGSLSDROPALHFRNY--DAPETVRE 555
DB 275 KYSSNGMEVYARAVTWTMEDSKMSIKHRAIVTVADTRMVPPLQLLFRSYRPEWPEACE 334
QY 556 P-RPNQNVNLRPPAQSDQLVMPAARSSGAAPTYFRNGRFLDGGLIANNPTIDAMTEIH 614
DB 335 HYKF-----LDPTKVELMKTLCRTTAAPYFFESFNGLSGGGLIANNPTLALISDFP 365
QY 615 EYNODLIRKQANKVK-----KLIVVSLGTGRSPQVPTCVDV 653
DB 366 LTKK--LEKSFASKSSERENKRNKWKICVSLGTGVPTFKIGIDIL 430

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RESULT 6

ankyrin-related unc-44 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282

R/Gating, S.

submitted to the EMBL Data Library, February 1996

A/Description: The sequence of C. elegans cosmid B0350.

A/Reference number: Z18332

A/Accession: T15347

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2039 <GAT>

A/Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA934

A/Accession: T15346

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1000, 'SKLQRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAORS', 1950, 'IVAI

32, 'S', 2034-2035, 'GSPTRSVPEERHSHOHDEHGST' <GA2>

A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1

A/Accession: T15344

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTVASTSEQVPE', 1934-1935, 'EK

<GA3>

A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1

A/Accession: T15345

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAORS', 1950, 'IVAES', 1956-1957, 'EQVPE'

PTRSVPEERHSHOHDEHGST' <GA4>

A/Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAORS', 1950, 'IVAES', 1956-1957, 'EQVPE'

R/Cenka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontakulpoor

U. Cell Biol. 129, 1081-1092, 1995

A/Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Caer

A/Reference number: A57282; NID:95263663; PMID:7744957

A/Accession: A57282

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-852, 'GGC', 856-1000, 'SKLQRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEEL

A/Residues: 1-852, 'GGC', 856-1000, 'SKLQRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEEL

A/Cross-references: GB:U21734; NID:g790607; PIDN:AAA5854.1; PID:g790608

A/Accession: B57282

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E'

V, 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRSVPEERHSH', 1984-1985, 'EDHGS', 1

A/Cross-references: GB:U21731

A/Accession: C57282

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'O', 414, 824, 'S', 826, 'ER', 829, 'S'

4, 'TIV', 1828, 'ESTS', 1833, 'OV', 1836, 'E', 1934-1935, 'EGS', 1939, 'SEES', 1944, 'REDDGTVTT', 194

A/Cross-references: GB:U21732; NID:g790603; PIDN:AAA5853.1; PID:g790604

C/Genetic:

A/Status: preliminary

A/Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1879/

C/Superfamily: ankyrin; ankyrin repeat homology

F/164-192/Domain: ankyrin repeat homology <AN0>

F/358-390/Domain: ankyrin repeat homology <AN1>

F/391-423/Domain: ankyrin repeat homology <AN11>

Query Match 9.0%; Score 324.5; DB 2; Length 2039;

Best Local Similarity 24.1%; Pred. No. 1.4e-16;

Matches 129; Conservative 77; Mismatches 207; Indels 123; Gaps 16;

```

QY 147 AENEBGCTPLHLACRKGDEILVELVQYCHTQWDVTDYGEVTFHYAVQGDNSQVLLQLG 206
DB 420 ATTESGLTPLHVAFAFGALINIVYLLQ-GANDVETVGEFPLHLAABANQDVRVLI 478
QY 207 RANVAGLNQVNNQGLTPLHLACQLGQEMVRVLLCNACNIMGRNGY-PHISAMKFSQK 265
DB 479 RRG-ARVDAQARLQPTPLHLASRLGNTDIVILLQAGANSNATTRNYPPLHLAAEGGE 537
QY 266 GCAEMIISDSSQIHSKD---PRYGASPLHMAK---NAEMARMLKRCQNVNSTSSAGN 318
DB 538 EVAGIILD-----HNADTLTKGFTPLHLASKNGNEVVRLLERSTPPVDIEKQNV 591
QY 319 TALHVGMBNRDPCATVLLTHGANADARGEHGNTPHLHMSKDNVEMIKALIVFGAEVDT 378
DB 592 TPLHVAANNDKDVANLLENGASAKAANKGTPLHLIAAKNQVMEIASTLLQFKADPVA 651
QY 379 PNDFGETPLFLASKIKLQDLNHLISRAKRPAPILGSMREKTKTHHLCLDGGGVKGLI 438
DB 652 KSRAGFTPLHLSQEGHKE-----ISGLL- 675
QY 439 IQLLIIEKASGATKDLFDWVAGTSGGILALAILHSSKMAVMKGMVFRMKDEVFRGSR 498
DB 676 -----IENGSDVGAK-----ANNGLTAMHLC-----AQEDHV----- 702

```

499 PYESGPLEBFLKREBGEHTWTIDVRKPKMLTGLTSDROPAABHLFRNYDAPETVREPRF 558
Db 703 -----PVAQJLLYNNAGAEINKTNAGTTPPLVACHFGGLNANKLVEAGDVGKTR- 754
Qy 559 NQNVNLRPPAPSDQLVWRARSSGAAPTYFRPNRGLDGLLANNFTLDAMTEIHEYNQ 618
Db 755 -SYTPLHQAQOQHNNCVRLLENGASP-----NEGTATGQTP- 792
Qy 619 DLIRKQANVKKLSTIVSLGTRSPDY--PVTCDV-FRPSNPWELAKVFGAKE 671
Db 793 -----SIAORLGYVSVETLRTVETTVITETTVDERKRPONPEANETTFSESE 843

RESULT 7
T13940
ankylin - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T13940
R/Dubreuil, R.R.; Yu, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
A/Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Drosophila
A/Reference number: Z17820; MUID:95024098; PMID:7937942
A/Accession: T13940
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1549 <DUB>
A/Cross-references: UNIPROT:Q24241; EMBL:L35601; NID:9557083; PID:9557084; PIDN:AA37208
C/Genetics:
A/Cross-references: FlyBase:Fbgn0011747

Query Match 8.8%; Score 320; DB 2; Length 1549;

Best Local Similarity 22.7%; Pred. No. 2, 1e-16; Matches 141; Conservative 79; Mismatches 179; Indels 222; Gaps 23;

Qy 45 ILFQNTNPTNTRDCVLVNPNSQSGFRLFOLEADALVNFHQVSSQL-----PFYESSP 99
Db 319 LLOQNP-----ILFTKTKGLSLAH-----AAQGHDEAHLLLNKAPVDEVTY 364
Qy 100 QVL-----HTEVLQHLTDLIRNHP-----NSVAHLA-----VELGIRECFH 136
Db 365 DYTALVNAHCGHVAKLLDYKANPNRANGFTPLHACKKRIKMWELLIK---H 421
Qy 137 HSNILISANCANEBEGCTPLHACRKGDEILVELVOYCHTQMDVDTYKSETVPHVAVOG 136
Db 422 GANI-----GATTESGLTPLHVASFWGCINIVITLQH-BASADLPTRIGETPLHLARA 475
Qy 197 DNGQVQLLGRNAV-----210
Db 476 NQADIRILRSKAVDAIVEGGCTPLHVASRLGNINIMLLQHGAEINMQSDKYSALH 535
Qy 211 -----AGLNVNNOGLTPLHACQLGQEMVRVILLNARCNINIGPN 252
Db 536 IAAKEGENTIVQVLLENGAENNAVTKKFTPLHACYKQNVQVILLQNGASIDFGKN 595
Qy 253 GY-PIISAMFSGQKCAEMIISDSS-----QT--HKD- 283
Db 596 DVTPLHATVATYNNPSIVLELLKNGSSPNLCARNGQCAIHACKKQVLEIMQVLQHDADV 655
Qy 284 ---PRYGASPLHMAK---NAEMARMLKRGCVNSTSAGNTALHVGEMRPFDCALVL 337
Db 656 NITSKGSFPLHLAAQGANVDVQVLLIEGY-ISAANKGLTPLHVAAGHGVAVSILL 714
Qy 338 THGANMARGEHGNTPLHLAMSKGNVEMIKALIVGAEDVTENDGETPTPLASKIGKQ 397
Db 715 EHGANISERTNRNGTPLHMAAHYGHLDLVKFIENDADIEMSNIGYTPHQAQOQ--- 771
Qy 398 DLWHISARPRAPFLISMRDEKRTHHDLCLDGGVGVGLIIQVLLIAEKASGATADLF 457
Db 772 ---HI-----MITNLHKKKNPNALTD- 792
Qy 458 DWVAGTSGGILALAILHKSMAV---MRGVYFRMKDEVFRGSRPYESGPLEBFLKREFG 514

Db 793 -----GNVALH-----ASNLCGYVWMSLKITVSTVINSN-----IGAIEBKLK----- 833
Qy 515 EHTKMTDVAKRKPMLTGLTSD 535
Db 834 -----VMTPELMQETLLSD 847

RESULT 8

A55575
ankylin 3, long splice form - human

N/Alternate names: ankylin G

C/Species: Homo sapiens (man)

C/Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004

A/Accession: A55575

R/Kordeli, E.; Lambert, S.; Bennett, V.

J. Biol. Chem. 270, 2352-2359, 1995

A/Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the axon initial segment

A/Reference number: A55575; MUID:95138209; PMID:7836469

A/Accession: A55575

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-4377 <KOR>

A/Cross-references: UNIPROT:Q12955; GB:U13616; NID:9608024; PIDN:AAA64834.1; PID:9608025

C/Genetics:

A/Genes: GDB:ANK3

A/Cross-references: GDB:424503; OMIM:600465

A/Map position: 10q21-10q21

C/Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

C/Keywords: alternative splicing; peripheral membrane protein

F/106-138/Domain: ankyrin repeat homology <AN01>
F/139-171/Domain: ankyrin repeat homology <AN02>
F/172-200/Domain: ankyrin repeat homology <AN03>
F/201-233/Domain: ankyrin repeat homology <AN04>
F/234-266/Domain: ankyrin repeat homology <AN05>
F/267-299/Domain: ankyrin repeat homology <AN06>
F/300-332/Domain: ankyrin repeat homology <AN07>
F/333-365/Domain: ankyrin repeat homology <AN08>
F/366-398/Domain: ankyrin repeat homology <AN09>
F/399-431/Domain: ankyrin repeat homology <AN10>
F/432-464/Domain: ankyrin repeat homology <AN11>
F/465-497/Domain: ankyrin repeat homology <AN12>
F/498-530/Domain: ankyrin repeat homology <AN13>
F/531-563/Domain: ankyrin repeat homology <AN14>
F/564-596/Domain: ankyrin repeat homology <AN15>
F/597-629/Domain: ankyrin repeat homology <AN16>
F/630-662/Domain: ankyrin repeat homology <AN17>
F/663-695/Domain: ankyrin repeat homology <AN18>
F/696-728/Domain: ankyrin repeat homology <AN19>
F/729-761/Domain: ankyrin repeat homology <AN20>
F/762-794/Domain: ankyrin repeat homology <AN21>
F/795-827/Domain: ankyrin repeat homology <AN22>
F/828-860/Domain: ankyrin repeat homology <AN23>

Query Match 8.2%; Score 296; DB 2; Length 4377;

Best Local Similarity 29.2%; Pred. No. 8, 1e-14; Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;

Qy 124 HLAVELGIRECFHRSIRISANCANEBEGCTPLHACRKGDEILVELVOYCHTQMDVTD 183
Db 504 HISARLGKADIVQQLLOQGSAPAAATTSQYTPHLHAREGHEVDVAFLLDH-CASISIT 562
Qy 184 YKGETVPHVAVQDNGVQLDGLGRNAVAGLNQVNNQGLTPLHACQLGQEMVRVILLCN 243
Db 563 KKEFTPLHVAARKGLKVANLLQKS-ASPDAAGSGLTPLHVAHYDNQKVALLLDDOG 621
Qy 244 ARGNINQNGY-PIISAMFSGQKCAEMIISDSSQIHSKDPYRGASPLHMAK---NA 297
Db 622 ASPHAAAKQYTPPLHLAAKKNQMDITLLEYGADANAV---TRGSIASVHLAAQEGHY 677
Qy 298 EMARMLKRGCVNSTSAGNTALHVGEMRPFDCALVLTTHGANMARGEHGNTPLHLA 357
Db 678 DWVSLILGRNAVNLNKSGLTPLHLAAQEDRVNVAEVLVNGAHVADAQTKMGYTPHVG 737

QY 358 MSKDNVEMIKALIVFGAEVDPNDPGETPTFLASKIG 394
 Db 738 CHYGNIKIVFLQHSKKNVAKKNGYTPHQAQGS 774

RESULT 9

T42714

ankyrin 3, splice form 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene

R:Peterson, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.

J. Cell Biol. 130, 313-330, 1995

A:Reference number: Z22237; MUID:95340633; PMID:7615634

A:Accession: T42714

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1765 <PET>

A:Cross-references: UNIPROT:Q61307; EMBL:LA0632; NID:g710548; PID:g710551; PIDN:AA01605

A:Experimental source: strain C57BL/6J; kidney

C:Genetics:

A:Gene: Ank3

A:Map position: 10

A:Intons: 1587/1

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

Query Match 8.1%; Score 294.5; DB 2; Length 1765;
 Best Local Similarity 24.7%; Pred. No. 2.6e-14;
 Matches 112; Conservative 81; Mismatches 191; Indels 69; Gaps 18;

QY 124 HLAVELG---IRECFHSRIISCANCAENEBGCTPLHACRGDDELIVELYCHTOM 179
 Db 421 HVAEFMGNVIVSOLMNH---GASPTTVNRGETALHMAASGQAEVVRVLQ-DGAQV 475
 QY 180 DVDYKGETVFHYAVOGDNSQVQLQLGRNAVAGLVNNOGLTPHLACQLGKQEMRVYL 239
 Db 476 EAKAKDDQTPHLISALRGKADIVQLQOG-ASPNAATTSCTPPLHAAEGHEVDVAFL 534
 QY 240 LLCNARCNINGPNGY-PIHSAMKFSQKCAEMTISDSSQIHSKDPRYGASPLHMA--K 295
 Db 535 LDHGASLSTTKKGFPLHVAAYGKLEVASLLQKASAP--DAAGSGILTPHVAANYD 592
 QY 296 NAEAMMLKRCGNVSTSSAGNTALHVGVRMRPFCALVILLHGANADARGHGTPLH 355
 Db 593 NQVALLLLDQGSPPAAAKNGYTPHLIAKKQMDIATSLLEYGADANAVTROGLASVH 652
 QY 356 LAMSKDNVEMIKALIVFGAEVDPNDPGETPTFLAS---KIGKLQDLM---HISRAKP 408
 Db 653 LAAQEGHVDVSVLLSRNANVNLSNKSGLTPHLAAQEDRVNVAEVLVNGAHVDAQTKM 712
 QY 409 AFLTGSMDKERTHDLCLDGGGVKGLIIQLLIAIEKASGVATYDLFDVWAGSTGGI 468
 Db 713 GY-----TPLVHGQ-HYGNIK---IVNELLQHSKVNKATKN-----GY 747
 QY 469 LALAILHKSMAVMRGVFRMKDEVRGSRPYE---SGPLEBFLKPEFGHTKMTDVRK- 524
 Db 748 TAA-----HQAQOQGHTHIINVLLONNASPNELTVNGTALAIARRLG-YISVVDTLKV 800
 QY 525 --PKVMLTGLSDRQPAELHLPFNYPADPTVRE 555
 Db 801 VTBEIMTTTTITTEK-----HKMNVPEPTMNE 825

RESULT 10

T42715

ankyrin 3, splice form 3 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42715

R:Peterson, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995

A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene ;
 the repeat domain.

A:Reference number: Z22237; MUID:95340633; PMID:7615634

A:Accession: T42715

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1940 <PET>

A:Cross-references: UNIPROT:Q61307; EMBL:LA0632; NID:g710548; PID:g710549; PIDN:AA01604.

A:Experimental source: strain C57BL/6J; kidney

C:Genetics:

A:Gene: Ank3

A:Map position: 10

A:Intons: 834/1

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

Query Match 8.1%; Score 294.5; DB 2; Length 1940;
 Best Local Similarity 24.7%; Pred. No. 3e-14;
 Matches 112; Conservative 81; Mismatches 191; Indels 69; Gaps 18;

QY 124 HLAVELG---IRECFHSRIISCANCAENEBGCTPLHACRGDDELIVELYCHTOM 179
 Db 421 HVAEFMGNVIVSOLMNH---GASPTTVNRGETALHMAASGQAEVVRVLQ-DGAQV 475
 QY 180 DVDYKGETVFHYAVOGDNSQVQLQLGRNAVAGLVNNOGLTPHLACQLGKQEMRVYL 239
 Db 476 EAKAKDDQTPHLISALRGKADIVQLQOG-ASPNAATTSCTPPLHAAEGHEVDVAFL 534
 QY 240 LLCNARCNINGPNGY-PIHSAMKFSQKCAEMTISDSSQIHSKDPRYGASPLHMA--K 295
 Db 535 LDHGASLSTTKKGFPLHVAAYGKLEVASLLQKASAP--DAAGSGILTPHVAANYD 592
 QY 296 NAEAMMLKRCGNVSTSSAGNTALHVGVRMRPFCALVILLHGANADARGHGTPLH 355
 Db 593 NQVALLLLDQGSPPAAAKNGYTPHLIAKKQMDIATSLLEYGADANAVTROGLASVH 652
 QY 356 LAMSKDNVEMIKALIVFGAEVDPNDPGETPTFLAS---KIGKLQDLM---HISRAKP 408
 Db 653 LAAQEGHVDVSVLLSRNANVNLSNKSGLTPHLAAQEDRVNVAEVLVNGAHVDAQTKM 712
 QY 409 AFLTGSMDKERTHDLCLDGGGVKGLIIQLLIAIEKASGVATYDLFDVWAGSTGGI 468
 Db 713 GY-----TPLVHGQ-HYGNIK---IVNELLQHSKVNKATKN-----GY 747
 QY 469 LALAILHKSMAVMRGVFRMKDEVRGSRPYE---SGPLEBFLKPEFGHTKMTDVRK- 524
 Db 748 TAA-----HQAQOQGHTHIINVLLONNASPNELTVNGTALAIARRLG-YISVVDTLKV 800
 QY 525 --PKVMLTGLSDRQPAELHLPFNYPADPTVRE 555
 Db 801 VTBEIMTTTTITTEK-----HKMNVPEPTMNE 825

RESULT 11

T42713

ankyrin 3, splice form 1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42713

R:Peterson, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.

J. Cell Biol. 130, 313-330, 1995

A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene ;
 the repeat domain.

A:Reference number: Z22237; MUID:95340633; PMID:7615634

A:Accession: T42713

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1943 <PET>

A:Cross-references: UNIPROT:Q61307; EMBL:LA0632; NID:g710548; PID:g710550; PIDN:AA01606.

A:Experimental source: strain C57BL/6J; kidney

C:Genetics:

A:Gene: Ank3
 A:Map position: 10
 A:Introns: 855/1
 C:Function:
 A:Description: supposed to play an important role in the polarized distribution of many
 A:Note: major kidney ankyrin
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing

Query Match 8.1%; Score 294.5; DB 2; Length 1943;
 Best Local Similarity 24.7%; Pred. No. 3e-14;
 Matches 112; Conservative 81; Mismatches 191; Indels 69; Gaps 18;

QY 124 HLAVELG-----IRECFHSHRIISCANCAENEBCGTPHLACRKGDEILVELVOYCHTQM 179
 DB 421 HVAAFMGHNVIVSOLMHH-----GASPTTNVAGETPLHAAASGQAEVRYLVQ-DGAYV 475
 QY 180 DVTYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVYL 239
 DB 476 EAKAKDDQPLHISARLGRADIVQQLLQOG-ASPNAATTSGYTPHLAAREGHEDVAAPL 534
 QY 240 LNCNACNIMGNGY-PHISAKPFSQKCAEMTISMSDSQHSKDPHYGASPLHMA---K 295
 DB 535 LDHGASLSTTTKKGFTPLHVAAYKGLVAVASLLQKSASP--DAAGKSGTTPHVAAYHD 592
 QY 296 NEMAMMLKRGCVNSTSAGNTALHVGMRFRPCATVLTTHGANADARGHGTPLH 355
 DB 593 NQKVALLLDQASPRAAAKNGTTPHLIAKKNQMDIATSLLEYGADANAATVROGLASVH 652
 QY 356 LAMSKDNVEMIKALIVFAGAEVDPDPGFTPLAS---KIGKLODLM---HISBARKP 408
 DB 653 LAAQEGHVDVMSLLSRNANVNLNKSGLTPHLAAGEDRVNVAEVLVQGAHVDAQTGM 712
 QY 409 AFLTSGMRDEKRTDHLCLDGGGVKGLIIQLLIAERASGVATKDLFDWVAGTSTGTI 468
 DB 713 GY-----TPLHVG-C-HYGNIK--IVNFLLOHSAKNVAKTKN-----GY 747
 QY 469 LALAILHSKMAVMRGVFRMKDEVFRGSRPYE---SGPLEBFLKREFEHTKMTDVRK- 524
 DB 748 TNL-----HQAQQGHTHTIIVNLONNASPBELTVNGTALAIARRLG-YISVVDTLKV 800
 QY 525 --PKWMLTGLSDROPALHLFRNYDAPETVRE 555
 DB 801 VTBEIMTTTITTEK-----HKMNVPEITMNE 825

RESULT 12

T42716
 Ankyrin 3, splice form 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42716
 R:Peterson, L.D.; John, K.M.; Lu, F.M.; Eicher, B.M.; Higgins, A.; Yialamas, M.; Turtzo, I.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A:Reference number: Z22237; MUID:95340633; PMID:7615634
 A:Accession: T42716
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1961 <PEP>
 A:Cross-references: UNIPROT:Q61307; EMBL:U40632; NID:9710548; PID:9710552; PIDN:AAB01607
 A:Experimental source: strain C57BL/6J; kidney
 C:Genetics:
 A:Gene: Ank3
 A:Map position: 10
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing

Query Match 8.1%; Score 294.5; DB 2; Length 1961;
 Best Local Similarity 24.7%; Pred. No. 3.1e-14;
 Matches 112; Conservative 81; Mismatches 191; Indels 69; Gaps 18;

QY 124 HLAVELG-----IRECFHSHRIISCANCAENEBCGTPHLACRKGDEILVELVOYCHTQM 179
 DB 421 HVAAFMGHNVIVSOLMHH-----GASPTTNVAGETPLHAAASGQAEVRYLVQ-DGAYV 475
 QY 180 DVTYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVYL 239
 DB 476 EAKAKDDQPLHISARLGRADIVQQLLQOG-ASPNAATTSGYTPHLAAREGHEDVAAPL 534
 QY 240 LNCNACNIMGNGY-PHISAKPFSQKCAEMTISMSDSQHSKDPHYGASPLHMA---K 295
 DB 535 LDHGASLSTTTKKGFTPLHVAAYKGLVAVASLLQKSASP--DAAGKSGTTPHVAAYHD 592
 QY 296 NEMAMMLKRGCVNSTSAGNTALHVGMRFRPCATVLTTHGANADARGHGTPLH 355
 DB 593 NQKVALLLDQASPRAAAKNGTTPHLIAKKNQMDIATSLLEYGADANAATVROGLASVH 652
 QY 356 LAMSKDNVEMIKALIVFAGAEVDPDPGFTPLAS---KIGKLODLM---HISBARKP 408
 DB 653 LAAQEGHVDVMSLLSRNANVNLNKSGLTPHLAAGEDRVNVAEVLVQGAHVDAQTGM 712
 QY 409 AFLTSGMRDEKRTDHLCLDGGGVKGLIIQLLIAERASGVATKDLFDWVAGTSTGTI 468
 DB 713 GY-----TPLHVG-C-HYGNIK--IVNFLLOHSAKNVAKTKN-----GY 747
 QY 469 LALAILHSKMAVMRGVFRMKDEVFRGSRPYE---SGPLEBFLKREFEHTKMTDVRK- 524
 DB 748 TNL-----HQAQQGHTHTIIVNLONNASPBELTVNGTALAIARRLG-YISVVDTLKV 800
 QY 525 --PKWMLTGLSDROPALHLFRNYDAPETVRE 555
 DB 801 VTBEIMTTTITTEK-----HKMNVPEITMNE 825

RESULT 13

B35049
 Ankyrin 1, erythrocyte splice form 3 - human
 N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N:Contents: ankyrin 2.2, erythrocyte
 C:Species: Homo sapiens (man)
 C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
 R:Lambert, S.; Yu, H.; Prechal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Ke
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A:Title: cDNA sequence for human erythrocyte ankyrin.
 A:Reference number: A35049; MUID:90175370; PMID:1689649
 A:Accession: B35049
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1656 <LAM>
 C:Genetics:
 A:Gene: GDB:ANK1; ANK
 A:Cross-references: GDB:118737; OMIM:182900
 A:Map position: 8p11.2-8p11.2
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:2-1866/Product: ankyrin 1, erythrocyte form 3 #status predicted <Mat>
 F:2-1513,1676-1866/Product: ankyrin 2.2, erythrocyte #status predicted <Mat>
 F:77-109/Domain: ankyrin repeat homology <AN01>
 F:110-142/Domain: ankyrin repeat homology <AN03>
 F:143-171/Domain: ankyrin repeat homology <AN04>
 F:172-204/Domain: ankyrin repeat homology <AN05>
 F:205-237/Domain: ankyrin repeat homology <AN06>
 F:238-270/Domain: ankyrin repeat homology <AN07>
 F:271-303/Domain: ankyrin repeat homology <AN08>
 F:304-336/Domain: ankyrin repeat homology <AN09>
 F:337-369/Domain: ankyrin repeat homology <AN10>
 F:370-402/Domain: ankyrin repeat homology <AN11>
 F:403-435/Domain: ankyrin repeat homology <AN12>
 F:436-468/Domain: ankyrin repeat homology <AN13>
 F:469-501/Domain: ankyrin repeat homology <AN14>
 F:502-534/Domain: ankyrin repeat homology <AN15>
 F:535-567/Domain: ankyrin repeat homology <AN16>

F:568-600/Domain: ankryn repeat homology <AN17>
 F:601-633/Domain: ankryn repeat homology <AN18>
 F:634-666/Domain: ankryn repeat homology <AN19>
 F:667-699/Domain: ankryn repeat homology <AN20>
 F:700-732/Domain: ankryn repeat homology <AN21>
 F:733-765/Domain: ankryn repeat homology <AN22>
 F:766-798/Domain: ankryn repeat homology <AN23>

Query Match 8.1%; Score 294; DB 2; Length 1856;
 Best Local Similarity 25.6%; Pred. No. 3,1e-14;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LQHLTDLIRNHPWSVAHLAVELGIRECFPH--SRIISCAENAE---EGCTPLHLACR 161
 DB 336 LDHLTPL-----HVA-----HCGHRAVAKVLDKGAKPNSBALNGFTPLHACK 380
 QY 162 KGGELIVELVOYCHTQMD-----VTDYKGET 188
 DB 381 KKHVRW-ELLKGTASIDAVTESGLTPLHVASFMGHLPIVKNLORGASPNVSVKVE 439
 QY 189 VPHYAVQDNGSOYLQLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVAVLLCNACNI 248
 DB 440 PLHMAARAGHTVAKVLLQNK-AKVNAKAKDDOTPLHCAARIGHTVAVLLLENNANPVL 498
 QY 249 MGENGY-----PIHSAMKFSQKCAEMIISM 274
 DB 499 ATTAGHTPLHIAAREGHVETVALLLEKESQACMTKGTPLHVAAYGKVAELLER 558
 QY 275 DSSQHSKDPRYGASPLHMA---KNAEMAMLLKRCGNVNSTSSAGNTALHVGVMNRFD 331
 DB 559 DAHP--NAAGKNGLTPLHVAHNNNDIVLLPRGSGPSHPMNGYTPPLHIAKONQVE 616
 QY 332 CAIVLTHGANADAREHNTPLHAMSNDNEMIKALIVFGABVDTPNDPGETPLFLS 391
 DB 617 VARSLLQYGSANABSVQGTPLHIAAQEGHAEVALLSKQANGNLGNKSGLTPLHLVA 676
 QY 392 KIG 394
 DB 677 QEG 679

RESULT 14

ankryn 1, erythrocyte splice form 2 - human
 N/Alternate names: ankryn 2.1, erythrocyte; ankryn-R
 N/Contains: ankryn 2.2, erythrocyte
 C/Species: Homo sapiens (man)
 C/Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004
 C/Accession: A35049
 R/Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A/Title: cDNA sequence for human erythrocyte ankryn.
 A/Reference number: A35049; MUID:9015370; PMID:1669849
 A/Accession: A35049
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1880 <LMA>
 A/Cross-references: UNIPROT:P16157; GB:M28880
 C/Genetics:
 A/Genes: GDB:ANK1, ANK
 A/Cross-references: GDB:118737; OMIM:182900
 A/Map position: 8p11.2-8p11.2
 C/Superfamily: ankryn repeat homology
 C/Keywords: alternative splicing; cytoskeleton
 F:2-1880/Product: ankryn 1, erythrocyte form 2 #status predicted <MAT>
 F:2-1513,1676-1880/Product: ankryn 2.2, erythrocyte #status predicted <MA2>
 F:74-76/Domain: ankryn repeat homology <AN01>
 F:77-109/Domain: ankryn repeat homology <AN02>
 F:110-142/Domain: ankryn repeat homology <AN03>
 F:143-171/Domain: ankryn repeat homology <AN04>
 F:172-204/Domain: ankryn repeat homology <AN05>
 F:205-237/Domain: ankryn repeat homology <AN06>
 F:238-270/Domain: ankryn repeat homology <AN07>

F:271-303/Domain: ankryn repeat homology <AN08>
 F:304-336/Domain: ankryn repeat homology <AN09>
 F:337-369/Domain: ankryn repeat homology <AN10>
 F:370-402/Domain: ankryn repeat homology <AN11>
 F:403-435/Domain: ankryn repeat homology <AN12>
 F:436-468/Domain: ankryn repeat homology <AN13>
 F:469-501/Domain: ankryn repeat homology <AN14>
 F:502-534/Domain: ankryn repeat homology <AN15>
 F:535-567/Domain: ankryn repeat homology <AN16>
 F:568-600/Domain: ankryn repeat homology <AN17>
 F:601-633/Domain: ankryn repeat homology <AN18>
 F:634-666/Domain: ankryn repeat homology <AN19>
 F:667-699/Domain: ankryn repeat homology <AN20>
 F:700-732/Domain: ankryn repeat homology <AN21>
 F:733-765/Domain: ankryn repeat homology <AN22>
 F:766-798/Domain: ankryn repeat homology <AN23>

Query Match 8.1%; Score 294; DB 2; Length 1880;
 Best Local Similarity 25.6%; Pred. No. 3,1e-14;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LQHLTDLIRNHPWSVAHLAVELGIRECFPH--SRIISCAENAE---EGCTPLHLACR 161
 DB 336 LDHLTPL-----HVA-----HCGHRAVAKVLDKGAKPNSBALNGFTPLHACK 380
 QY 162 KGGELIVELVOYCHTQMD-----VTDYKGET 188
 DB 381 KKHVRW-ELLKGTASIDAVTESGLTPLHVASFMGHLPIVKNLORGASPNVSVKVE 439
 QY 189 VPHYAVQDNGSOYLQLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVAVLLCNACNI 248
 DB 440 PLHMAARAGHTVAKVLLQNK-AKVNAKAKDDOTPLHCAARIGHTVAVLLLENNANPVL 498
 QY 249 MGENGY-----PIHSAMKFSQKCAEMIISM 274
 DB 499 ATTAGHTPLHIAAREGHVETVALLLEKESQACMTKGTPLHVAAYGKVAELLER 558
 QY 275 DSSQHSKDPRYGASPLHMA---KNAEMAMLLKRCGNVNSTSSAGNTALHVGVMNRFD 331
 DB 559 DAHP--NAAGKNGLTPLHVAHNNNDIVLLPRGSGPSHPMNGYTPPLHIAKONQVE 616
 QY 332 CAIVLTHGANADAREHNTPLHAMSNDNEMIKALIVFGABVDTPNDPGETPLFLS 391
 DB 617 VARSLLQYGSANABSVQGTPLHIAAQEGHAEVALLSKQANGNLGNKSGLTPLHLVA 676
 QY 392 KIG 394
 DB 677 QEG 679

RESULT 15

ankryn 1, erythrocyte splice form 1 - human
 N/Alternate names: ankryn 2.1, erythrocyte; ankryn-R
 N/Contains: ankryn 2.2
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C/Accession: S08275; A33219; EC2220; A35443
 R/Lux, S.E.; John, K.M.; Bennett, V.
 Nature 344, 36-42, 1990
 A/Title: Analysis of cDNA for human erythrocyte ankryn indicates a repeated structure w/
 A/Reference number: S08275; MUID:90158830; PMID:2137557
 A/Accession: S08275
 A/Molecule type: mRNA
 A/Residues: 1-1881 <LNU>
 A/Cross-references: UNIPROT:P16157; EMBL:X16609; NID:G28701; P1DN:CAA34610.1; P1D:G28702
 A/Accession: A33219
 A/Molecule type: protein
 A/Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30, '733-749', 'A', 751-753, 828-833, 'X', 835-855, 'X',
 'X', 1367,1383-1427,1601-1630,1686-1698, 'D', 1700,1763-1772 <LUX>
 A/Note: 845-Arg and 1392-Thr were also found
 R/Hermann, U.; Barrel, M.; Fraide, R.
 Biochem. Biophys. Res. Commun. 204, 453-460, 1994

A>Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A/Reference number: PC2220; MUID:95071346; PMID:7526850
A/Accession: PC2220
A/Molecule type: protein
A/Residues: 910-929 <HER>
R/Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A>Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A/Reference number: A35443; MUID:90285190; PMID:2141335
A/Accession: A35443
A/Molecule type: protein
A/Residues: 'X',5,'X',7-12,403-417,'X',419-422,'H',424,'LQ',797-800,'L',802-814,862-863,
C/Genetics:
A/Genes: GDB:ANK1; ANK
A/Cross-references: GDB:118737; OMIM:182900
A/Map position: 8p11.2-8p11.2
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keywords: alternative splicing; phosphoprotein
F/2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F/2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
F/2-827/Domain: 89K #status predicted <DOM1>
F/2-827/Region: anion exchange protein binding
F/44-76/Domain: ankyrin repeat homology <AN01>
F/77-109/Domain: ankyrin repeat homology <AN02>
F/110-142/Domain: ankyrin repeat homology <AN03>
F/143-171/Domain: ankyrin repeat homology <AN04>
F/172-204/Domain: ankyrin repeat homology <AN05>
F/205-237/Domain: ankyrin repeat homology <AN06>
F/238-270/Domain: ankyrin repeat homology <AN07>
F/271-303/Domain: ankyrin repeat homology <AN08>
F/304-336/Domain: ankyrin repeat homology <AN09>
F/337-369/Domain: ankyrin repeat homology <AN10>
F/370-402/Domain: ankyrin repeat homology <AN11>
F/403-435/Domain: ankyrin repeat homology <AN12>
F/436-468/Domain: ankyrin repeat homology <AN13>
F/469-501/Domain: ankyrin repeat homology <AN14>
F/502-534/Domain: ankyrin repeat homology <AN15>
F/535-567/Domain: ankyrin repeat homology <AN16>
F/568-600/Domain: ankyrin repeat homology <AN17>
F/601-633/Domain: ankyrin repeat homology <AN18>
F/634-666/Domain: ankyrin repeat homology <AN19>
F/667-699/Domain: ankyrin repeat homology <AN20>
F/700-732/Domain: ankyrin repeat homology <AN21>
F/733-765/Domain: ankyrin repeat homology <AN22>
F/766-798/Domain: ankyrin repeat homology <AN23>
F/828-1382/Domain: 62K #status predicted <DOM2>
F/828-1382/Region: spectrin binding
F/1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 8.1%; Score 294; DB 1; Length 1881;

Best Local Similarity 25.6%; Pred. No. 3.2e-14; Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LQHLTDLIRNHPSSVAHLAVELGIRCEPHH--SRIISCAWCAENE---EGCTPLHACR 161
DB 336 LDHITPL-----HVAA-----HGHHRVAKVLLDKAKPNSRALNGFTPLHIAK 380
QY 162 KGDGEILVELVOYCHTQMD-----VTDYKGET 188
DB 381 KNHYRVM-ELLKTKGASIDAVTESGLTPHVASFHGLPIYKNLLQRGASPNVSNVAKET 439
QY 189 VFHYAVGDNDSQVQLIGRNAVAGLNOVNNQGLTPHLACQLGQEMVRVILLCNARCN 248
DB 440 PLHVAAPAGHTEVAKYLLQNR-AKVNAKAKDDQTPHICARIGHTNNVKLLNNANPNL 498
QY 249 MGPNXY-----PIHSAMKPSOKCAEMTISM 274
DB 499 ATTAGHTPLHIAAREGHVETVLLLEKASQACMTKGFPLHVAATYGVKRVAVELLER 558
QY 275 DSSQIHSKDPRYGASPLHMA---KNAEMARMLLRGCNVNSTSAGNTALHVGVRNRF 331
DB 559 DAHP--NAAGNGLTPLHVAVHHNNLDIVKLLPRGSPHSFANNGYTPHLIAKQNDVE 616

QY 332 CATVLTGANDARGEHGNTPLHLSMKNVEMIKALIVGAEVDTPNDPGETPTFLAS 391
DB 617 VAKSLQIGGSANASVQGVTPHLAAQGHAEVALLSKQANGNLGKSGITPLHIVA 676
QY 392 KIG 394
DB 677 QEG 679

Search completed: December 15, 2004, 13:14:20
Job time: 34.0226 sec

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:25 ; Search time 149.609 Seconds
(without alignments)
2642.105 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
Sequence: 1 MCFRGLVNTFSGVTNLFNS.....GAKELGMVVDCTDPDGRP 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|--------------------|
| 1 | 3566.5 | 98.5 | 806 | 1 PA26_HUMAN | O60733 homo sapien |
| 2 | 3566.5 | 98.5 | 806 | 1 CAG30429 | Cag30429 homo sapi |
| 3 | 3289.5 | 91.1 | 752 | 1 PA26_MOUSE | P97819 mus musculu |
| 4 | 3289.5 | 90.9 | 752 | 2 Q7TPX2 | Q7tpx2 mus musculu |
| 5 | 3272 | 90.4 | 807 | 2 Q9JK61 | Q9jk61 mus musculu |
| 6 | 3272 | 90.4 | 807 | 2 AAH57209 | Aah57209 mus muscu |
| 7 | 3257 | 90.0 | 751 | 1 PA26_RAT | P97570 rattus norv |
| 8 | 2210.5 | 61.1 | 756 | 2 Q6DDFO | Q6ddfo xenopus lae |
| 9 | 1977.5 | 54.6 | 818 | 2 Q6NW10 | Q6nw10 brachydanto |
| 10 | 1977.5 | 54.6 | 818 | 2 AAH67375 | Aah67375 brachydan |
| 11 | 1164 | 32.1 | 879 | 2 Q7Q2U1 | Q7q2u1 anopheles g |
| 12 | 1163.5 | 32.1 | 877 | 2 Q9VTE6 | Q9vte6 drosophila |
| 13 | 1163.5 | 32.1 | 877 | 2 AAH50194 | Aah50194 drosophi |
| 14 | 1163.5 | 32.1 | 887 | 2 Q7KUD4 | Q7kud4 drosophila |
| 15 | 1163.5 | 32.1 | 887 | 2 AAH11936 | Aah11936 drosophi |
| 16 | 742 | 20.5 | 386 | 2 Q8MR13 | Q8mr13 drosophila |
| 17 | 647.5 | 17.9 | 1071 | 2 Q20500 | Q20500 caenorhabdi |
| 18 | 634.5 | 17.5 | 1023 | 2 Q62398 | Q62398 caenorhabdi |
| 19 | 629.5 | 17.4 | 1021 | 2 Q81006 | Q81006 caenorhabdi |
| 20 | 458 | 12.7 | 762 | 2 Q95YD2 | Q95yd2 caenorhabdi |
| 21 | 357.5 | 9.9 | 501 | 2 Q9NSJ3 | Q9nsj3 caenorhabdi |
| 22 | 338 | 9.3 | 843 | 2 P97582 | P97582 rattus norv |
| 23 | 338 | 9.3 | 1219 | 2 Q8C8R3 | Q8c8r3 mus musculu |
| 24 | 332 | 9.2 | 1219 | 2 Q7Z3L5 | Q7z3l5 homo sapien |
| 25 | 332 | 9.2 | 3924 | 1 ANK2_HUMAN | ANK2 human sapien |
| 26 | 324.5 | 9.0 | 1004 | 2 Q7JNZ0 | Q7jnz0 caenorhabdi |
| 27 | 324.5 | 9.0 | 1004 | 2 AAQ91911 | Aaq91911 caenorhab |
| 28 | 324.5 | 9.0 | 1786 | 2 Q17344 | Q17344 caenorhabdi |
| 29 | 324.5 | 9.0 | 1786 | 2 Q17487 | Q17487 caenorhabdi |
| 30 | 324.5 | 9.0 | 1815 | 2 Q17488 | Q17488 caenorhabdi |
| 31 | 324.5 | 9.0 | 1841 | 2 Q8MG00 | Q8mg00 caenorhabdi |

ALIGNMENTS

| RESULT 1 | PA26_HUMAN | STANDARD; | PRT; | 806 AA. |
|----------|--|-----------|------|---------|
| AC | O60733; Q75645; Q8N452; Q9UG29; Q9YU70; Q9Y671; | | | |
| DT | 30-MAY-2000 (Rel. 39, Created) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last sequence update) | | | |
| DT | 01-OCT-2004 (Rel. 45, Last annotation update) | | | |
| DE | 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cat-PLA2) (Group VI phospholipase A2) (GVI PLA2). | | | |
| GN | Name=iPLA2G6; Synonyms=iPLA2; | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2). | | | |
| RC | TISSUE=B-cell, and Testis; | | | |
| RX | MEDLINE=98079046; PubMed=9417066; | | | |
| RA | Larsen P.K.A., Claesson H.-E., Kennedy B.P.; | | | |
| RT | "Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity."; | | | |
| RL | J. Biol. Chem. 273:207-214 (1998). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2). | | | |
| RC | TISSUE=Pancreatic islets; | | | |
| RX | MEDLINE=99194813; PubMed=10092647; | | | |
| RA | Ma Z., Wang X., Nowatke W., Ramanadham S., Turk J.; | | | |
| RT | "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1."; | | | |
| RL | J. Biol. Chem. 274:9607-9616 (1999). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. | | | |
| RX | MEDLINE=99269033; PubMed=10336645; | | | |
| RA | Larsen Forell P.K.A., Kennedy B.P., Claesson H.-E.; | | | |
| RT | "The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene."; | | | |
| RL | Eur. J. Biochem. 262:575-585 (1999). | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM LH-IPLA). | | | |
| RC | TISSUE=Testis; | | | |
| RA | Amorje W., Winkler U., Mewes H.-W., Gassenhuber J., Wiemann S.; | | | |
| RL | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [5] | | | |
| RP | SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343. | | | |
| RA | Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., | | | |
| RA | Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., | | | |
| RA | Sherwood J.K., Sherwood A.M., Leitauer B.J., Nickerson D.A.; | | | |
| RT | "NIH-SNPs, environmental genome project. NIH S515478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; | | | |
| RL | Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases. | | | |

[6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clamp M., Smith L.J., Alnecough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Copley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leverhwa M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McMan O.T.,
 RA McCally J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Rose M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Stewart C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minochina S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mituyama S.,
 RA Roe B.A., Chen F., Chu Y., Hu P., Hua A., Kenton S., Lai H., Lo T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lo T.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
 RA Phan Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisose S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bennis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinde K., Kemp K., Latreille P., Layman D., Ozerky P., Rottling T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Delmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
 RA Peyrard M., Kedra D., Seroussi E., Pransoni I., Tapa I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodentelch H., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tiliahun Y., Wright H.,
 RT "The DNA sequence of human chromosome 22."
 RL Nature 402:489-495(1999).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS LH-1PLA2 AND SH-1PLA2).
 RC TISSUE=Brain;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uudin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and

CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -1- FUNCTION: Isoform ankyrin-1PLA2-1 and isoform ankyrin-1PLA2-2,
 CC which lack the catalytic domain, are probably involved in the
 CC negative regulation of 1PLA2 activity.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC SUBUNIT: Forms large oligomeric 270-350 kDa structures.
 CC -1- SUBCELLULAR LOCATION: Isoform LH-1PLA2 was found to be membrane
 CC bound. Isoform SH-1PLA2 is cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=LH-1PLA2;
 CC IsoId=O60733-1; Sequence=Displayed;
 CC Name=SH-1PLA2;
 CC IsoId=O60733-2; Sequence=VSP_000278;
 CC Name=Ankyrin-1PLA2-1;
 CC IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
 CC Name=Ankyrin-1PLA2-2;
 CC IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
 CC TISSUE SPECIFICITY: Four different transcripts were found to be
 CC expressed in a distinct tissue distribution.
 CC -1- SIMILARITY: Contains 7 ANK repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
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DR HSSP; 060778; 10Y3.
DR Genew; HSCNC:9039; PLA2G6.

Query Match 98.5%; Score 3566.5; DB 1; Length 806;
Best Local Similarity 92.3%; Pred. No. 5.8e-265;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;

QY 1 MOFFGRVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREGQILFQNTPNRTWDCVLY 60
DB 1 MOFFGRVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREGQILFQNTPNRTWDCVLY 60
QY 61 NPNRSQSGFRLLFOLELEADALVNFHOYSQQLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120
DB 61 NPNRSQSGFRLLFOLELEADALVNFHOYSQQLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHACRKDGELIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHACRKDGELIVELVOYCHTQMD 180
QY 181 VTDYKGETVHYAVQGNDSQVQLLGRNVAAGLNVNNOGLTPHLACOLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVQGNDSQVQLLGRNVAAGLNVNNOGLTPHLACOLGKQEMRVLL 240
QY 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMTISMSQSIHSDPRYGASPLHAKNAEMA 300
DB 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMTISMSQSIHSDPRYGASPLHAKNAEMA 300
QY 301 RMLIKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLSMSK 360
DB 301 RMLIKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLSMSK 360
QY 361 DNEMTKALIVFGAEVDPNDPGETPTFLASKIGRLVTRKAILTLRTVGAECFPPIHG 420
DB 361 DNEMTKALIVFGAEVDPNDPGETPTFLASKIGRLVTRKAILTLRTVGAECFPPIHG 420
QY 396 -----LQDLMIHSRAKPAFIIGSMRDEKRTDHL 425
DB 421 VPAEQSAAHHHPFSLERAPPISLNLELQDLMIHSRAKPAFIIGSMRDEKRTDHL 480
QY 426 LCIDGGGVKGLIIITQLIAIEKASGVAATKDLFDWVAGTSTGGILALAILHKSMAVYRGM 485
DB 481 LCIDGGGVKGLIIITQLIAIEKASGVAATKDLFDWVAGTSTGGILALAILHKSMAVYRGM 540
QY 486 YFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKWMLTGLISROPALHLFR 545
DB 541 YFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKWMLTGLISROPALHLFR 600
QY 546 NYDAPEIVREPRFNQNNLRPPAOPSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 605
DB 601 NYDAPEIVREPRFNQNNLRPPAOPSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 660
QY 606 TLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGSPQVPTCVDFRPSNWEIHLAKT 665
DB 661 TLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGSPQVPTCVDFRPSNWEIHLAKT 720
QY 666 VFGAKELGKRVVDCCTDPDGR 686
DB 721 VFGAKELGKRVVDCCTDPDGR 741

RESULT 2

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AC CAG30429;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE PLA2G6 protein.
GN PLA2G6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1];
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Gingham J.A.,
RA Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle B.J.,
RA Beare D.M., Dunham I.,
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456543; CAG30429.1; -
SQ SEQUENCE 806 AA; 89902 MW; 8E55CDAEB9ACAD8B CRC64;

Query Match 98.5%; Score 3566.5; DB 2; Length 806;
Best Local Similarity 92.3%; Pred. No. 5.8e-265;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;

QY 1 MOFFGRVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREGQILFQNTPNRTWDCVLY 60
DB 1 MOFFGRVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREGQILFQNTPNRTWDCVLY 60
QY 61 NPNRSQSGFRLLFOLELEADALVNFHOYSQQLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120
DB 61 NPNRSQSGFRLLFOLELEADALVNFHOYSQQLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHACRKDGELIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHACRKDGELIVELVOYCHTQMD 180
QY 181 VTDYKGETVHYAVQGNDSQVQLLGRNVAAGLNVNNOGLTPHLACOLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVQGNDSQVQLLGRNVAAGLNVNNOGLTPHLACOLGKQEMRVLL 240
QY 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMTISMSQSIHSDPRYGASPLHAKNAEMA 300
DB 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMTISMSQSIHSDPRYGASPLHAKNAEMA 300
QY 301 RMLIKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLSMSK 360
DB 301 RMLIKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLSMSK 360
QY 361 DNEMTKALIVFGAEVDPNDPGETPTFLASKIGRLVTRKAILTLRTVGAECFPPIHG 420
DB 361 DNEMTKALIVFGAEVDPNDPGETPTFLASKIGRLVTRKAILTLRTVGAECFPPIHG 420
QY 396 -----LQDLMIHSRAKPAFIIGSMRDEKRTDHL 425
DB 421 VPAEQSAAHHHPFSLERAPPISLNLELQDLMIHSRAKPAFIIGSMRDEKRTDHL 480
QY 426 LCIDGGGVKGLIIITQLIAIEKASGVAATKDLFDWVAGTSTGGILALAILHKSMAVYRGM 485
DB 481 LCIDGGGVKGLIIITQLIAIEKASGVAATKDLFDWVAGTSTGGILALAILHKSMAVYRGM 540
QY 486 YFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKWMLTGLISROPALHLFR 545
DB 541 YFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKWMLTGLISROPALHLFR 600
QY 546 NYDAPEIVREPRFNQNNLRPPAOPSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 605
DB 601 NYDAPEIVREPRFNQNNLRPPAOPSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 660
QY 606 TLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGSPQVPTCVDFRPSNWEIHLAKT 665
DB 661 TLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGSPQVPTCVDFRPSNWEIHLAKT 720
QY 666 VFGAKELGKRVVDCCTDPDGR 686
DB 721 VFGAKELGKRVVDCCTDPDGR 741

RESULT 3

PA26_MOUSE
ID PA26_MOUSE STANDARD; PRT; 752 AA.
AC P97819; 099LA9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (PLA2) (Cat-
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _
RP SEQUENCE FROM N.A.
RC STRAIN=DRA/2;
RX MEDLINE=97236816; PubMed=9079688;
RA Balboa M.A., Balazide J., Jones S.S., Dennis E.A.;
RT "Identity between the Ca²⁺-independent phospholipase A2 enzymes from
RT P3881 macrophages and Chinese hamster ovary cells";
RN J. Biol. Chem. 272:8576-8580(1997).
RN [2]
RP REVISIONS TO 2-3; 9; 11 AND 211.
RA Balboa M.A., Balazide J., Jones S.S., Dennis E.A.;
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RX SEQUENCE FROM N.A.
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diachenko L., Marutha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toohyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalek U., Smallue D.E.,
RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
CC or send an email to license@1sb-sib.ch).
CC -----
CC EMBL: U88624; AAB4511.2; -;
CC EMBL: BC003487; AAH03487.1; -;
CC HSSP: Q60778; 10Y3.
CC MGD: MGI:1859152; Pla2g6.
CC InterPro: IPR002110; ANK.
CC Pfam: PF00023; ANK_6.
CC PRINTS: PR01415; ANKYRIN.
CC SMART: SM00248; ANK_6.
CC PROSITE: PS50088; ANK_REPEAT; 4.
CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
CC ANK repeat; Hydrolase; Lipid degradation; Repeat.
CC REPEAT 151 181 ANK 1.
CC REPEAT 185 215 ANK 2.
CC REPEAT 219 248 ANK 3.
CC REPEAT 251 281 ANK 4.
CC REPEAT 286 312 ANK 5.
CC REPEAT 316 345 ANK 6.
CC REPEAT 349 378 ANK 7.

FT ACT_SITE 465 465 Potential.
SQ SEQUENCE 752 AA; 83702 MW; AAC3347B0E1292E9 CRC64;
Query Match 91.1%; Score 3299.5; DB 1; Length 752;
Best Local Similarity 90.5%; Pred. No. 1.7e-241;
Matches 622; Conservative 29; Mismatches 35; Indels 1; Gaps 1;
QY 1 MGFGRGLVNTVFSQVNTLFSNPFPRKVEAVADYTSRDRVEEGQLIFONTPNRTWDCVLY 60
DB 1 MGFGRGLVNTVLSVTNLFSPNPFPRKVEVSLTDYVSSEVREEGQLILQVNSNRTWDCVLY 60
QY 61 NPNNSGSGRLPDLLEADALVNFHYSSQLLPFYSSQVLTETVQLHLDLIRNHPN 120
DB 61 SPNPPSGGRLFLLEADALVNFQFSSQLPFPYSSVQVLHVEVLQHLTDLIRNHPN 120
QY 121 SVNLAVELGIRCFPHSRILISCANCAENEGCTPLHLCRKDGELVELVQYCHTOMD 180
DB 121 TVTHLAVELGIRCFPHSRILISCANSTENEGCTPLHLCRKDGSELVELVQYCAQMD 180
QY 181 VTQYKGETVFHYAVQGDNSQVTLQILGRNAVAGLNQVNNQGLTPHLACQLGQKQEVRL 240
DB 181 VTQNKGETAFHYAVQGDNPQVTLQILGKNASAGLNQVNNQGLTPHLACQKQKQEVRL 240
QY 241 LCNARCNINPNCQYPTHSAMKPSQKCAEMTISMSDSQHSKDPKRGASPLHAKNAEMA 300
DB 241 LCNARCNINPNCQYPTHTAKPSQKCAEMTISMSDSQHSKDPKRGASPLHAKNAEMA 300
QY 301 RMLLKSGCWNSTYSAGNTALHYGVNRNRFDCALVELTHGANADARGEHNTPLHAMS 360
DB 301 RMLLKSGCVDSTSSSGNTALHYAVNRNRFDCVMTLTGANGANGEHNTPLHAMS 360
QY 361 DNVETKALIVGAEDVTPNDGEPTFLASKTGK-LQDLMHISRRKPAFTIGSRDEK 419
DB 361 DNVEMKALIVFAGVADTPNDFETPALASKISKLOLDMPTSRARKPAFTIGSRDEK 420
QY 420 RTHDHLCLDGGVKGILIIILIALEKASGVATKOLPMVAGTSGGILALILSKSN 479
DB 421 RSHDHLCLDGGVKGILVILQILIALEKASGVATKOLPMVAGTSGGILALILSKSN 480
QY 480 AYVRGMYPRMKDEVPRGSRPYESGPLEEFLKREFGHTKMTDVRKPKWLTGTLSDRPA 539
DB 481 AYVRGYVPRMKDEVPRGSRPYESGPLEEFLKREFGHTKMTDVRKPKWLTGTLSDRPA 540
QY 540 ELHLFNYDAPETVREPRFNQVNLPRPAQPSQVLYWRAARSSGAAPYFRNGRLDGG 599
DB 541 ELHLFNYDAPETVREPRFNQVNLPRPAQPSQVLYWRAARSSGAAPYFRNGRLDGG 600
QY 600 LLANNPTLAMEIHEYNQDLIRKQANVYKLSIVSLGTGSPQVPTCVVFRPSNP 659
DB 601 LLANNPTLAMEIHEYNQDMIRKQGNVYKLSIVSLGTGSPQVPTCVVFRPSNP 660
QY 660 WEIAKTVPFAGKELGKRVVDCCTDPDGR 686
DB 661 WEIAKTVPFAGKELGKRVVDCCTDPDGR 687
RESULT 4
Q7TPX2 PRELIMINARY; PRT; 752 AA.
ID 07TPX2;
AC 07TPX2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Phospholipase A2, group VI.
GN Name=PLA2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; Tissue=Osteoblast;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Krzywnicki M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He; TISSUE=osteoblast;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC052845; AAS52845.1; -
 DR GO, GO:0003824; F: catalytic activity; IEA.
 DR GO, GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro, IPR002110; ANK.
 DR InterPro, IPR002641; Pataatin.
 DR Pfam, PF000023; Ank; 6.
 DR Pfam, PF01234; Pataatin; 1.
 DR SMART, SM00248; ANK; 6.
 DR PROSITE, PSS00088; ANK_REPEAT; 4.
 DR PROSITE, PSS0297; ANK_REGION; 1.
 DR ANK repeat.
 SQ SEQUENCE 752 AA; 83717 MW; DAC3347B0E14AFC CRC64;

Query Match 90.9%; Score 3289.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 1e-243;
 Matches 621; Conservative 29; Mismatches 36; Indels 1; Gaps 1;
 QY 1 MOPFGRVNTFSGYTNLFSPNFRKVEAVADVTSDDRYRSGQILPONTNRTWDCVLY 60
 DB 1 MOPFGRVNTLSTVTLFSPNFRKVEAVSLDYSSERVRGGQILQVNSNRKWDVLY 60
 QY 61 NPNRSQSGFRLFQLEADALVNFHOYSSQILPFYESSPOVLTATEVLQHLTDLIRNPSW 120
 DB 61 SPNRPQSGFRLFQLEADALVNFHOYSSQILPFYESSPOVLTATEVLQHLTDLIRNPSW 120
 QY 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACKRGDEILVELVOYCTQMD 180
 DB 121 TVHLAVELGIRCFHHSRIISCANSTENEGCTPLHLACKRGDEILVELVOYCHAQMD 180
 QY 181 VTQYKGTVFHYAVQGNNSQVLTQIGRNAVAGLVQVNNQGLTPHLACOLGKQMVLYL 240
 DB 181 VTQYKGTVFHYAVQGNNSQVLTQIGRNAVAGLVQVNNQGLTPHLACOLGKQMVLYL 240
 QY 241 LCNARCINMGPGYPIHSAMKFSQKCAEMTISDSSQHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCINMGPGYPIHSAMKFSQKCAEMTISDSSQHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLIKRGCVNVSISAGNTALHVGVMNRNRPFCALVLTGKANADARGHGTPLHLAMSK 360
 DB 301 RMLIKRGCVNVSISAGNTALHVGVMNRNRPFCALVLTGKANADARGHGTPLHLAMSK 360
 QY 361 DNVEMLKALIVFGABVDTPNDPGETPLAKICK-LQDLNHSIRARAPATILSMDEK 419
 DB 361 DNVEMLKALIVFGABVDTPNDPGETPLAKICK-LQDLNHSIRARAPATILSMDEK 419
 QY 420 RTHDHLCLDGGGVKGLIIQDLIAIEKASGVATKDLFDVAVAGTSGGIIALAILHSM 479
 DB 420 RTHDHLCLDGGGVKGLIIQDLIAIEKASGVATKDLFDVAVAGTSGGIIALAILHSM 479
 QY 421 RSHDHLCLDGGGVKGLIIQDLIAIEKASGVATKDLFDVAVAGTSGGIIALAILHSM 480
 DB 421 RSHDHLCLDGGGVKGLIIQDLIAIEKASGVATKDLFDVAVAGTSGGIIALAILHSM 480

QY 480 AYKRGVFRKQDEVRPGSRPYESGPLEEFKRFEGHTKMTVVRKPKWLTGTLSDRPA 539
 DB 481 AYKRGVFRKQDEVRPGSRPYESGPLEEFKRFEGHTKMTVVRKPKWLTGTLSDRPA 540
 QY 540 ELHLPFNRYDAPEVTRBPRFQNVNLRPPAPQSPDQVWRARSSGAAPTYFRPGRFLDGG 599
 DB 541 ELHLPFNRYDAPEVTRBPRFQNVNLRPPAPQSPDQVWRARSSGAAPTYFRPGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHERYQDLIRKQANRYKSLIVSISGTGRSPQVPTCVDFRPSNP 659
 DB 601 LLANNPTLDAMTEIHERYQDLIRKQANRYKSLIVSISGTGRSPQVPTCVDFRPSNP 660
 QY 660 WEIAKTVFGAKELGRVNVDOCTDPDGR 686
 DB 661 WEIAKTVFGAKELGRVNVDOCTDPDGR 687
 RESULT 5
 ID Q9UK61 PRELIMINARY; PRT; 807 AA.
 AC Q9UK61;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE C22+-independent phospholipase A2 long form (Pla2g6 protein).
 GN Name=Pla2g6;
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NH/Swiss;
 RA Chiu C.-H., Jackowski S.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MNR1; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Krzywnicki M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=MNR1; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF259401; AAF72651.1; -
 DR EMBL, BC057209; AAS7209.1; -
 DR HSSP, O60768; IOY3.
 DR MGD, MGI1859152; Pla2g6.
 DR GO, GO:0003824; F: catalytic activity; IEA.
 DR GO, GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro, IPR002110; ANK.
 DR InterPro, IPR002641; Pataatin.

DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF01734; Patatin; 1.
 DR PRINTS; PR01415; ANKYRN.
 DR PROSITE; PSS0088; ANK_REPEAT; 4.
 DR PROSITE; PSS0297; ANK_REPEAT; 1.
 DR ANK repeat.
 KW ANK repeat.
 SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 90.4%; Score 3272; DB 2; Length 807;
 Best Local Similarity 83.8%; Pred. No. 2,5e-242;
 Matches 622; Conservative 29; Mismatches 35; Indels 56; Gaps 1;

QY 1 MGFGRVLTFFSGVTNLFSPNPRKVEVAADYTSDDREBEGQLIFONTNRTWCVLV 60
 DB 1 MGFGRVLTNLTSSVTNLFSPNPRKVEVSLTDYSSERBEGQLILQNTSNRTWCVLV 60
 QY 61 NPNNSGGRFLFQLELEADALVNFHQSSQLPFYESSPOVLTEVLOHITDLIRNPSW 120
 DB 61 SPNPSGGRFLFQLESEADALVNFQPSQLPFYESSVVLHVEVLQHTDLIRNPSW 120
 QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHACRKGDEILVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRCFHHSRIISCANSTENEBEGCTPLHACRKGDEILVELVOYCHTQMD 180
 QY 181 VTQKETEYHVAVQGDNSQVLQLGRNAVAGLVNNOGVLTPHLACQKQEMRVLL 240
 DB 181 VTQKETEYHVAVQGDNPQVLQLGRNAGLVNNOGVLTPHLACQKQEMRVLL 240
 QY 241 LCNARCNINPNGYPIHSAKFSQKCAEMTISDSQIHSKDPRYGASPLHAKNAEMA 300
 DB 241 LCNARCNINPNGYPIHTAMKFSQKCAEMTISDSQIHSKDPRYGASPLHAKNAEMA 300
 QY 301 RMLKRGCVNSTSSAGNTALHGVNMRPDCAILLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNSTSSAGNTALHVAVMNRPCVAVLLTYGANAGARGEHNTPLHLAMSK 360
 QY 361 DNVEIMKALIVGAEDVTPNDPGETPTFLASKIGK----- 395
 DB 361 DNVEIMKALIVGAEDVTPNDPGETPTFLASKIGK----- 395
 QY 396 ----- 420
 DB 396 ----- 420
 QY 421 VSTEQSGAAATHPLFSLDRTQPPAISLNLELDQIMTISRAKPAFTLSMRBCKSHD 480
 DB 421 VSTEQSGAAATHPLFSLDRTQPPAISLNLELDQIMTISRAKPAFTLSMRBCKSHD 480
 QY 481 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGSTGGILALAIHKSMAVMRG 540
 DB 481 LCLDGGGVKGLVIQLLIAIEKASGVATKDLFDWVAGSTGGILALAIHKSMAVMRG 540
 QY 541 MYRMKDEVFRSGRPYSGPLSEFLKKEFGSHYKMTDVRKPYMLTGLSDROPALHLF 600
 DB 541 VYFRMKDEVFRSGRPYSGPLSEFLKKEFGSHYKMTDVRKPYMLTGLSDROPALHLF 600
 QY 601 RNDAPETVEPRPNQVNLNRPAPQSDOLVRAABSGAAPTFRNGSFLGGILLAN 660
 DB 601 RNDAPETVEPRPNQVNLNRPAPQSDOLVRAABSGAAPTFRNGSFLGGILLAN 660
 QY 661 PTIDAMTEIHEYNODMIRKQGNKVKLSIVSLGTGRSPQVPTCDVFRPSNPELAK 720
 DB 661 PTIDAMTEIHEYNODMIRKQGNKVKLSIVSLGTGRSPQVPTCDVFRPSNPELAK 720
 QY 721 TVFGAKELGKVVVDCCTDPDGR 686
 DB 721 TVFGAKELGKVVVDCCTDPDGR 742

RESULT 6

AAH57209 PRELIMINARY; PRT; 807 AA.
 AC AAH57209;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE Pfaz66 protein.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollay S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.T., Skalska U., Smalios D.E., Schmechel A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RA "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057209; AAH57209.1; -
 SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 90.4%; Score 3272; DB 2; Length 807;
 Best Local Similarity 83.8%; Pred. No. 2,5e-242;
 Matches 622; Conservative 29; Mismatches 35; Indels 56; Gaps 1;

QY 1 MGFGRVLTFFSGVTNLFSPNPRKVEVAADYTSDDREBEGQLIFONTNRTWCVLV 60
 DB 1 MGFGRVLTNLTSSVTNLFSPNPRKVEVSLTDYSSERBEGQLILQNTSNRTWCVLV 60
 QY 61 NPNNSGGRFLFQLELEADALVNFHQSSQLPFYESSPOVLTEVLOHITDLIRNPSW 120
 DB 61 SPNPSGGRFLFQLESEADALVNFQPSQLPFYESSVVLHVEVLQHTDLIRNPSW 120
 QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHACRKGDEILVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRCFHHSRIISCANSTENEBEGCTPLHACRKGDEILVELVOYCHTQMD 180
 QY 181 VTQKETEYHVAVQGDNSQVLQLGRNAVAGLVNNOGVLTPHLACQKQEMRVLL 240
 DB 181 VTQKETEYHVAVQGDNPQVLQLGRNAGLVNNOGVLTPHLACQKQEMRVLL 240
 QY 241 LCNARCNINPNGYPIHSAKFSQKCAEMTISDSQIHSKDPRYGASPLHAKNAEMA 300
 DB 241 LCNARCNINPNGYPIHTAMKFSQKCAEMTISDSQIHSKDPRYGASPLHAKNAEMA 300
 QY 301 RMLKRGCVNSTSSAGNTALHGVNMRPDCAILLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNSTSSAGNTALHVAVMNRPCVAVLLTYGANAGARGEHNTPLHLAMSK 360
 QY 361 DNVEIMKALIVGAEDVTPNDPGETPTFLASKIGK----- 395
 DB 361 DNVEIMKALIVGAEDVTPNDPGETPTFLASKIGK----- 395
 QY 396 ----- 420
 DB 396 ----- 420
 QY 421 VSTEQSGAAATHPLFSLDRTQPPAISLNLELDQIMTISRAKPAFTLSMRBCKSHD 480
 DB 421 VSTEQSGAAATHPLFSLDRTQPPAISLNLELDQIMTISRAKPAFTLSMRBCKSHD 480
 QY 481 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGSTGGILALAIHKSMAVMRG 540
 DB 481 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGSTGGILALAIHKSMAVMRG 540


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DB 481 LLLDGGVGVGLVITLIQLLIERKASGATDLPFWAGTGTGILALAILHSSSMAYMRG 540
QY 485 MYFRMKDEVFRGSRPYESGPLEBEFLKKEFGSHNTMTDVRKPKWLTGTLSDROPALHLF 544
DB 541 VYFRMKDEVFRGSRPYESGPLEBEFLKKEFGSHNTMTDVRKPKWLTGTLSDROPALHLF 600
QY 545 RNYDAPETVREPRFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGGILLANN 604
DB 601 RNYDAPETVREPRFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGGILLANN 660
QY 605 PTIDAMTEIHEYNODLIRKQOANKVKLSIVSLGTRSPQVPYTCVDVFRPSNPMEIAX 664
DB 661 PTIDAMTEIHEYNODMIRKQGNKVKLSIVSLGTRSPQVPYTCVDVFRPSNPMEIAX 720
QY 665 TVFGAKELGKRVVDCCTDPDGR 686
DB 721 TVFGAKELGKRVVDCCTDPDGR 742

RESULT 7
PA26_RAT STANDARD; PRT; 751 AA.
AC P97570;
AT 30-MAY-2000 (Rel. 39, last sequence update)
DT 30-MAY-2000 (Rel. 39, last sequence update)
DE 01-OCT-2004 (Rel. 45, last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (PLA2) (Cat-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
RX MEDLINE=97259008; PubMed=9111008;
RA Ma Z., Ramachandram S., Kempe K., Chi X.S., Ladenson J., Turk J.;
RT "Pancreatic islets express a Ca2+-independent phospholipase A2 enzyme that contains a repeated structural homologue to the integral membrane protein binding domain of ankyrin.";
RT J. Biol. Chem. 272.11118-11127(1997).
RL J. Biol. Chem. 272.11118-11127(1997).
CC -FUNCTION: Catalyzes the release of fatty acids from phospholipids. It has been implicated in normal phospholipid remodeling, nitric oxide-induced or vasopressin-induced arachidonic acid release and in leukotriene and prostaglandin production. May participate in fas mediated apoptosis and in regulating transmembrane ion flux in glucose-stimulated B-cells.
CC -CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.
CC -SUBCELLULAR LOCATION: Cytoplasmic.
CC -TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver, heart and skeletal muscle.
CC -SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; U51898; AAC53136.1; -.
CC HSSP; Q60798; 10Y3.
CC RGD; 628867; PLA2G6.
CC InterPro: IPR002110; ANK.
CC Pfam; PF00023; ANK_6.
CC PRINTS; PR01415; ANKYRIN.
CC SMART; SM00248; ANK_6.
CC PROSITE; PS50088; ANK_REPEAT; 4.
CC PROSITE; PS50297; ANK_REPEAT_REGION; 1.

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KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 150 180 ANK 1.
FT REPEAT 184 214 ANK 2.
FT REPEAT 218 247 ANK 3.
FT REPEAT 250 280 ANK 4.
FT REPEAT 285 311 ANK 5.
FT REPEAT 315 344 ANK 6.
FT REPEAT 348 377 ANK 7.
FT ACT SITE 464 464 Potential.
SQ SEQUENCE 751 AA; 83582 MW; 393BBADAVFC99B CRC64;

Query Match 90.0%; Score 3257; DB 1; Length 751;
Best Local Similarity 89.7%; Pred. No. 3,2e-241;
Matches 616; Conservative 29; Mismatches 40; Indels 2; Gaps 2;

QY 1 MGFGRVINTFGSVTLNLSNPPRVKAVADYSSQVRVREBGLIFONTPNRTWCCLV 60
DB 1 MGFGRVINTVTLSSVTNLSNPPRVKAVADYSSQVRVREBGLIFONTPNRTWCCLV 60
QY 61 NPNSSGSRPLPOLLEADALVNFHOYSSQLAPYESSPOVLTETVLOHITDLIRHPSK 120
DB 61 NPNSSGSRPLPOLLEADALVNFHOYSSQLAPYESSPOVLTETVLOHITDLIRHPSK 119
QY 121 SVANLAVELGIRCFHSHRIISCANCAENEBGCTPLHLACRKGSHIVELVQYCHTQND 180
DB 121 SVANLAVELGIRCFHSHRIISCANCAENEBGCTPLHLACRKGSHIVELVQYCHTQND 179
QY 120 TVTHLAVELGIRCFHSHRIITCANSTENEBGCTPLHLACRKGSHIVELVQYCHTQND 179
DB 120 TVTHLAVELGIRCFHSHRIITCANSTENEBGCTPLHLACRKGSHIVELVQYCHTQND 179
QY 181 VTDYKGVFHHVAVQDQNSQVTLQGRNVAAGLVNNOGLTPHLACQKQKQKQKQK 240
DB 181 VTDYKGVFHHVAVQDQNSQVTLQGRNVAAGLVNNOGLTPHLACQKQKQKQKQK 239
QY 180 VTDYKGVFHHVAVQDQNSQVTLQGRNVAAGLVNNOGLTPHLACQKQKQKQKQK 239
DB 180 VTDYKGVFHHVAVQDQNSQVTLQGRNVAAGLVNNOGLTPHLACQKQKQKQKQK 239
QY 241 LCNARININGPNQYPLHSAMKPSQKCAEMTISMSQSHSDQRYGASPLHAKNAEMA 300
DB 241 LCNARININGPNQYPLHSAMKPSQKCAEMTISMSQSHSDQRYGASPLHAKNAEMA 299
QY 240 LCNARININGPNQYPLHSAMKPSQKCAEMTISMSQSHSDQRYGASPLHAKNAEMA 299
DB 240 LCNARININGPNQYPLHSAMKPSQKCAEMTISMSQSHSDQRYGASPLHAKNAEMA 299
QY 301 RMLLKSGCVNVSSTASAGNTALHGVNRNRPDCAIVLITGANADAGEHNTPLHLAMSK 360
DB 301 RMLLKSGCVNVSSTASAGNTALHGVNRNRPDCAIVLITGANADAGEHNTPLHLAMSK 359
QY 300 RMLLKSGCVNVSSTASAGNTALHGVNRNRPDCAIVLITGANADAGEHNTPLHLAMSK 359
DB 300 RMLLKSGCVNVSSTASAGNTALHGVNRNRPDCAIVLITGANADAGEHNTPLHLAMSK 359
QY 361 DNVEIMKALIVGAVDTPNDPGETPFLASKIGK-LQDLMHSRARKPAFLIGSWRDEK 419
DB 361 DNVEIMKALIVGAVDTPNDPGETPFLASKIGK-LQDLMHSRARKPAFLIGSWRDEK 419
QY 360 DNVEIMKALIVGAVDTPNDPGETPFLASKIGK-LQDLMHSRARKPAFLIGSWRDEK 419
DB 360 DNVEIMKALIVGAVDTPNDPGETPFLASKIGK-LQDLMHSRARKPAFLIGSWRDEK 419
QY 420 RTHDHLCLDGGVGVGLVITLIQLLIERKASGVATKOLPFWAGTGTGILALAILHSSKM 479
DB 420 RTHDHLCLDGGVGVGLVITLIQLLIERKASGVATKOLPFWAGTGTGILALAILHSSKM 479
QY 480 AYVRGMYFRMKDEVFRGSRPYESGPLEBEFLKKEFGSHNTMTDVRKPKWLTGTLSDROPA 539
DB 480 AYVRGMYFRMKDEVFRGSRPYESGPLEBEFLKKEFGSHNTMTDVRKPKWLTGTLSDROPA 539
QY 540 ELHLFRNYDAPETVREPRFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGG 559
DB 540 ELHLFRNYDAPETVREPRFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGG 559
QY 540 ELHLFRNYDAPETVREPRFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGG 559
DB 540 ELHLFRNYDAPETVREPRFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGG 559
QY 600 LLAANNPTLAMEIHEYNODLIRKQOANKVKLSIVSLGTRSPQVPYTCVDVFRPSNP 659
DB 600 LLAANNPTLAMEIHEYNODLIRKQOANKVKLSIVSLGTRSPQVPYTCVDVFRPSNP 659
QY 660 WELAKTVFGAKELGKRVVDCCTDPDGR 686
DB 660 WELAKTVFGAKELGKRVVDCCTDPDGR 686

RESULT 8
Q6DDKO PRELIMINARY; PRT; 756 AA.
AC Q6DDKO;
AT 01-OCT-2004 (TRENBERG, 28, Created)
DT 01-OCT-2004 (TRENBERG, 28, last sequence update)
DE 01-OCT-2004 (TRENBERG, 28, last annotation update)
DE Hypothetical protein.
DE Xenopus laevis (African clawed frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomihyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez Y., Bouffard G.G.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Klein S., Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073558; AAH7558.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 756 AA; C0278741CA52A71 CRC64;
 Query Match 61.1%; Score 2210.5; DB 2; Length 756;
 Best Local Similarity 59.9%; Pred. NO. 8.5e-161;
 Matches 413; Conservative 120; Mismatches 152; Indels 5; Gaps 2;
 QY 1 MGFGRVNTFSQVTNLFSPNPRKVEVAVADYTSSDRREGLLFPONTNPTWDCVLV 60
 DB 1 MGFGRVNTFSQVTNLFSPNPRKVEVAVADYTSSDRREGLLFPONTNPTWDCVLV 60
 QY 61 NPNSQSGFPLFOLEADLVNPHQYSSQLPPYESSPOLVHTVQLHTDLIRNPSW 120
 DB 61 NPSSPQNAVYLFPLESEPEALCFQEAVALKLRPFYESSRGLCLETIQQQLDTCIRSHPM 120
 QY 121 SVNHLVGLGIRCFPHSRIRISNCANCAENEGCGPLHLARKDGEIVLVOYCHTMD 180
 DB 121 SLNHLVGLGIRCFPHSRIRISNCANCAENEGCGPLHLARKDGEIVLVOYCHTMD 180
 QY 121 SLNHLVGLGIRCFPHSRIRISNCANCAENEGCGPLHLARKDGEIVLVOYCHTMD 180
 DB 121 SLNHLVGLGIRCFPHSRIRISNCANCAENEGCGPLHLARKDGEIVLVOYCHTMD 180
 QY 181 VTDYKGTVEFVAVQDGNQVQLDGLGNNAVAGLNQVNNQGLTPHLACQLGKQEMVAVLL 240
 DB 181 VTDYKGTVEFVAVQDGNQVQLDGLGNNAVAGLNQVNNQGLTPHLACQLGKQEMVAVLL 240
 QY 181 IADQNGETVYVHHAQQNNPRVIELGSPVGVVHKSNNMETPLHVCRLGKTELVALLL 240
 DB 181 IADQNGETVYVHHAQQNNPRVIELGSPVGVVHKSNNMETPLHVCRLGKTELVALLL 240
 QY 241 LCNARCTIMPNGYPTIHSANKFGKCAEMTISMDSSQHSKDPRIYASPLHAKAEMA 300
 DB 241 LCNARCTIMPNGYPTIHSANKFGKCAEMTISMDSSQHSKDPRIYASPLHAKAEMA 300
 QY 241 RCHARCDIIGKDGPIPTAMKYSQKCEVBAILDVSAQHLAEBPRYQATPIHAKAEMA 300
 DB 241 RCHARCDIIGKDGPIPTAMKYSQKCEVBAILDVSAQHLAEBPRYQATPIHAKAEMA 300
 QY 301 RMLLKGGCVNNTSSAGNTALHYGVMBNPDCAIVLLTHQANDARGHNTPLHLSMSK 360
 DB 301 RMLLKGGCVNNTSSAGNTALHYGVMBNPDCAIVLLTHQANDARGHNTPLHLSMSK 360
 QY 301 RLTIERGCVNNTSCKTLDPLHTVWKDRPEALMVAVLTNVADPVKGEHNTPLHLSMK 360
 DB 301 RLTIERGCVNNTSCKTLDPLHTVWKDRPEALMVAVLTNVADPVKGEHNTPLHLSMK 360

QY 361 DNEMTKALIVFGAEVDPNDPFGERTPLASKIGK-LQDLMIHSRARK----PAFLGSM 415
 DB 361 DQELIKALMVFAVDVQHNDFEGTETGLTAARSXKGRFVYVSTALSGMLVQDVRDFR 420
 QY 416 RDEKRTDHLCLDGGVKGGLITIQLLIAEKASGATDLPFWAGSTGGIATAIILH 475
 DB 421 EDGLRKYDRLCLDGGGIRGLVLMQLLIAEKAGAPRIELFPWVGSTGGIATAIYH 480
 QY 476 SKSMAYWRGMYPMKQEVFGSRPYESGPLSEPLKXREPGHTMTQVRPKVLTGLTSD 535
 DB 481 GPMESVRYCLYFMKQEVFGSRPYESGPLSEPLKXREPGHTMTQVRPKVLTGLTSD 540
 QY 536 RQPAELHLPFANYDAPETVREPRNQVNLRRPAQPSDOLVWRARSSGAAPYFRNGRF 595
 DB 541 RHPAEHLFPFANYDAPETVREPRNQVNLRRPAQPSDOLVWRARSSGAAPYFRNGRF 600
 QY 596 LDGGLANPTLDAMEIHEHYNODLRKQANKKLSIVSLGTRSPQVPTCVDR 655
 DB 601 LDGGLSNPTLDAMEIHEHYNCLKKGAGGVKKGIVSLGTRSPQVPTCVDR 660
 QY 656 PSNPWEIAKTVFGAKELGKVVVDCCTDPDG 685
 DB 661 PSNPWEIAKTVFGAKELGKVVVDCCTDPDG 690
 RESULT 9
 ID 06NMYO PRELIMINARY; PRT; 818 AA.
 AC 06NMYO;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Zgc:77476.
 GN Name=zgc:77476;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomihyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez Y., Bouffard G.G.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC067375; AAH67375.1; -;
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Pataatin.
 DR Pfam; PF00023; Ank; 6.

QY 438 IIOIIAIEKASGATKDFDVAAGTSGIILALAIHSGMAVMGMYPKMDVEFRGS 497
 DB 480 LIIILLALIEGASRPRIELFDWISGISTGIIALAIHSGMSEYKLYIRMEQVFKGS 539
 QY 498 RPYESGPLEBFLKREGEHTKMTDVKKKMYLTGTLSDRQPAELHFRNYDAETVREPR 557
 DB 540 RPYESGPLEBFLKREGEHTKMTDVTHPRVMTSVLADRHGELHFRNYDPAEQDPP 599
 QY 558 FNNNNLPRPAQ-----SPOLYRARSSGAAPTYFRPN 592
 DB 600 YKSTATFQPLTVQGWEDDLIVGYTRPRKRYTDEQLVWRARSSGAAPTYFRPN 659
 QY 593 GRFLDGLIANNPTLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTGRSPQVPTCYD 652
 DB 660 GRFLDGLIANNPTLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTGRSPQVPTCYD 719
 QY 653 VFRSPNPWEIATVFGAKELGKRVVDCCTDPDG 685
 DB 720 VFRSPNPWEIATVFGAKELGKRVVDCCTDSDG 752

RESULT 11

QY 070201 PRELIMINARY; PRT; 879 AA.

AC 070201; PRELIMINARY; PRT; 879 AA.
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE EBI3359 (Fragment).
 GN Name=eb1G3359; ORFNames=ENSANG00000002698;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 NCBI_TaxID=180454;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

CC EMBL: AAAB01008968; EMBL3225.1; -
 DR GO: GO:0003824; F: catalytic activity; IEA.
 DR GO: GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000560; HisAc_phosphatase.
 DR InterPro: IPR002641; Patalin.
 DR Pfam: PF00023; Ank; 6.
 DR Pfam: PF01734; Patalin; 1.
 DR PRINTS: PRO1415; ANKYRIN.
 DR PROSITE: PS50088; ANK_REPEAT. 3.
 DR PROSITE: PS50297; ANK_REPEAT_REGION. 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW ANK repeat.
 FT NON_TER 1 1
 FT NON_TER 879 879
 SQ SEQUENCE 879 AA; 96484 MW; 3491E003CF637188 CRC64;

Query Match 32.2%; Score 1164; DB 2; Length 879;
 Best Local Similarity 32.1%; Pred. No. 2.8e-80;
 Matches 260; Conservative 134; Mismatches 269; Indels 146; Gaps 9;

QY 21 PFVKEVAVADYSSDRVREEGQILFQNTPNR-----TWDCLVAPRNS--OSGRLFLQ 73
 DB 11 PNVQAEKVESYINLPVQNESMRLEFAPNNSPDKLVYEILIERHSESTINTSYSLR 70
 QY 74 LELEADLVVPHOYSSQLPFYESSPOVLTHTVLOHTLDIRHNSVVAHLVGLIRE 133
 DB 71 ATTQSAEEKEFEAPHQRLPELVKIVREMYINGIQKCLDVLINDPSLSLHVAVFYLTLD 130
 QY 134 CFHHSRIISCANCAENEGCTPLHLACRKDGELVELVGYCHTQMDVTDTYKGETVFHYA 193

DB 131 YISNPSIIFLDYABESENMTPELOVAVKANNIEFVALLIQSNOCNIEHDKNSNSVFHYA 190
 QY 194 VQDSDNQVQLGGRNAVAGLQNNNGLTPLHLAQLQKQEMVRYLLCNACNIMSPNG 253
 DB 191 A-STTKEMTNMLANSTSNLNCNDGYTPHLACLADKPCVKALLAGADTKMA-RG 248
 QY 254 YPIHSAKKSOKGCAEMISMSQIHSKDPYRGASPLHMAKVAEMARMILKRGCVNST 313
 DB 249 AGTSYSKSLPSSNVADFLVS-NPNKLFQDMKGKGTPLHSSSREVLNLSIERGCVNLV 307
 QY 314 SSAGNTALVGVKRNRPDCALVLLTGGANADARGEHTPLHLMSKNVEMIKALIVRG 373
 DB 308 NENGQTPPLHVMVARDLECVALLAHDAEIDVDVNSGNTPLHIAVEKKLPIYQCLVFG 367
 QY 374 AEVDTPNDGERTPTL-----ASKIGKQLDMH----- 401
 DB 368 ADFNKNKDKGKTPRLHVGKDSGSKSMILYILHSYAKRCPEKSKCPCGCAAGTYNG 427
 QY 402 -----ISRA 405
 DB 428 IPPAQPETTEQREHIQVLAFTTTSKHSNVSPLSINTIRATIPERERPEVKTVDVSGE 487
 QY 406 RKDPAFLGSM-----RDEKRTHD----- 423
 DB 488 RKGASMDALLSMFMSKVEAASKPTSTSSSLKXCAGSGQRDTSRFRSSCEAGSGE 547
 QY 424 -----HLICLOGGGVGLIIIOIIAIEKASGATKDFDVAAGTSGIILALAIHSG 477
 DB 548 SYNGRRLCLDGGGKRGVLAQMLDEIENLAQTPVHLFDIAGTSGIILALAIHSG 607
 QY 478 SMAVMGMYPKMDVEFRGSRPYESGPLEBFLKREGEHTKMTDVKKKMYLTGTLSDRQ 537
 DB 608 TMKQGCCLYLRMKDQAFVGSRPYSDQLFTVKEQGEFTVMSDIGPRLMTGVVADRK 667
 QY 538 PABLHFRNYDAETVREPRFNQNNVLRPPAOSDQLVWRARSSGAAPTYFRPNRFLD 597
 DB 668 PVNLHLFRNYEASDLSIVTSPNNRGPPPEBQLVWRARATGAASYFAFGRLD 727
 QY 598 GGLIANNPTLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTGRSPQVPTCYDVFERS 657
 DB 728 GGLIANNPTLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTGRSPQVPTCYDVFERS 787
 QY 658 NPWEIATVFGAKELGKRVVDCCTDPDGR 686
 DB 788 SIWATAKVAVGISTITLLVDQATADGR 816

RESULT 12

QY 09VT60 PRELIMINARY; PRT; 877 AA.

AC 09VT60; PRELIMINARY; PRT; 877 AA.
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE CG6718-PA.
 GN ORFNames=CG6718;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.

RP MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Geiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amandites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H., Blazek R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Avril J.F., Agdayant A., An H.U., Andrews-Pfennoch C., Baldwin D.,
 RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle K.C., Daventport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hestlin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,
 RA Jatalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Klamm B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Noshvili A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
 RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodagel, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RA Science 287:2185-2195 (2000).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537566;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frisbe E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RA "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RA *melanogaster* euchromatic genome sequence.";
 RA Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frisbe E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RA "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RA a genomic perspective.";
 RA Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu U., Bergman B.P.,
 RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RA systematic review.";
 RA Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 [5]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 EMBL; AEO03550; AAF50194.3; -.

DR HSP: Q60778; 10Y3.
 DR FLYBASE; FBgn0036053; CG6718.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF000023; Ank; 5.
 DR Pfam; PF017343; Patatin; 1.
 DR PRINTS; PR01415; ANKTRIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PSS0088; ANK_REPEAT; 3.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.
 SQ SEQUENCE 877 AA; 96862 MW; C9DC2C06C282869B CRC64;
 Query Match 32.1%; Score 1163.5; DB 2; Length 877;
 Best Local Similarity 31.9%; Pred. No. 3e-80;
 Matches 257; Conservativity 135; Mismatches 248; Indels 165; Gaps 12;
 QY 17 LPSNPVAVNAADVTSSDRVREBQGLIFQTPTRMTDVCVIVNRNSGFRLEL 76
 DB LFAVPF-----NSSNEKRAVVEIILQRTSD-----SNTSFLRSVP 78
 QY 77 EADALVNFQYSSQLLPFYESSPOVLTTEVLTQHLTLIRHPMSVAHLAVEIGRECFH 136
 DB 79 QQEAERFRNAPLQRLPVFVIVRYVYVNVNGLQACALADNPSTWLSHLAYFNVDYIS 138
 QY 137 HSRBIISCANCAENEBEGCTPLHLACRKGDEIVELVQYCHTQMDVTDTYKGETVFRYAVQG 196
 DB 139 NPKMLQCVDDADATATLMSFPQALIKQGHMEVYKALPL--SKLHHDINSNSVFHYAA-S 195
 QY 197 DNSQVQLGRNAVAGLVNNOGLTPHLACQLGQGEQVWVYLLCNARINIGPNCPYI 256
 DB 196 TTKELINLLIDKSTVNLNHLNSDGYTPPLHVAACADPEVYKALLGAVNLT--NAKDI 252
 QY 257 HSAKFSQKCAEMTISMSDSQHSKDPYRGASPLHMAKNAEVARMLKRCGVNSTSSA 316
 DB 253 RKYYTSAPTTVSSFLRTNVSKITYTDMKYGTPLMCSRETLHLIMGCVNATNFD 312
 QY 317 GNTALHVGVRNRPDCAIVLLTGHANADARGEHTPLHLAMSKDVEMIKALIVGAEV 376
 DB 313 GRTALHVMVARNFECEVTLTADAEIDVLDKGNALHIAIKLVPIVQCLVVEGCDI 372
 QY 377 DTENDGERP-----TFLASKG----- 394
 DB 373 NLNKKQKTPRANVNDASGNKDEILYILHSVGARKCKDTGSKCPGCAKNVNGIPP 432
 QY 395 ----KLQDLMIHR-----ARKPAFI----- 411
 DB 433 EAESEVQRHIEHMLATTSROMMGFLNAAANGILEKQPAQPVVVDTEKELKQSIM 492
 QY 412 -----LGSNR-----DEKTHDH 424
 DB 493 DALLGMFTTVNADENKENSSDSLASGQKSVSSPEQLPSPSPIAAEIGKPYGRGR 552
 QY 425 LTLCDGGVYKGLIILQLLAIEKASGVATKDPDMVAGSTGGIILALILHSMAMVRG 484
 DB 553 LTLCDGGKRGVLVQMLLEIKLSRPIIHMVDWLAGSTGGIILALGCGTMOQWG 612
 QY 485 MYFRMKDEVGRSPYSGPLFEFLKREFGCHTKMTDVKPKYMLTGLTSDRPAELHLF 544
 DB 613 LYIRMEGCTVGRSPNSEFESILKDNIGEFVMTDINKPKIMGVWADRKPVDLHLF 672
 QY 545 RNYDADETVR--EPFNQNVNLRPPAOPSDQVLPAAASSGAAPYFRPNRFPDGLGL 601
 DB 673 RNYTASDILIGIVTPINNRI---PPQPSQQLVMPAABATGAAPSPYAFGRFLDGLGI 729
 QY 602 ANNPPTDAMTEIHEYNQDLIRKQANKYKLSIVSLGCRSQVAVVTCVVDVPRSPNPS 661
 DB 730 ANNPPTDAMTEIHEYNMALRSAGRESEALPVSVVMSLGTGHLPTVELKQIDVFRPESIDW 789
 QY 662 LAKTVEGAKELGKRVVDCCTDPDGR 686

DB 790 TAKLAVISTGNLVDQATCSGDR 814

RESULT 13

AAFS0194 PRELIMINARY; PRT: 877 AA.

ID AAF50194; (TREMBlrel. 27, Created)

AC AAF50194; (TREMBlrel. 27, Last sequence update)

DT 01-APR-2004 (TREMBlrel. 27, Last annotation update)

DE CG6718-PA.

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

SEQUENCE FROM N.A.

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L., Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballow R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P., Burdits K.C., Busam D.A., Butler H., Cadelis E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Deodson K., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M., Durbin K.J., Evans G.C., Ferraz C., Ferriere S., Fleischmann W., Foster A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Goadet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hottel D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Jafarizadeh S., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Maccubbin A.E., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M., Palazzolo M., Pittman G.S., Sanders R.D., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Smit E., Spradling A.C., Stapleton M., Strong R., Sun B., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wasserman D.A., Weinstock G.M., Wu D., Yang S., Ye Q.A., Ye J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Ye Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195(2000).

SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R., Paclab J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.C., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the *Drosophila melanogaster* euchromatic genome sequence." Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

SEQUENCE FROM N.A.

MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bellenkourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.; "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review." Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

SEQUENCE FROM N.A.

MEDLINE=22426070; PubMed=12537573;

Celniker S.E., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celinker S.E.; "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomic perspective." Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

SEQUENCE FROM N.A.

FLYBASE; (SEP-2002) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.

Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

EMBL; AEO03550; AAF50194.3; -

FLYBASE; FBgn0036053; CG6718.

SEQUENCE 877 AA; 96863 MW; C9DC2CD6C282869B CRC64;

Query Match 32.1%; Score 163.5; DB 2; Length 877;

Best Local Similarity 31.9%; Pred. No. 3e-80;

Matches 257; Conservative 155; Mismatches 248; Indels 165; Gaps 12;

17 LPSNPVAKVANAADTSSPRVREBQGLIFQVTPKRTMDVLRNRSQSSGRLEQLDEL 76

40 LFAAPF-----NSSNEKVAVEILLQRTSP-----SNTSFLRSPV 78

77 EALALVNFHOYSQQLPFYESSPOVLTTEVLQHLTLIRNPSMSVAHLAVELGIECFH 136

79 QQAERFNAFLQRLVVFVSIVKEYVNVANGLOACALADNPWTSLHLAYENLVDIYS 138

137 HSRILCANCAENEBECSTPLHLACRKGDELVELVQVCTQMDVTYKGETVFHYAVQG 196

139 NPKMLQCVDPADATLMSFPQLAKQGHMEVYKALPL--SKLEHNDINSNSVFHAA-S 195

197 DNGOVLQGLGRNAVAGLNVNNGGLPRLHACQLGQEGQEMVRVLLLCNRCNMGPRGYP 256

196 TTYEILNLIIDKSTVNLNHLNSDGYVPLHACADLPENVKALLLAGANVL--NAKD 252

257 HSAKFSQKCAEMIISMDSQTHSKDPYRGASPLHMAKVAEMARMILKRCNVNSTSSA 316

253 RKYKTSAPRTTSSFLRTNVSKLYTQDMKYGGRPLMCSSERLHLLIMEGCVNNTNPD 312

317 GNTALHGVGRNFPDCAVLVLTGANADARGHGNTPLHLANSKDNVEIKALIVGAIV 376

313 GRTALHYMVARNFECVTLADAEIDVLKDKGNALHIAIEKKLVPTVQCLVVGCDI 372

377 DTENDFGEP-----TFLASKIG----- 394

373 NLKNKQKTPRHVNVGNDASGNKDEILYILSHVAGRCCKDTGSKPPCGCAKNYNGIPP 432

395 ----KLQDLMIHR-----ARKPAFI----- 411

433 EAPESVQRHIIHMLATTSRQMGFLVAAAAGILEKQAPKPPVVDTEKSLKQGSIM 492

412 -----LGSNR-----DEKTHDH 424

493 DALLGMFTTVNADENKENSDSLASGQKSVSSPEQLPSPSPAIAGIDKPYRGGR 552

425 LLLDGGGVKGLIIQLLAIERKASGVATKDLFDWVAGTSGTLLALILHSSMYMNG 484

DB 553 LILCDGGGIRGLVLYOMLEIEKLSRTPIIHFMDWIACTSTGILALALGCGKTRQCMG 612

QY 485 MYRMDEVRFRGSRPESGLESLEFKRESEHTRKTDVDRPKMVLGTSLDRPAAHLHF 544

DB 613 LYLKMEQOCVGRSPNSEPFESILKDMGSEFVMMDDIKPKIMVGVMDRCPVLLHF 672

QY 545 RNDABEYTR---EPPFNQVNNRPPAPSDOLVWRAASGAAPYFRNGRFLDGLL 601

DB 673 RNTTASDLIGITYTPINNRI---PPQSEQLVWRAARATGAAPSTRFGRFLDGLI 729

QY 602 ANPTIDAMTEIHEYNODLIRKQANKKSLIVSLGTSRSPQVPTCVDFRPSNPM 661

DB 730 ANPTIDAMTEIHEYNMAMASAGRESEALIVSVVMSLGTCHIEVTLEKOIDVFRPSIND 769

QY 662 LATTVGAKELGKVVVDCCCTDPRGR 686

DB 790 TATLAVGISTGIMLVDAQATCSGR 814

RESULT 14

Q7KUD4 PRELIMINARY; PRT; 887 AA.

AC 07KUD4; 05-JUL-2004 (TEMBLrel. 27, Created)

DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

DE CG6718-PB (CG6718-PC).

GN ORFNames=CG6718;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_taxid=7227;

OK [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10711132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sulten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abil J.F., Aghayani A., An H.J., Andrews-Pfannkoch L., Basley E.M.,

RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolnakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,

RA Foslter C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegan C.,

RA Jatali M., Kalush F., Kapren G.H., Ke Z., Kemison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasbo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mpherson D.,

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RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [31]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Belcencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [32]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Belcencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [33]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Belcencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [34]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Belcencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [35]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Belcencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [36]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA H

| | | | |
|----|-----|---|-----|
| Qy | 17 | LFSNPFVKEVAADVADTSSDRVREBGOILLFONTPNRTWCVLVNERNOSGFRLEFOLEL | 76 |
| Dz | 50 | LFAPFP-----NSSNEKRAVEIILQRPSTD-----SWTSFSLRSPV | 88 |
| Qy | 77 | EADLVNFHOYSOQLPPFESSPOVLHTEVLOHTDULRNHBSWAHLAVELGIPECH | 136 |
| Dz | 89 | OQEERNAEFORLPVFVSIVKEYYNNGLOKACALANDSMTLSHLAFNLVDYIS | 148 |
| Qy | 137 | HSRIISCANCAENEGCTPLHLACKRGDEILLVELVOUCHTOVDYDKGETVFHYAOG | 196 |
| Dz | 149 | NPKMLQCVDQDAATLMSPFOALIKQHHEMVKALLPL--SKLEHDINSNSVFHYAA-S | 205 |
| Qy | 197 | DNSOVTLQLGNNAVAGLANOVNOGLTPLHLAQOLGQEWVRULLCNARCNIMGPRGYI | 256 |
| Dz | 206 | TTKEIINIINIDKSTVNHLINLDGYTPPLHVACLADPENVVKALLLAGAVNL--NAKDI | 262 |
| Qy | 257 | HSAMFSQKCGCAEMIIISMDSOIHSNDPRYGASPLHMANKMAEMARMLIRGCNVNSTSA | 316 |
| Dz | 263 | RKVYTSAPTYVSSFRLRTNVSKLTLYQDMKGGTGPLHMCSSRETIAHLIMEGCDVANIND | 322 |
| Qy | 317 | GNTALHVGMRNRFPCAIVLLTHGANADARGHGNTPLHLAMSNDVNEMI KALIYGAEV | 376 |
| Dz | 323 | GRTALHWVARRRFEVCVTLLAHDAEIDVLDKGNALHAIAIEKKLPIVQCLVNEGCDI | 382 |
| Qy | 377 | DTPNDFGTP-----TFASKIG----- | 394 |
| Dz | 383 | NLKNDXGKTPRHMGVNDASGNKDDELITYLHSVAGRCCKDTOSKCPGNCANKNYNGIRP | 442 |
| Qy | 395 | ----KLQDLMIHSR-----ARKPAFI----- | 411 |
| Dz | 443 | EAPESVEQREHI EHNLAATTSRQMGGFLMAANGILEKQOPAKPVVDTBELKQSJM | 502 |
| Qy | 412 | -----LGSNR-----LGSNR-----DEKTRDH | 424 |
| Dz | 503 | DALLGMFTTKVNADEMKEKNESSDSLASGQKAVSSPEOLPSFTSDIAEIOGKPYGGR | 562 |
| Qy | 425 | LLCDDGGGVKGLIILQILAIEKASGVATKDLFDWVAGSTGGIILALITLHKSMAVMRG | 484 |
| Dz | 553 | LLCDDGGGIRGLVLYOMLIEIKLSTPTIHHFDWJAGSTGGIILALAGCGKTMQCMG | 622 |
| Qy | 485 | MYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVKRPKVMLTGSLSDROPAELHF | 544 |
| Dz | 623 | LYLRMEKCOCFVSGRPNSSEFFESILKDNJGSEFVVMTDIGHPKIMVGNADRXPVDLHF | 682 |
| Qy | 545 | RNYDAPEYVR---EEFPNONVMLRPAOSDOLVMPAAARSAGAAPPYRPNGBFLDGILL | 601 |
| Dz | 683 | RNYTSASDILGIVTPINNRRI---PPQPSEOLVWMAAARAATGAAPSIFRAFGFELDGILL | 739 |
| Qy | 602 | ANNPTLDANTEIHEYNUODLIRKGOANKVKKLSIVSLTGRSPQVNVTCVDVFERPBNPME | 661 |
| Dz | 740 | ANNPTLDAMTBHEHNMALRSAGRSEALPVSVMVSLGTGHIPVTELKOVIDPREPSIND | 799 |
| Qy | 662 | LAKTVFGAKEJGKMVVDCCTDPGR | 686 |
| Dz | 800 | TAKLAVGISITIGNLLVDAQTCSDGR | 824 |

Search completed: December 15, 2004, 13:13:14
Job time : 153.609 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:51:45 ; Search time 139.101 Seconds
(without alignments)
1771.710 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620
Sequence: 1 MGFPGRLVNTFGSVTVTLFNSN.....GAKELGKRVVDCCTDGR 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-----------------------|
| 1 | 3620 | 100.0 | 687 | 2 | AAW17847 Cytochrome c |
| 2 | 3620 | 100.0 | 687 | 5 | ABR82231 Human pro |
| 3 | 3606.5 | 99.6 | 688 | 2 | AAW17848 Cytochrome c |
| 4 | 3606.5 | 99.6 | 688 | 5 | ABR82232 Human pro |
| 5 | 3593.5 | 99.3 | 784 | 7 | ADD93407 Human 11p |
| 6 | 3566.5 | 98.5 | 806 | 5 | AAE25968 Human PLA |
| 7 | 3566.5 | 98.5 | 806 | 8 | ADO19776 Human PRO |
| 8 | 3302.5 | 91.2 | 752 | 2 | AAW01479 Calcium-i |
| 9 | 3302.5 | 91.2 | 752 | 2 | AAW01479 Calcium-i |
| 10 | 3302.5 | 91.2 | 752 | 2 | AAW13163 Ca-indupe |
| 11 | 3302.5 | 91.2 | 752 | 2 | AAW17849 Hamster c |
| 12 | 3302.5 | 91.2 | 752 | 2 | AAW81825 Chinese h |
| 13 | 3302.5 | 91.2 | 752 | 5 | ABR82215 Calcium i |
| 14 | 3257 | 90.0 | 751 | 7 | ADD46244 Rat Prote |
| 15 | 3257 | 90.0 | 751 | 7 | ADDE6532 Rat Prote |
| 16 | 3257 | 90.0 | 751 | 7 | ADDE5230 Rat Prote |
| 17 | 3257 | 90.0 | 751 | 7 | ADDE6036 Rat Prote |
| 18 | 2723 | 75.2 | 667 | 7 | ADM05093 Human pro |
| 19 | 2084 | 57.6 | 394 | 5 | AAW17845 Cytochrome c |
| 20 | 2084 | 57.6 | 394 | 5 | ABR8229 Calcium i |
| 21 | 1690.5 | 46.7 | 401 | 4 | AAW92811 Human pro |
| 22 | 1531 | 42.3 | 292 | 2 | AAW17846 Cytochrome c |
| 23 | 1531 | 42.3 | 292 | 5 | ABR82230 Calcium i |
| 24 | 1163.5 | 32.1 | 877 | 4 | ABR62624 Drosophila |
| 25 | 338 | 9.3 | 843 | 7 | ADD27861 Rat ankyr |

| | | | | | |
|----|-------|-----|------|---|---------------------|
| 26 | 332 | 9.2 | 1839 | 7 | ADD27862 Human bxa |
| 27 | 332 | 9.2 | 1872 | 4 | AAW79160 Human pro |
| 28 | 324 | 9.0 | 1330 | 7 | ADM04552 Human pro |
| 29 | 320 | 8.8 | 1549 | 4 | ABR67412 Drosophila |
| 30 | 320 | 8.8 | 1549 | 4 | ABR85328 Drosophila |
| 31 | 305.5 | 8.4 | 1745 | 2 | AAW76776 Drosophila |
| 32 | 305.5 | 8.4 | 1745 | 2 | AAW70608 Full leng |
| 33 | 305.5 | 8.4 | 1745 | 3 | AAW11589 Drosophila |
| 34 | 305.5 | 8.4 | 1745 | 5 | AAW021368 Ankyrin p |
| 35 | 302.5 | 8.4 | 2443 | 4 | ABR60521 Drosophila |
| 36 | 302 | 8.3 | 763 | 3 | AAW79154 Mouse pro |
| 37 | 302 | 8.3 | 786 | 3 | AAW69163 Mouse pro |
| 38 | 302 | 8.3 | 786 | 6 | AAW69163 Mouse pro |
| 39 | 302 | 8.3 | 786 | 7 | ABW02414 Mouse pro |
| 40 | 302 | 8.3 | 786 | 7 | ABW02422 Human PKK |
| 41 | 302 | 8.3 | 786 | 7 | ABW02423 Human PKK |
| 42 | 302 | 8.3 | 786 | 7 | ABW02424 Human PKK |
| 43 | 302 | 8.3 | 787 | 3 | AAW76079 Human PKK |
| 44 | 302 | 8.3 | 787 | 4 | ABW56018 Skin cell |
| 45 | 302 | 8.3 | 787 | 5 | ABW72218 Murine pr |

ALIGNMENTS

RESULT 1
AAW17847 standard; protein; 687 AA.

AAW17847: (first entry)

07-AUG-1997

Cytochrome phospholipase A2/B (alternatively spliced clone 19a).

Cytochrome phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

inflammation; inhibitor; antiinflammatory.

Homo sapiens.

MO9717448-A2.

15-MAY-1997.

07-NOV-1996; 96MO-US017794.

08-NOV-1995; 95US-00555568.

(GENE) GENETICS INST INC.

Jones S, Tang J;

WPI; 1997-281037/25.

N-PSDB; AAT68825.

Calcium independent phospholipase A2/B - used to reduce inflammation in a

mammalian subject.

Claim 12; Page 49-51; 74pp; English.

A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is

characterized by activity in the absence of calcium, by activity in a

mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-

phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a

lack of stimulation by ATP, and by including in its sequence at least one

of the amino acid sequences given in AAW17839-44). It is an

alternatively spliced variant of another isolated polypeptide (AAW17845)

and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes

(AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are

thought to be involved in the release of arachidonic acid in specific

tissues. Recombinant sPLA2/B polypeptides produced in transformed host

cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory

drugs which inhibit the arachidonic acid cascade

XX SQ Sequence 687 AA;

Query Match 100.0%; Score 3620; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSNPFVKEVAADYSSDRVREEGQLIFONTPNRTWDCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSNPFVKEVAADYSSDRVREEGQLIFONTPNRTWDCVLV 60

QY 61 NPNRSQGFRLFOLEADALVNFHOYSSQLLPFYESSPOVLTEVLOHITDLIRNHP 120
 DB 61 NPNRSQGFRLFOLEADALVNFHOYSSQLLPFYESSPOVLTEVLOHITDLIRNHP 120

QY 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBGCTPLHLCKRGDGLVLELVQYCHTQMD 180
 DB 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBGCTPLHLCKRGDGLVLELVQYCHTQMD 180

QY 181 VTDYKGETVFNHVAOQDNSQVLLQLRNNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFNHVAOQDNSQVLLQLRNNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKAEMA 300
 DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKAEMA 300

QY 301 RMLLKGCNNVNTSSAGNTALHGVNRNRPDCAVLLTTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLKGCNNVNTSSAGNTALHGVNRNRPDCAVLLTTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDPNDPFGETPTFLASKIGKLODLWHISRAKPAFILGSMDEKR 420
 DB 361 DNVEIMKALIVFGAEVDPNDPFGETPTFLASKIGKLODLWHISRAKPAFILGSMDEKR 420

QY 421 THHHLCTLDGGYKGLIITQLLAIKASGVATDLPDWAAGSTGGIILALILHSKMA 480
 DB 421 THHHLCTLDGGYKGLIITQLLAIKASGVATDLPDWAAGSTGGIILALILHSKMA 480

QY 481 YMGMYFRMDEVFRGSRPYESGPLEBEFLKREGEHNTKMTDVKPKMLAGTISDRQPAE 540
 DB 481 YMGMYFRMDEVFRGSRPYESGPLEBEFLKREGEHNTKMTDVKPKMLAGTISDRQPAE 540

QY 541 LHLFRNYDAETVREPRNQNVNLRPPAOPSDQLWBAARS SGAAPTYFRPNRGFLDQGL 600
 DB 541 LHLFRNYDAETVREPRNQNVNLRPPAOPSDQLWBAARS SGAAPTYFRPNRGFLDQGL 600

QY 601 LANNPTLDANTEIHEYNQDLIRKQANKVKKLSTIVSLGTRSPQVVTCDVFRPSNPW 660
 DB 601 LANNPTLDANTEIHEYNQDLIRKQANKVKKLSTIVSLGTRSPQVVTCDVFRPSNPW 660

QY 661 ELAKTVFGAKELGKMNVDCCCTDPGRP 687
 DB 661 ELAKTVFGAKELGKMNVDCCCTDPGRP 687

RESULT 2
 ABB82231
 ID ABB82231 standard; protein; 687 AA.
 AC ABB82231;
 DE 08-JAN-2003 (first entry)
 XX Human cPLA2/B splice variant (clone 19a).
 XX
 KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiarthritic; antipneumatic; antirheumatic; cytosolic;
 KW antilesthetic; human.
 OS Homo sapiens.
 XX
 PN US2002106364-A1.

XX PD 08-AUG-2002.
 XX PF 09-AUG-2001; 2001US-00927180.
 XX PR 27-JUL-1994; 94US-00281193.
 XX PR 14-APR-1995; 95US-00422106.
 XX PR 14-APR-1995; 95US-00422420.
 XX PR 26-JUN-1995; 95MO-US008069.
 XX PR 08-NOV-1995; 95US-00555568.
 XX PR 09-SEP-1998; 98US-00149988.
 XX PR 06-MAR-2000; 2000US-00519223.
 XX PA (GEMV) GENETICS INST INC.
 XX PI Jones S, Tang J;
 XX DR WPI, 2002-739923/80.
 XX DR N-PSDB; ABV73010.
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 PS Claim 6; Page 23-25; 41pp; English.
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19a)
 XX
 XX SQ Sequence 687 AA;

Query Match 100.0%; Score 3620; DB 5; Length 687;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSNPFVKEVAADYSSDRVREEGQLIFONTPNRTWDCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSNPFVKEVAADYSSDRVREEGQLIFONTPNRTWDCVLV 60

QY 61 NPNRSQGFRLFOLEADALVNFHOYSSQLLPFYESSPOVLTEVLOHITDLIRNHP 120
 DB 61 NPNRSQGFRLFOLEADALVNFHOYSSQLLPFYESSPOVLTEVLOHITDLIRNHP 120

QY 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBGCTPLHLCKRGDGLVLELVQYCHTQMD 180
 DB 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBGCTPLHLCKRGDGLVLELVQYCHTQMD 180

QY 181 VTDYKGETVFNHVAOQDNSQVLLQLRNNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFNHVAOQDNSQVLLQLRNNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKAEMA 300
 DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKAEMA 300

QY 301 RMLLKGCNNVNTSSAGNTALHGVNRNRPDCAVLLTTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLKGCNNVNTSSAGNTALHGVNRNRPDCAVLLTTHGANADARGEHNTPLHLAMSK 360

Db 301 RMLKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Qy 361 DNVEIMKALIVFGAEVDTPNDPFGETPTFLASKIGKLODLMHISARKPAFIIIGSRDEK 420
 Db 361 DNVEIMKALIVFGAEVDTPNDPFGETPTFLASKIGKLODLMHISARKPAFIIIGSRDEK 420
 Qy 421 THHLLCLDGGVKGKLIILQLLAIERKASGVATKDLFDWVAGTSTGGIILALAIHSKMA 480
 Db 421 THHLLCLDGGVKGKLIILQLLAIERKASGVATKDLFDWVAGTSTGGIILALAIHSKMA 480
 Qy 481 YMRGMVFRMKDEVRGSRPYESGPLEEFLLKREFGEHTKMTDVRKPKVMTGLTSLDRQPAE 540
 Db 481 YMRGMVFRMKDEVRGSRPYESGPLEEFLLKREFGEHTKMTDVRKPKVMTGLTSLDRQPAE 540
 Qy 541 LHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
 Db 541 LHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
 Qy 601 LANNPTLDAMTEIHEYNODLIRKQANKVKKLSIVSLGTGRSPQVPTCVDFRPSNP 660
 Db 601 LANNPTLDAMTEIHEYNODLIRKQANKVKKLSIVSLGTGRSPQVPTCVDFRPSNP 660
 Qy 661 ELAKTVFGAKELGKRVVDCCTDPDGR 687
 Db 661 ELAKTVFGAKELGKRVVDCCTDPDGR 687

RESULT 3

AAW17848 standard; protein; 688 AA.

AAW17848;

07-AUG-1997 (first entry)

Cytosolic phospholipase A2/B (alternatively spliced clone 19b).

Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

inflammation; inhibitor; antiinflammatory.

Homo sapiens.

MO9717448-A2.

15-MAY-1997.

07-NOV-1996; 96WO-US017794.

08-NOV-1995; 95US-00555568.

(GEMV) GENETICS INST INC.

Jones S, Tang J;

WPI: 1997-281037/25.

N-PSDB; AAT68826.

Calcium independent phospholipase A2/B - used to reduce inflammation in a

mammalian subject.

Claim 12; Page 54-56; 74pp; English.

CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is
 CC characterised by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-
 CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAW17839-44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17846)
 CC and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes
 CC (AAW17847) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host

CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory

CC drugs which inhibit the arachidonic acid cascade

XX Sequence 688 AA;

Query Match 99.6%; Score 3606.5; DB 2; Length 688;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MGFPGRLVNTFGSVTNLFSPNFRVKEVAVADYTSRDRVREEGQLIFONTPARTWCVLV 60
 Db 1 MGFPGRLVNTFGSVTNLFSPNFRVKEVAVADYTSRDRVREEGQLIFONTPARTWCVLV 60
 Qy 61 NPNRSOSGFRPLFLELEADALVNFHYSQQLPFYESSPOVLTETVLOHTDILRNHPSW 120
 Db 61 NPNRSOSGFRPLFLELEADALVNFHYSQQLPFYESSPOVLTETVLOHTDILRNHPSW 120
 Qy 121 SVAHIAVELGIRRCFHHSRILISCANCAENEGCTPLHLACRKDGELVELVQYCHTQMD 180
 Db 121 SVAHIAVELGIRRCFHHSRILISCANCAENEGCTPLHLACRKDGELVELVQYCHTQMD 180
 Qy 181 VTQKGETVFHVAVOGDNSQVTLQGRNVAAGLNQVNNQGLTPHLACQLGKQEMVRVL 240
 Db 181 VTQKGETVFHVAVOGDNSQVTLQGRNVAAGLNQVNNQGLTPHLACQLGKQEMVRVL 240
 Qy 241 LCNARCNIMGPNQVPIHSAMKFSOKGCAEMTISMDSSQHSKDPYRGASPLHAKNAEMA 300
 Db 241 LCNARCNIMGPNQVPIHSAMKFSOKGCAEMTISMDSSQHSKDPYRGASPLHAKNAEMA 300
 Qy 301 RMLKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Qy 361 DNVEIMKALIVFGAEVDTPNDPFGETPTFLASKIGKLODLMHISARKPAFIIIGSRDEK 419
 Db 361 DNVEIMKALIVFGAEVDTPNDPFGETPTFLASKIGKLODLMHISARKPAFIIIGSRDEK 419
 Qy 420 RTHDHLCLDGGVKGKLIILQLLAIERKASGVATKDLFDWVAGTSTGGIILALAIHSKSM 479
 Db 420 RTHDHLCLDGGVKGKLIILQLLAIERKASGVATKDLFDWVAGTSTGGIILALAIHSKSM 479
 Qy 481 AYMRGMVFRMKDEVRGSRPYESGPLEEFLLKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 539
 Db 481 AYMRGMVFRMKDEVRGSRPYESGPLEEFLLKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 539
 Qy 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 599
 Db 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 599
 Qy 600 LANNPTLDAMTEIHEYNODLIRKQANKVKKLSIVSLGTGRSPQVPTCVDFRPSNP 659
 Db 600 LANNPTLDAMTEIHEYNODLIRKQANKVKKLSIVSLGTGRSPQVPTCVDFRPSNP 659
 Qy 660 WEIAKTVFGAKELGKRVVDCCTDPDGR 687
 Db 660 WEIAKTVFGAKELGKRVVDCCTDPDGR 687

RESULT 4

ABB82232 standard; protein; 688 AA.

ABB82232;

08-JAN-2003 (first entry)

Human cPLA2/B splice variant (clone 19b).

Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;

antiinflammatory; antiarthritic; antipsoaritic; antirheumatic; cytosolic;

Homo sapiens.

PT infections.
 XX Claim 69, Page 206-207, 238pp; English.
 PS
 XX The present sequence is the protein sequence of human lipid-associated
 CC molecule LIPAM-14 (Incyte polypeptide 751262CD1), a protein that shows
 CC homology to human Ca2+-independent phospholipase A2 short isoform. This
 CC is one of 19 LIPAM polypeptides of the invention. The invention relates
 CC to these novel LIPAMs and the nucleic acids encoding them, and to the use
 CC of nucleic acids and proteins in the diagnosis, treatment and prevention
 CC of disorders associated with abnormal expression or activity of LIPAM
 CC such as neurodegenerative disorders (e.g. Parkinson's disease,
 CC Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,
 CC cataractia), endocrine disorders (e.g. diabetes, Grave's disease), cancers
 CC (e.g. leukemia, cervical or breast cancers), immunological disorders
 CC (e.g. scleroderma, systemic lupus erythematosus, allergies),
 CC gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.
 CC gastroparesis syndrome), infections (e.g. viral, bacterial, fungal,
 CC parasitic, protozoal, helminthic), cardiovascular disorders (e.g.
 CC atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention
 CC also relates to the assessment of the effects of exogenous compounds on
 CC the expression of nucleic acids and LIPAMs. The invention provides
 CC expression vectors, host cells, antibodies, agonists and antagonists,
 CC transgenic organisms, and arrays and microarrays of the polynucleotides.
 CC
 XX
 SQ Sequence 784 AA;
 Query Match 99.3%; Score 3593.5; DB 7; Length 784;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 684; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 1 MOFFGRLVNTFSGVTNLFSPNFRKVEAVADYSSDRVRESGQLIFONTPNRTWDCV 60
 DB 33 MOFFGRLVNTFSGVTNLFSPNFRKVEAVADYSSDRVRESGQLIFONTPNRTWDCV 92
 QY 61 NPNRSQGFRLFOLELEADALVNFHOYSQQLPFYESSPOVLAHTEVLOHITDILRNHPSW 120
 DB 93 NPNRSQGFRLFOLELEADALVNFHOYSQQLPFYESSPOVLAHTEVLOHITDILRNHPSW 152
 QY 121 SVAHLAVELGIRCEFHHSRIISCANCAENBEGCTPLHACRKDGILVELVOYCHTQMD 180
 DB 153 SVAHLAVELGIRCEFHHSRIISCANCAENBEGCTPLHACRKDGILVELVOYCHTQMD 212
 QY 181 VTQYKGETVTHYAVQGNQSVQLQLGRNAVAGLNQVNNQGITPLHLACQLCKQEMRVLL 240
 DB 213 VTQYKGETVTHYAVQGNQSVQLQLGRNAVAGLNQVNNQGITPLHLACQLCKQEMRVLL 272
 QY 241 LCNARCNIMGPNNGPIHSAMKFSQKCAEMTISDSSQHSKDPHYGASPLHAKNAEMA 300
 DB 273 LCNARCNIMGPNNGPIHSAMKFSQKCAEMTISDSSQHSKDPHYGASPLHAKNAEMA 332
 QY 301 RMLKRGCVNSTSSAGNTALHVGWNRNPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 DB 333 RMLKRGCVNSTSSAGNTALHVGWNRNPDCAIVLLTHGANADARGEHNTPLHLAMSK 392
 QY 361 DNVEMITQALIVFGAEVUTPDNDFGETPTPLASKIKG-LQDLMLHISRAKRPATILSMDK 419
 DB 393 DNVEMITQALIVFGAEVUTPDNDFGETPTPLASKIKGRODLMLHISRAKRPATILSMDK 452
 QY 420 RTDHLCLDGGGKGLIITLQLAIEKASGATKDLFDWVAGSTGGIATLALILHKSMM 479
 DB 453 RTDHLCLDGGGKGLIITLQLAIEKASGATKDLFDWVAGSTGGIATLALILHKSMM 512
 QY 480 AYNGMGTFRMKDEVFRGSRPYESGPLEBFLKREFGHTKMTDVAKPKVMTLGTLSDRQPA 539
 DB 513 AYNGMGTFRMKDEVFRGSRPYESGPLEBFLKREFGHTKMTDVAKPKVMTLGTLSDRQPA 572
 QY 540 ELHIFRYVDAEETREPRFNQNNLRRPAQPSDOLVWRRAASSGAAPTPYPRNKRFLDGG 599
 DB 573 ELHIFRYVDAEETREPRFNQNNLRRPAQPSDOLVWRRAASSGAAPTPYPRNKRFLDGG 632
 QY 600 LLANNPTLDMTEIHEYNODLIRKQANKVKLSIVSLGTRSPQVPTCVDFRPSNP 659

DB 633 LLANNPTLDMTEIHEYNODLIRKQANKVKLSIVSLGTRSPQVPTCVDFRPSNP 692
 QY 660 WEIATKTVFGAKELGKRWVDCCTDPDGR 686
 DB 693 WEIATKTVFGAKELGKRWVDCCTDPDGR 719
 RESULT 6
 AAE25968
 ID AAE25968 standard; protein; 806 AA.
 XX
 AC AAE25968;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human PLA2 group VI (Ca2+-independent) protein.
 XX
 KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
 XX antisense therapy; PLA2 protein.
 OS Homo sapiens.
 PN US6410325-B1.
 XX
 PD 25-JUN-2002.
 XX
 PE 09-MAY-2001, 2001US-00851896.
 XX
 PR 09-MAY-2001, 2001US-00851896.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Freier SM, Watt AT;
 XX
 DR WPI; 2002-616513/66.
 XX
 DR N-PSDB; AAD42941.
 XX
 PT Novel antisense compounds useful for inhibiting gene expression of human
 PT phospholipase A2, group VI and for treating diseases associated with
 PT expression of phospholipase A2, group VI.
 PS
 XX Disclosure; Col 109-116; 72pp; English.
 CC
 CC The present invention relates to novel antisense compounds which inhibit
 CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 CC (Ca2+-independent) in human cells or tissues and for treating an animal,
 CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnostics, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) protein
 CC
 XX
 SQ Sequence 806 AA;
 Query Match 98.5%; Score 3566.5; DB 5; Length 806;
 Best Local Similarity 92.3%; Pred. No. 0;
 Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;
 QY 1 MOFFGRLVNTFSGVTNLFSPNFRKVEAVADYSSDRVRESGQLIFONTPNRTWDCV 60
 DB 1 MOFFGRLVNTFSGVTNLFSPNFRKVEAVADYSSDRVRESGQLIFONTPNRTWDCV 60
 QY 61 NPNRSQGFRLFOLELEADALVNFHOYSQQLPFYESSPOVLAHTEVLOHITDILRNHPSW 120
 DB 61 NPNRSQGFRLFOLELEADALVNFHOYSQQLPFYESSPOVLAHTEVLOHITDILRNHPSW 120
 QY 121 SVAHLAVELGIRCEFHHSRIISCANCAENBEGCTPLHACRKDGILVELVOYCHTQMD 180
 DB 121 SVAHLAVELGIRCEFHHSRIISCANCAENBEGCTPLHACRKDGILVELVOYCHTQMD 180
 QY 181 VTQYKGETVTHYAVQGNQSVQLQLGRNAVAGLNQVNNQGITPLHLACQLCKQEMRVLL 240

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Db      181 VTQYKGETVFHYAVQGDNSQVLTQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
Qy      241 LCNARCNINPNGYPPIHSAMKFSQKCAEMTISMSDSQIHSKOPRYASFLHAKNAEMA 300
Db      241 LCNARCNINPNGYPPIHSAMKFSQKCAEMTISMSDSQIHSKOPRYASFLHAKNAEMA 300
Qy      301 RMLLKGCNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db      301 RMLLKGCNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Qy      361 DNVEIMKALIVFGAEVDTENDFGETPTFLASKIGK----- 395
Db      361 DNVEIMKALIVFGAEVDTENDFGETPTFLASKIGRLVTRKAILTLRTVGAECFPPIHG 420
Qy      396 -----LQDLMIHSRARKPAFLIGSMRDEKRTDHL 425
Db      421 VPAEQSAAHPHPSIERAOPPPISLNNLELQDLMIHSRARKPAFLIGSMRDEKRTDHL 480
Qy      426 LCLDGGGVKGLIITQLLIAIEKASGVATKDLFDWVAGTSGTGLIALALHLSKSMAYMRGM 485
Db      481 LCLDGGGVKGLIITQLLIAIEKASGVATKDLFDWVAGTSGTGLIALALHLSKSMAYMRGM 540
Qy      486 YFRMKDEVFRGSRPYESGPLBEFLKREFGHTKMTDVRKPKWMLTGLSDROPABELHLFR 545
Db      541 YFRMKDEVFRGSRPYESGPLBEFLKREFGHTKMTDVRKPKWMLTGLSDROPABELHLFR 600
Qy      546 NYAPETVPRPNQVNNLRPPAOPSDQLVWRARSSGAAPTYFRNGRFLDGGLLANNP 605
Db      601 NYAPETVPRPNQVNNLRPPAOPSDQLVWRARSSGAAPTYFRNGRFLDGGLLANNP 660
Qy      606 TLDAMTEIHEYNODLIRKQANVKKLSIVSLGTGRSPQVPTCVDFRPSNPWELAKT 665
Db      661 TLDAMTEIHEYNODLIRKQANVKKLSIVSLGTGRSPQVPTCVDFRPSNPWELAKT 720
Qy      666 VFGAKELGKRVVDDCTDPDGR 686
Db      721 VFGAKELGKRVVDDCTDPDGR 741

RESULT 7
AD019776
ID      AD019776 standard; protein; 806 AA.
AC      AD019776;
XX      12-AUG-2004 (first entry)
DT      Human PRO polypeptide #350.
DE      Human PRO polypeptide #350.
XX      Human; PRO; immune related disorder; systemic lupus erythematosus;
XX      rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
XX      systemic scleroderma; Sjogren's syndrome; vasculitis; sarcoidosis;
XX      autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
XX      diabetes mellitus; renal disease; demyelinating disease;
XX      central nervous system; peripheral nervous system;
XX      demyelinating polyneuropathy; Guillain-Barre syndrome;
XX      chronic inflammatory demyelinating polyneuropathy.
OS      Homo sapiens.
PN      MO200404361-A2.
PD      27-MAY-2004.
XX      06-NOV-2003; 2003WO-US035268.
XX      08-NOV-2002; 2002US-0425235P.
PA      (GETH ) GENENTECH INC.
PI      Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM,
        Wood WI, Wu TD;

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XX      WPI; 2004-42067/39.
DR      N-SDS; AD019775.
XX      Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT      treating an immune related disorder such as systemic lupus erythematosus,
PT      rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
XX      spondyloarthritis.
PS      Claim 7; SEQ ID NO 700; 1731DP; English.
XX      The invention relates to human PRO polypeptides and the polynucleotides
CC      encoding them. The polypeptides and polynucleotides are useful for
CC      treating and diagnosing immune related disorders in mammals. The immune
CC      related disorders include systemic lupus erythematosus, rheumatoid
CC      arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC      sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC      haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC      mellitus, immune-mediated renal disease, demyelinating diseases of the
CC      central or peripheral nervous system, demyelinating polyneuropathy,
CC      Guillain-Barre syndrome and chronic inflammatory demyelinating
CC      polyneuropathy. This sequence represents a human PRO polypeptide of the
CC      invention.
XX      Sequence 806 AA;
SQ
Query Match      98.5%; Score 3566.5; DB 8; Length 806;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;
Qy      1 MOFFGRLVNTFSQVTLFSPNFRVKEVAADYSSDRVBEQGLIFQTPNRTMDCVLY 60
Db      1 MOFFGRLVNTFSQVTLFSPNFRVKEVAADYSSDRVBEQGLIFQTPNRTMDCVLY 60
Qy      61 NPNRSQSGRRLPOLLEADALVNFHOYSSQLBFYSSPOVLTETLQHLTDLIRNHPM 120
Db      61 NPNRSQSGRRLPOLLEADALVNFHOYSSQLBFYSSPOVLTETLQHLTDLIRNHPM 120
Qy      121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVQYCTOMD 180
Db      121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVQYCTOMD 180
Qy      181 VTQYKGETVFHYAVQGDNSQVLTQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
Db      181 VTQYKGETVFHYAVQGDNSQVLTQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
Qy      241 LCNARCNINPNGYPPIHSAMKFSQKCAEMTISMSDSQIHSKOPRYASFLHAKNAEMA 300
Db      241 LCNARCNINPNGYPPIHSAMKFSQKCAEMTISMSDSQIHSKOPRYASFLHAKNAEMA 300
Qy      301 RMLLKGCNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db      301 RMLLKGCNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Qy      361 DNVEIMKALIVFGAEVDTENDFGETPTFLASKIGK----- 395
Db      361 DNVEIMKALIVFGAEVDTENDFGETPTFLASKIGRLVTRKAILTLRTVGAECFPPIHG 420
Qy      396 -----LQDLMIHSRARKPAFLIGSMRDEKRTDHL 425
Db      421 VPAEQSAAHPHPSIERAOPPPISLNNLELQDLMIHSRARKPAFLIGSMRDEKRTDHL 480
Qy      426 LCLDGGGVKGLIITQLLIAIEKASGVATKDLFDWVAGTSGTGLIALALHLSKSMAYMRGM 485
Db      481 LCLDGGGVKGLIITQLLIAIEKASGVATKDLFDWVAGTSGTGLIALALHLSKSMAYMRGM 540
Qy      486 YFRMKDEVFRGSRPYESGPLBEFLKREFGHTKMTDVRKPKWMLTGLSDROPABELHLFR 545
Db      541 YFRMKDEVFRGSRPYESGPLBEFLKREFGHTKMTDVRKPKWMLTGLSDROPABELHLFR 600
Qy      546 NYAPETVPRPNQVNNLRPPAOPSDQLVWRARSSGAAPTYFRNGRFLDGGLLANNP 605
Db      601 NYAPETVPRPNQVNNLRPPAOPSDQLVWRARSSGAAPTYFRNGRFLDGGLLANNP 660

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PT inflammatory agents for treating e.g. rheumatoid arthritis.
 XX
 PS Claim 1; Col 15-22; 24pp; English.

CC The present sequence is that of a calcium-independent cytosolic
 CC phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release
 CC of arachidonic acid in specific tissues characterized by unique membrane
 CC phospholipids. The invention provides a process for producing such an
 CC enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence
 CC of one or more amino acid sequences selected from AAM01480-92, cPLA2/B
 CC has activity in a mixed micelle assay with 1-palmitoyl-2-[14C]-
 CC arachidonyl-1-phosphatidylcholine. The enzyme is useful for screening anti-
 CC -inflammatory agents mediated by the arachidonic acid cascade, for
 CC treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF
 CC field.)

XX
 SQ Sequence 752 AA:

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MGFEGVLVNTFSGVNTLFSNPRVKEVAVADYSSDRVREBQGLIFONTPTNTWCULV 60
 DB 1 MGFEGVLVNTLSSVTNLFSNPRVKEISVADYTSHERVREBQGLIFONASNRITWCILV 60
 QY 61 NPNNSGGRFLFQLELEADALVNFHOYSQQLPFYESSQVLAHTEVLOHLDLIRNHP 120
 DB 61 SPNPHSGRFLFQLESEADALVNFQPSQLPFYESSQVLAHTEVLOHLDLIRNHP 120
 QY 121 SVAAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTOMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDEILVELVOYCHAQMD 180
 QY 181 VTDYKGETVPHYAVGDSNQVQLGLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 DB 181 VTDNKETAHYAVVQGNQSVQLGLGRNASAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 QY 241 LCNARCNMGPNVPIHSAMKFSQKCAEMIIISMDSQHSKDPKRYGASPLHAKNAEMA 300
 DB 241 LCNARCNWQSPGFPIHTAMKFSQKCAEMIIISMDSQHSKDPKRYGASPLHAKNAEMA 300
 QY 301 RMLKRGCVNSTSSAGNTALHVGVMNRPDCAI VILLTGANADANGHGNTPLHLAMSK 360
 DB 301 RMLKRGCDVSTSAAGNTALHVAVMNRPDCAI VILLTGANAGTPEHGNTPLHLAISK 360
 QY 361 DNVEMLKALIVFAEVDTPNDPGETPFLASKTIGK-LQDLMHSRARKPAFIISMRDEK 419
 DB 361 DNNEMLKALIVFAEVDTPNDPGETPFLASKTIGK-LQDLMHSRARKPAFIISMRDEK 420
 QY 420 RTDHDLCLDGGGVKGLIITQLIAIEKASGVAATKDLFDVAVAGTSTGIIALAILHNSKM 479
 DB 421 RTDHDLCLDGGGVKGLIITQLIAIEKASGVAATKDLFDVAVAGTSTGIIALAILHNSKM 480
 QY 480 AYVRGMYFRMKDEVFRRSGRPYESGPLEEFLKREFGHEHTKMTDYRKPRMLTGLISDRQPA 539
 DB 481 AYVRGVYFRMKDEVFRSGRPYESGPLEEFLKREFGHEHTKMTDYRKPRMLTGLISDRQPA 540
 QY 540 ELHLFNNYDAPEVREPRFNQNNLRPPAPSPQVLYRARSSGAATYRPRNGRFLDDG 559
 DB 541 ELHLFNNYDAPEVREPRFNQNNLRPPAPSPQVLYRARSSGAATYRPRNGRFLDDG 600
 QY 600 ILANNPTLDAMTEIHEYNQDLIRKQANVKYKLSIVSLGTGRSPQVLYCVVFRPSNP 659
 DB 601 ILANNPTLDAMTEIHEYNQDLIRKQANVKYKLSIVSLGTGRSPQVLYCVVFRPSNP 660
 QY 660 WEIAKTVFGAKELGKVVVDCCTDPDGR 686
 DB 661 WEIAKTVFGAKELGKVVVDCCTDPDGR 687

RESULT 10
 AAM13163

ID AAM13163 standard; protein; 752 AA.

XX AAM13163;

DT 17-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1997 (first entry)

DE Ca-independent phospholipase A2/B protein.

KM Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
 KM chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
 KM heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;
 KM CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.

OS Crictetus griseus; ovary cells.

PN US5589170-A.

PD 31-DEC-1996.

PF 14-APR-1995; 95US-00422106.

PR 27-UTL-1994; 94US-00281193.

PA (GEMV) GENETICS INST INC.

PI Tang J, Jones S;

XX WPI; 1997-076789/07.

DR N-PSDB; AAT59199.

PT Compen. comprising calcium-independent phospholipase enzyme - for

PT screening for anti-inflammatory agents.

PS Claim 5; Col 15-22; 24pp; English.

CC This is the amino acid sequence of the Ca-independent phospholipase A2/B
 CC from Chinese hamster ovary cells. The protein was isolated from these
 CC cells by conventional chromatographic methods e.g. DEAE anion exchange,
 CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20
 CC chromatofocusing chromatography. The purified protein has mol. wt. of 86
 CC kD and an optimum pH 6. The protein was used for amino acid sequencing
 CC from which pools of degenerate probes were synthesized. The probes were
 CC used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 40000
 CC recombinant phages screened, 12 positive plaques were isolated. One of
 CC these, designated clone 9, contained this sequence. The phospholipase
 CC gene can be inserted into eukaryotic vectors for expression in COS or CHO
 CC cells. The protein, or peptides derived from it e.g. AAM13164-76, can be
 CC used to identify phospholipase inhibitors that can be used as anti-
 CC inflammatory agents, esp. against components of the arachidonic acid
 CC cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT
 CC -2003 to standardise OS field)

XX SQ Sequence 752 AA:

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MGFEGVLVNTFSGVNTLFSNPRVKEVAVADYSSDRVREBQGLIFONTPTNTWCULV 60
 DB 1 MGFEGVLVNTLSSVTNLFSNPRVKEISVADYTSHERVREBQGLIFONASNRITWCILV 60
 QY 61 NPNNSGGRFLFQLELEADALVNFHOYSQQLPFYESSQVLAHTEVLOHLDLIRNHP 120
 DB 61 SPNPHSGRFLFQLESEADALVNFQPSQLPFYESSQVLAHTEVLOHLDLIRNHP 120
 QY 121 SVAAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTOMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDEILVELVOYCHAQMD 180
 QY 181 VTDYKGETVPHYAVGDSNQVQLGLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240

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DB 181 VTNNKSTAPHYAVGQNSQVQLQLGKNASAGLNQVKKGLTPLHLACQNGKQEMRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMTISMDSSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNWMPGSPPIHTAMKFSQKCAEMTISMDSSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKRGCVNVTSSAGNTALHVGWNRFPDCAIVLLTHGANDARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVTSSAGNTALHVGWNRFPDCAIVLLTHGANDARGEHNTPLHLAMSK 360
QY 361 DNVEMLKALIVFGAEVDPNDPFGETPTFLASKIGK-LQDLMHSRARKPAFIILGSMDK 419
DB 361 DNVEMLKALIVFGAEVDPNDPFGETPTFLASKIGK-LQDLMHSRARKPAFIILGSMDK 420
QY 420 RTHDHLCLDGGGVKGLIITQLLIAIEKASGAVTKDLFDWVAGTSTGIIALAILHSSKM 479
DB 421 RTHDHLCLDGGGVKGLIITQLLIAIEKASGAVTKDLFDWVAGTSTGIIALAILHSSKM 480
QY 480 AYNRGMVFRMKDEVFGSRPYESGPLEEFLKREFGHTKMTDVKKRKMVLTGTLSDRQPA 539
DB 481 AYNRGMVFRMKDEVFGSRPYESGPLEEFLKREFGHTKMTDVKKRKMVLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQNNVLRPPAOPSDQLVWRARSSGAFTYFRPNRFLDGG 539
DB 541 ELHLFRNYDAPETVREPRFNQNNVLRPPAOPSDQLVWRARSSGAFTYFRPNRFLDGG 600
QY 600 LLANNPTLDMTEIHEYNODLIRKGOANKYKLSIVSLGTGRSPQVPTCVDFRPSNP 659
DB 601 LLANNPTLDMTEIHEYNODMIRKGOANKYKLSIVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WEIAKTVFGAKELGKMWVDDCTDPDGR 686
DB 661 WEIAKTVFGAKELGKMWVDDCTDPDGR 687

RESULT 11
AAW17849
ID AAW17849 standard; protein: 752 AA.
XX
AC AAW17849;
XX
DT 27-AUG-2003 (revised)
DT 07-AUG-1997 (first entry)
XX
DE Hamster cytosolic phospholipase A2/B.
XX
KM Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
XX inflammation; inhibitor; antiinflammatory; CHO.
XX
OS Cricetus.
XX
FH Key Location/Qualifiers
FT Active-site 465
FT /note= "mutagenesis of Ser-465 results in loss of
activity"
XX
PN W09717448-A2.
XX
PD 15-MAY-1997.
XX
PF 07-NOV-1996; 96WC-US017794.
XX
PR 08-NOV-1995; 95US-00555568.
XX
PA (GEMV ) GENETICS INST INC.
XX
PI Jones S, Tang J;
XX
DR MPI, 1997-281037/25.
XX
PT N-PSDB; AAT68827.
XX
Calcium independent phospholipase A2/B - used to reduce inflammation in a

```

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PT mammalian subject.
XX
XX Example 4; Page 33-36; 74pp; English.
XX
CC A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is
CC thought to be involved in the arachidonic acid cascade. Its amino acid
CC sequence was deduced from a cDNA clone (AAT68827) obt'd. from a CHO-CDX
CC cDNA library. The recombinant enzyme has been expressed in CHO and COS
CC host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also
CC been isolated. These can be used to screen for inhibitors useful as
CC antiinflammatory agents that block the arachidonic acid cascade in
CC mammals. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 752 AA;
XX
Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOPFGLVMTFSGVTNLFSNPFYKREVAADYSSDRVREEGQLIFONTPNRTMPCVLY 60
DB 1 MOPFGLVMTLSSVTNLFSPNFRVKELSVADYTSHERVREEGQLIFONASNTMPCILV 60
QY 61 NPNNSGGRFLFQLELEADALVNFHOYSSQLPFYESSPOVLTTEVLOHITDILRNHPSV 120
DB 61 SPNPHSGRFLFQLESEADALVNFQFSSQLPFYESSQVVLHVEVLQHLSDILRSHPSV 120
QY 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBEGCTPLHACKRKGDEILVELVOYCHTQMD 180
DB 121 TVTHLAVEIGIRCEFHHSRIISCANSTENEBEGCTPLHACKRKGDSILVELVOYCHAQMD 180
QY 181 VTQYKSTAPHYAVGQNSQVQLQLGRNAVAGLNQNNQGLPPLHLACQNGKQEMRVLL 240
DB 181 VTNNKSTAPHYAVGQNSQVQLQLGKNASAGLNQVKKGLTPLHLACQNGKQEMRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMTISMDSSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNWMPGSPPIHTAMKFSQKCAEMTISMDSSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKRGCVNVTSSAGNTALHVGWNRFPDCAIVLLTHGANDARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVTSSAGNTALHVGWNRFPDCAIVLLTHGANDARGEHNTPLHLAMSK 360
QY 361 DNVEMLKALIVFGAEVDPNDPFGETPTFLASKIGK-LQDLMHSRARKPAFIILGSMDK 419
DB 361 DNVEMLKALIVFGAEVDPNDPFGETPTFLASKIGK-LQDLMHSRARKPAFIILGSMDK 420
QY 420 RTHDHLCLDGGGVKGLIITQLLIAIEKASGAVTKDLFDWVAGTSTGIIALAILHSSKM 479
DB 421 RTHDHLCLDGGGVKGLIITQLLIAIEKASGAVTKDLFDWVAGTSTGIIALAILHSSKM 480
QY 480 AYNRGMVFRMKDEVFGSRPYESGPLEEFLKREFGHTKMTDVKKRKMVLTGTLSDRQPA 539
DB 481 AYNRGMVFRMKDEVFGSRPYESGPLEEFLKREFGHTKMTDVKKRKMVLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQNNVLRPPAOPSDQLVWRARSSGAFTYFRPNRFLDGG 539
DB 541 ELHLFRNYDAPETVREPRFNQNNVLRPPAOPSDQLVWRARSSGAFTYFRPNRFLDGG 600
QY 600 LLANNPTLDMTEIHEYNODLIRKGOANKYKLSIVSLGTGRSPQVPTCVDFRPSNP 659
DB 601 LLANNPTLDMTEIHEYNODMIRKGOANKYKLSIVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WEIAKTVFGAKELGKMWVDDCTDPDGR 686
DB 661 WEIAKTVFGAKELGKMWVDDCTDPDGR 687

RESULT 12
AAW81825
ID AAW81825 standard; protein: 752 AA.
XX
XX AAW81825;
AC

```

XX 02-FEB-1999 (first entry)
 DT Chinese hamster calcium independent cPLA2/B protein.
 XX
 DE
 XX
 KM Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening;
 KM anti-inflammatory; arachidonic acid cascade; chinese hamster.
 XX
 OS Crictetus griseus.
 XX
 PN US840511-A.
 PD 24-NOV-1998.
 XX
 XX 23-OCT-1996; 96US-00735716.
 PF
 XX 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 PI Tang J, Jones S;
 XX
 XX WPI; 1999-034032/03.
 DR N-PSDB; AAV64840.
 XX
 XX Screening assay for phospholipase inhibitors - using specified
 PT phospholipase polypeptide.
 XX
 PS Claim 1b; Col 21-24; 24pp; English.
 XX
 XX This sequence represents a novel calcium independent cytosolic
 CC phospholipase A2/B enzyme isolated from chinese hamster ovary cells. This
 CC protein can be used for screening unknown compounds for anti-inflammatory
 CC activity mediated by the arachidonic acid cascade
 CC
 XX Sequence 752 AA;
 SQ

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 62; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MGFGRGLVNTFSQVNTLFSNPFRKVEAVADYSSDVRREGGQILFQNTPNRTWCVLV 60
 DB 1 MGFGRGLVNTFSQVNTLFSNPFRKVEAVADYSSDVRREGGQILFQNTPNRTWCVLV 60
 QY 61 NPNRSOSGFRFLFOLELEADALVNFHOVSQQLPPEYSSPOVLTVEVQHLTDLRNPSM 120
 DB 61 SPNPHSGFRFLFOLELEADALVNFHOVSQQLPPEYSSPOVLTVEVQHLTDLRNPSM 120
 QY 121 SVAAVLAVELGIRRCFHHRSRIISCANCAENEGCTPLHLACRKDGELVELVOYCHTOMD 180
 DB 121 TVTHLAVELGIRRCFHHRSRIISCANSTENEGCTPLHLACRKDGSELVELVOYCHTOMD 180
 QY 181 VTQYKGTVHYAVQGNQVQLLGRNAVAGLANQVNNQGITPLHLACQIGKQEMRVVL 240
 DB 181 VTQYKGTVHYAVQGNQVQLLGRNAVAGLANQVNNQGITPLHLACQIGKQEMRVVL 240
 QY 241 LCNARCNIMGNGYPIHSNAKFSQKCAEMTISDSSQIHSKOPRYGASPLHAKNAEMA 300
 DB 241 LCNARCNIMGNGYPIHSNAKFSQKCAEMTISDSSQIHSKOPRYGASPLHAKNAEMA 300
 QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAILVLTGHNADARGHNTPLHLAMSK 360
 DB 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAILVLTGHNADARGHNTPLHLAMSK 360
 QY 361 DNVEMLKALVFGAEVDTPNDPFGTPTPLASKIGK-LQDLMHISRARKPAFIISNMDEK 419
 DB 361 DNVEMLKALVFGAEVDTPNDPFGTPTPLASKIGK-LQDLMHISRARKPAFIISNMDEK 419
 QY 420 RTHDHLICLGGGKGLIITLAIKASGVAFTKDFDVAAGSTGGIILALHHSKSM 479
 DB 420 RTHDHLICLGGGKGLIITLAIKASGVAFTKDFDVAAGSTGGIILALHHSKSM 479
 QY 421 RTHDHLICLGGGKGLIITLAIKASGVAFTKDFDVAAGSTGGIILALHHSKSM 480

QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLLEEF.LKBEFGHTKMTDVRKPKVMTGLTSDROPA 539
 DB 481 AYMRGMYFRMKDEVFRGSRPYESGPLLEEF.LKBEFGHTKMTDVRKPKVMTGLTSDROPA 540
 QY 540 ELHLFRNYDAPEVIRBPRFRQNNLPPAPQSPQLVWRARSSGAPTYFRPNGRFLDGG 599
 DB 541 ELHLFRNYDAPEVIRBPRFRQNNLPPAPQSPQLVWRARSSGAPTYFRPNGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTGRSPQVPTCVDFVFRSPNP 659
 DB 601 LLANNPTLDAMTEIHEYNODMIRKGOANKVKLSIVSLGTGRSPQVPTCVDFVFRSPNP 660
 QY 660 WEIAKTVFGAKELGKRVVDCCTDPDGR 686
 DB 661 WEIAKTVFGAKELGKRVVDCCTDPDGR 687

RESULT 13
 ABB82215
 ID ABB82215 standard; protein; 752 AA.
 XX
 AC ABB82215;
 XX
 XX 08-JAN-2003 (first entry)
 DT
 XX
 XX Calcium independent phospholipase A2/B (cPLA2/B) (clone 9).
 DE
 XX
 KM Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KM anti-inflammatory; antiarthritic; antipneumatic; antirheumatic; cytosolic;
 KM antileukemic.
 XX
 XX Unidentified.
 OS
 XX
 PN US2002106364-A1.
 XX
 PD 08-AUG-2002.
 XX
 XX 09-AUG-2001; 2001US-00927180.
 PF
 XX 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422106.
 PR 26-JUN-1995; 95WO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 XX WPI; 2002-739923/80.
 DR N-PSDB; ABV73007.
 DR
 XX Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX
 PS Example 4; Page 10-12; 41pp; English.
 XX
 XX The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis, and
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated

CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (i) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a cPLA2/B enzyme (clone 9)

XX Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 5; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGRLVNTEGVTNLFSPNPRKVEAVADYSSDVRBEGQLIFONTPNRTWDCVLY 60
 DB 1 MOFFGRLVNTEGVTNLFSPNPRKVEAVADYSSDVRBEGQLIFONTPNRTWDCVLY 60
 QY 61 NPNRSQGFRLFOLEBDAALVNFHQSQQLPFYESSPOVLATEVLOHLTDLIRNHPW 120
 DB 61 SPNPSGDFRLFOLEBDAALVNFHQSQQLPFYESSPOVLATEVLOHLTDLIRNHPW 120
 QY 121 SVNHLAVELGIRCFHHSRIITSCANCAENBEGCTPLHLACRKDGSLIVELVOYCHTOMD 180
 DB 121 TVTHLAVELGIRCFHHSRIITSCANSTENBEGCTPLHLACRKDGSLIVELVOYCHTOMD 180
 QY 181 VTDYKGETVHVAVQDGNQVQLQLGKNAVAGLNQVNNQGLTPLHLACQKQEMVRL 240
 DB 181 VTDYKGETVHVAVQDGNQVQLQLGKNAVAGLNQVNNQGLTPLHLACQKQEMVRL 240
 QY 241 LCNARCINMGPNNGYPIHSAKFSGKCAEMIISSDSSQHSKDPYRGASPLHMAKNEMA 300
 DB 241 LCNARCINMGPNNGYPIHSAKFSGKCAEMIISSDSSQHSKDPYRGASPLHMAKNEMA 300
 QY 301 RMLLKRCGCVDSISMAQNTALHVAWNNRPFCCVWVLTTCGMMAGTPEGHGTPLHLAISK 360
 DB 301 RMLLKRCGCVDSISMAQNTALHVAWNNRPFCCVWVLTTCGMMAGTPEGHGTPLHLAISK 360
 QY 361 DNEMTIALVFGAEVTPDNGFTPTPLASKIGK-LQDLMHSRARKPAFITGSMDEK 419
 DB 361 DNEMTIALVFGAEVTPDNGFTPTPLASKIGK-LQDLMHSRARKPAFITGSMDEK 419
 QY 420 RTDHLCLDGGGVKGLIIQLAIEKASGATKDLFDWAGTSGGILALAILHSKSM 479
 DB 420 RTDHLCLDGGGVKGLIIQLAIEKASGATKDLFDWAGTSGGILALAILHSKSM 479
 QY 480 AYNGMTFRMKDVFRCSPRESGPLEPLKREGEHTKMTDVKPYVMTLGTLSDRQA 539
 DB 480 AYNGMTFRMKDVFRCSPRESGPLEPLKREGEHTKMTDVKPYVMTLGTLSDRQA 539
 QY 540 ELHLFRVYDAPEVTRERFNONVNLARPAPSDQLVRAARSSGAATYFRPNRFLDGG 599
 DB 540 ELHLFRVYDAPEVTRERFNONVNLARPAPSDQLVRAARSSGAATYFRPNRFLDGG 599
 QY 600 LLANNPTLDAMTEIHEYNODLIRKQANKYKSLIVSLGTGRSPQVPTCVDFRPSNP 659
 DB 600 LLANNPTLDAMTEIHEYNODLIRKQANKYKSLIVSLGTGRSPQVPTCVDFRPSNP 659
 QY 660 WEIAKTVFGAKELGKMYVDCCTDPGR 686
 DB 660 WEIAKTVFGAKELGKMYVDCCTDPGR 686
 QY 661 WEIAKTVFGAKELGKMYVDCCTDPGR 687
 DB 661 WEIAKTVFGAKELGKMYVDCCTDPGR 687

RESULT 14
 ADD6244
 ID ADD6244 standard; protein; 751 AA.

XX ADD6244;

XX 29-JAN-2004 (first entry)

XX Rat Protein P97570, SEQ ID NO 11919.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002MO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GENO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; P97570.
 XX New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 XX or human polynucleotides or a polynucleotide which represents a fragment,
 XX derivative or allelic variation of the nucleic acid sequence. Also
 XX claimed are a vector comprising the novel polynucleotide, a host cell
 XX comprising the vector, a method for identifying a nucleotide sequence
 XX which is differentially regulated in an animal subjected to pain and a
 XX kit to perform the method, an array, a method for identifying an agent
 XX that increases or decreases the expression of the polynucleotide sequence
 XX that is differentially expressed in neuronal tissue of a first animal
 XX subjected to pain, a method for identifying a compound which regulates
 XX the expression of a polynucleotide sequence which is differentially
 XX expressed in an animal subjected to pain, a method for identifying a
 XX compound that regulates the activity of one or more of the
 XX polynucleotides, a method for producing a pharmaceutical composition, a
 XX method for identifying a compound or small molecule that regulates the
 XX activity in an animal of one or more of the polypeptides given in the
 XX specification, a method for identifying a compound useful in treating
 XX pain and a pharmaceutical composition comprising the one or more
 XX polypeptides or their antibodies. The polynucleotide or the compound that
 XX modulates its activity is useful for preparing a medicament for treating
 XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 XX therapy). The sequence presented is a rat protein (shown in Table 2 of
 XX the specification) which is differentially expressed during pain. Note:
 XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic form directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 751 AA;

Query Match 90.0%; Score 3257; DB 7; Length 751;
 Best Local Similarity 89.7%; Pred. No. 0;
 Matches 616; Conservative 29; Mismatches 40; Indels 2; Gaps 2;

QY 1 MOFFGRLVNTEGVTNLFSPNPRKVEAVADYSSDVRBEGQLIFONTPNRTWDCVLY 60
 DB 1 MOFFGRLVNTEGVTNLFSPNPRKVEAVADYSSDVRBEGQLIFONTPNRTWDCVLY 60
 QY 61 NPNRSQGFRLFOLEBDAALVNFHQSQQLPFYESSPOVLATEVLOHLTDLIRNHPW 120
 DB 61 SPNPSGDFRLFOLEBDAALVNFHQSQQLPFYESSPOVLATEVLOHLTDLIRNHPW 119
 QY 121 SVNHLAVELGIRCFHHSRIITSCANCAENBEGCTPLHLACRKDGSLIVELVOYCHTOMD 180
 DB 121 TVTHLAVELGIRCFHHSRIITSCANSTENBEGCTPLHLACRKDGSLIVELVOYCHTOMD 179
 QY 181 VTDYKGETVHVAVQDGNQVQLQLGKNAVAGLNQVNNQGLTPLHLACQKQEMVRL 240
 DB 181 VTDYKGETVHVAVQDGNQVQLQLGKNAVAGLNQVNNQGLTPLHLACQKQEMVRL 240

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Db      180 VTNNKGTAFHYAVQGDNPVQLGLGKNASAGLQVNNQGLTPHLALCQWQKQEMRVLL 239
Qy      241 LCNARCNIMGPNPGPIHISAMKFSQKCAEMTISMDSSQIHSKDPRYGASPLHAKNAEMA 300
Db      240 LCNARCNIMGPGPIHTTAMKFSQKCAEMTISMDSSQIHSKDPRYGASPLHAKNAEMA 299
Qy      301 RMLLKRGCVNSTSSAGNTALHGVNMRPDCAVLLTHGANADARGEHNTPLHLSMSK 360
Db      300 RMLLKRGCVNSTSSAGNTALHVAVTNRFPDCVWVLLTGYANNAGARHGNTPLHLSMSK 359
Qy      361 DNVEIMKALIVFGAEVDTPNDPGETPTPLASKTGK-LQDLMHISRAKRPFIISMRDEK 419
Db      360 DNNEVMKALIVFGAEVDTPNDPGETPTPLASKTGK-LQDLMHISRAKRPFIISMRDEK 419
Qy      420 RTDHLCLDGGGKGLIIQLLAIKASGVAATKDLFDWVAGSTGGIALLHLSKSM 479
Db      420 RTDHLCLDGGGKGLIIQLLAIKASGVAATKDLFDWVAGSTGGIALLHLSKSM 479
Qy      480 AYNRGMYFRMKDEVFRGSRPYESGPLEEPLKREFGHTKMTDVKRPMVLTGTLSDRQPA 539
Db      480 AYNRGMYFRMKDEVFRGSRPYESGPLEEPLKREFGHTKMTDVKRPMVLTGTLSDRQPA 539
Qy      540 ELHLFRNYDAPEYRERFQNVNLRPPAPSDQVWRAARSSGAATYFRPNRFLDGG 599
Db      540 ELHLFRNYDAPEYRERFQNVNLRPPAPSDQVWRAARSSGAATYFRPNRFLDGG 599
Qy      600 LLANNPFLDAMTEIHEYNQDLIRKQANKYKLSIVSLGTSRSPQVPTCVDFRPSNP 659
Db      600 LLANNPFLDAMTEIHEYNQDLIRKQANKYKLSIVSLGTSRSPQVPTCVDFRPSNP 659
Qy      660 WELAKTVFGAKELGKRVVDDCTDPDGR 686
Db      660 WELAKTVFGAKELGKRVVDDCTDPDGR 686

RESULT 15
ADE60532 standard; protein; 751 AA.
AC      ADE60532;
DT      29-JAN-2004 (first entry)
DE      Rat Protein P97570, SEQ ID NO 6441.
XX      Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM      chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS      Rattus norvegicus.
PN      MO2003016475-A2.
PD      27-FEB-2003.
PF      14-AUG-2002; 2002WC-US025765.
XX      14-AUG-2001; 2001US-0312147P.
PR      01-NOV-2001; 2001US-0346382P.
XX      26-NOV-2001; 2001US-0333347P.
PA      (GEHO ) GEN HOSPITAL CORP.
PA      (FARB ) BAYER AG.
PI      WOOLF C, D'urao D, Befort K, Costigan M;
XX      WPI, 2003-268312/26.
DR      GENBANK; P97570.
XX      New composition comprising two or more isolated polypeptides, useful for
PT      preparing a medicament for treating pain in an animal.
XX      Claim 1, Page, 1017pp, English.

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XX      The invention discloses a composition comprising two or more isolated rat
CC      or human polynucleotides or a polynucleotide which represents a fragment,
CC      derivative or allelic variation of the nucleic acid sequence. Also
CC      claimed are a vector comprising the novel polynucleotide, a host cell
CC      comprising the vector, a method for identifying a nucleotide sequence
CC      which is differentially regulated in an animal subjected to pain and a
CC      kit to perform the method, an array, a method for identifying an agent
CC      that increases or decreases the expression of the polynucleotide sequence
CC      that is differentially expressed in neuronal tissue of a first animal
CC      subjected to pain, a method for identifying a compound which regulates
CC      the expression of a polynucleotide sequence which is differentially
CC      expressed in an animal subjected to pain, a method for identifying a
CC      compound that regulates the activity of one or more of the
CC      polynucleotides, a method for producing a pharmaceutical composition, a
CC      method for identifying a compound or small molecule that regulates the
CC      activity in an animal of one or more of the polypeptides given in the
CC      specification, a method for identifying a compound useful in treating
CC      pain and a pharmaceutical composition comprising the one or more
CC      polypeptides or their antibodies. The polynucleotide or the compound that
CC      modulates its activity is useful for preparing a medicament for treating
CC      pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC      injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC      therapy). The sequence presented is a rat protein (shown in Table 2 of
CC      the specification) which is differentially expressed during pain. Note:
CC      The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic form directly from WIPD at
CC      ftp.wipo.int/pub/published_pct_sequences.
XX
SQ      Sequence 751 AA;

```

```

Query Match      90.0%; Score 3257; DB 7; Length 751;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 616; Conservative 29; Mismatches 40; Indels 2; Gaps 2;

```

```

Qy      1 MOFFGRVNTFGGVTMLFNSPRFKEVAVADYSSDRVREEGQLIFONTPTNWCQVY 60
Db      1 MOFFGRVNTLSSVTMLFNSPRFAKEVSLADYASSRVEEGQLIQNASNTWCQDLY 60
Qy      61 NPNRSQGFRLFQLEADALVNFQYSSQLLPFYSSPQVLTTEVLOHLLTDLIRNHPN 120
Db      61 SPNRPQSDRLFLQLEADALVNFQYSSQLLPFYSSQVLAHEVLQ-LTDLIRNHPN 119
Qy      121 SVAHAVELGIRECFHRSRIISCANCAENBEGCTPLHLACRKGDSIIVELVOYCTQND 180
Db      120 TVTHLAVELGIRECFHRSRIITCANSTENBEGCTPLHLACRKGDSIIVELVOYCHAQND 179
Qy      181 VTPYKGETVPHYAVQGDNPVQLGLGKNASAGLQVNNQGLTPHLALCQWQKQEMRVLL 240
Db      180 VTNNKGTAFHYAVQGDNPVQLGLGKNASAGLQVNNQGLTPHLALCQWQKQEMRVLL 239
Qy      241 LCNARCNIMGPNPGPIHISAMKFSQKCAEMTISMDSSQIHSKDPRYGASPLHAKNAEMA 300
Db      240 LCNARCNIMGPGPIHTTAMKFSQKCAEMTISMDSSQIHSKDPRYGASPLHAKNAEMA 299
Qy      301 RMLLKRGCVNSTSSAGNTALHGVNMRPDCAVLLTHGANADARGEHNTPLHLSMSK 360
Db      300 RMLLKRGCVNSTSSAGNTALHVAVTNRFPDCVWVLLTGYANNAGARHGNTPLHLSMSK 359
Qy      361 DNVEIMKALIVFGAEVDTPNDPGETPTPLASKTGK-LQDLMHISRAKRPFIISMRDEK 419
Db      360 DNNEVMKALIVFGAEVDTPNDPGETPTPLASKTGK-LQDLMHISRAKRPFIISMRDEK 419
Qy      420 RTDHLCLDGGGKGLIIQLLAIKASGVAATKDLFDWVAGSTGGIALLHLSKSM 479
Db      420 RTDHLCLDGGGKGLIIQLLAIKASGVAATKDLFDWVAGSTGGIALLHLSKSM 479
Qy      480 AYNRGMYFRMKDEVFRGSRPYESGPLEEPLKREFGHTKMTDVKRPMVLTGTLSDRQPA 539
Db      480 AYNRGMYFRMKDEVFRGSRPYESGPLEEPLKREFGHTKMTDVKRPMVLTGTLSDRQPA 539
Qy      540 ELHLFRNYDAPEYRERFQNVNLRPPAPSDQVWRAARSSGAATYFRPNRFLDGG 599

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| | | | |
|----|-----|--|-----|
| Db | 540 | ELHLFRNYDAPBAVREBRCPTPINLKPPTQPADQLVWRAARSSGAAPTFFRPNGRFLDGG | 599 |
| Qy | 600 | LLANNPTLDAMTEIHEYNODLIRKQANKYKLSIVVSLGTRSPQVPTVCVDVFRPSNP | 659 |
| Db | 600 | LLANNPTLDAMTEIHEYNODMIRKQGNKYKLSIVVSLGTRSPQVPTVCVDVFRPSNP | 659 |
| Qy | 660 | WEIAKTVFGAKELGKRVVDCCTDPDGR | 686 |
| Db | 660 | WEIAKTVFGAKELGKRVVDCCTDPDGR | 686 |

Search completed: December 15, 2004, 13:08:08
 Job time : 142.101 secs

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OM protein - protein search, using bw model

Run on: December 15, 2004, 12:52:55 ; Search time 17.7917 Seconds
(without alignments)
2130.736 Million cell updates/sec

Title: US-10-612-668-17
Perfect score: 2084
Sequence: 1 MGFGRVLTVPFSGVTNLFPSN.....EVDTPNDPGETPTFLASKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------------|
| 1 | 2078 | 99.7 | 851 | 2 | T12503 hypothetical prote |
| 2 | 332 | 15.9 | 3924 | 2 | S37431 ankylrin 2, neutro |
| 3 | 318 | 15.3 | 2039 | 2 | T15347 ankylrin-related un |
| 4 | 313.5 | 15.0 | 1549 | 2 | T13940 ankylrin - fruit fl |
| 5 | 296 | 14.2 | 4377 | 2 | A55575 ankylrin 3, long sp |
| 6 | 294 | 14.1 | 1856 | 2 | B35049 ankylrin 1, erythro |
| 7 | 294 | 14.1 | 1880 | 2 | A35049 ankylrin 1, erythro |
| 8 | 294 | 14.1 | 1881 | 1 | S3H0K ankylrin 1, erythro |
| 9 | 293 | 14.1 | 1765 | 2 | T42714 ankylrin 3, splice |
| 10 | 293 | 14.1 | 1940 | 2 | T42715 ankylrin 3, splice |
| 11 | 293 | 14.1 | 1943 | 2 | T42713 ankylrin 3, splice |
| 12 | 293 | 14.1 | 1961 | 2 | T42716 ankylrin 3, splice |
| 13 | 285 | 13.7 | 1848 | 2 | S37771 ankylrin, erythrocy |
| 14 | 285 | 13.7 | 1862 | 2 | T49502 ankylrin - mouse |
| 15 | 281.5 | 13.5 | 397 | 2 | T46445 hypothetical prote |
| 16 | 258 | 12.4 | 1023 | 2 | T26261 hypothetical prote |
| 17 | 255.5 | 12.3 | 1411 | 2 | S30355 alpha-latrotosecto |
| 18 | 249 | 11.9 | 791 | 2 | T42691 hypothetical prote |
| 19 | 248.5 | 11.9 | 1435 | 2 | T32930 hypothetical prote |
| 20 | 244 | 11.7 | 247 | 2 | D84448 probable ankylrin l |
| 21 | 237 | 11.4 | 1401 | 2 | S11577 alpha-latrotoxin p |
| 22 | 236 | 11.3 | 2437 | 2 | S42612 transmembrane prot |
| 23 | 234 | 11.2 | 1423 | 1 | T37275 death-associated p |
| 24 | 233 | 11.2 | 1436 | 1 | AE2149 hypothetical prote |
| 25 | 231 | 11.1 | 934 | 1 | H71274 probable ankylrin - |
| 26 | 225 | 10.8 | 1071 | 2 | T22377 hypothetical prote |
| 27 | 218.5 | 10.5 | 368 | 2 | T18184 ankylrin repeat pro |
| 28 | 216.5 | 10.4 | 633 | 2 | T27499 hypothetical prote |
| 29 | 216.5 | 10.4 | 1184 | 2 | T00253 gene Ankhnz protel |

| | | | | | |
|----|-------|------|------|---|----------------------------|
| 30 | 215 | 10.3 | 907 | 2 | I50404 p50B/p97 (Lyt-10) |
| 31 | 213.5 | 10.2 | 933 | 2 | S17233 transcription fact |
| 32 | 213 | 10.2 | 1662 | 2 | T14151 inv protein - mous |
| 33 | 212 | 10.2 | 1062 | 2 | T30255 inverain - mouse |
| 34 | 208.5 | 10.0 | 606 | 2 | AC2508 hypothetical prote |
| 35 | 206.5 | 9.9 | 2352 | 2 | T30201 Notch homolog prot |
| 36 | 206 | 9.9 | 2531 | 2 | A46019 notch-1 protein - |
| 37 | 205 | 9.8 | 662 | 2 | E84725 ankylrin-like prote |
| 38 | 205 | 9.8 | 900 | 2 | A42024 transcription fact |
| 39 | 202 | 9.7 | 664 | 2 | A56695 notch2 protein hom |
| 40 | 202 | 9.7 | 2471 | 2 | A49128 cell-fate determin |
| 41 | 201 | 9.6 | 1031 | 2 | T43458 hypothetical prote |
| 42 | 200.5 | 9.6 | 2584 | 2 | T24158 hypothetical prote |
| 43 | 200.5 | 9.6 | 2606 | 2 | T24157 notch protein hom |
| 44 | 199.5 | 9.6 | 2531 | 2 | S18188 notch protein hom |
| 45 | 199.5 | 9.6 | 2535 | 2 | A40043 notch protein hom |

ALIGNMENTS

| | |
|--|---|
| RESULT 1 | |
| T12503 | hypothetical protein DKFZp434A102.1 - human (fragment) |
| C:Species: Homo sapiens (man) | |
| C:Date: 23-Jul-1999 | #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999 |
| C:Accession: T12503 | |
| R:Annotator: W. J. Wilkner, U. J. Newes, H. W. J. Gassenhuber, J. J. Wiemann, S. | |
| A:Submitted to the Protein Sequence Database, June 1999 | |
| A:Reference number: Z17527 | |
| A:Accession: T12503 | |
| A>Status: preliminary | |
| A:Molecule type: mRNA | |
| A:Residues: 1-851 <AMS> | |
| A:Cross-references: EMBL:AL080187 | |
| A:Experimental source: adult testis; clone DKFZp434A102 | |
| C:Genetics: | |
| A>Note: DKFZp434A102.1 | |
| Query Match | 99.7%; Score 2078; DB 2; Length 851; |
| Best Local Similarity | 99.7%; Pred. No. 1.6e-168; |
| Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | |
| QY | 1 MGFGRVLTVPFSGVTNLFPSNPFVKXAVADYTSSDRVREBQGLIFONTPNRTWCVLV 60 |
| DB | 46 MGFGRVLTVPFSGVTNLFPSNPFVKXAVADYTSSDRVREBQGLIFONTPNRTWCVLV 105 |
| QY | 61 NPNNSQSGFRLPQLEADALVNFHQSQQLPFYESSPOVLHTEVLQHLTDLIRNHPGW 120 |
| DB | 106 NPNNSQSGFRLPQLEADALVNFHQSQQLPFYESSPOVLHTEVLQHLTDLIRNHPGW 165 |
| QY | 121 SVAHLAVELGIRECFHSHRIISCANCAENEBGCTPLHLACRKDGGLVLEVOYCHTQMD 180 |
| DB | 166 SVAHLAVELGIRECFHSHRIISCANCAENEBGCTPLHLACRKDGGLVLEVOYCHTQMD 225 |
| QY | 181 VVDYKGETVPHYAVQDNGSOVLQLGRNAVAGLNQNNQGLPLHLACOLGKQEMRVLL 240 |
| DB | 226 VVDYKGETVPHYAVQDNGSOVLQLGRNAVAGLNQNNQGLPLHLACOLGKQEMRVLL 285 |
| QY | 241 LCNARCNINMGPNPYPIHSAKMSQKCAEMIISMDSQIHSKDPRIYGAASPLHAKNAEMA 300 |
| DB | 286 LCNARCNINMGPNPYPIHSAKMSQKCAEMIISMDSQIHSKDPRIYGAASPLHAKNAEMA 345 |
| QY | 301 RMLIKRGCVNVSSTSSAGNTALHYGVNRNRPDCAIYVLTGANAADARGEGNTPPLHAKMSK 360 |
| DB | 346 RMLIKRGCVNVSSTSSAGNTALHYGVNRNRPDCAIYVLTGANAADARGEGNTPPLHAKMSK 405 |
| QY | 361 DNVEMTKALIVGAEVDPNDGEPTPTFLASKIG 394 |
| DB | 406 DNVEMTKALIVGAEVDPNDGEPTPTFLASKIG 439 |
| RESULT 2 | |

S37431
 ankyrin 2, neuronal long splice form - human
 N:Alternate names: ankylrin B, 440K splice form; ankylrin-B; brain ankylrin; non-erythroid
 N:Contains: ankylrin 2, short form
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
 C:Accession: S37431, A39643, B39643; A40334, A49462; S14533, S14569
 R:Chan, W.
 Submitted to the EMBL Data Library, September 1993
 A:Reference number: S37431
 A:Accession: S37431
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-3924 <CHA>
 A:Cross-references: UNIPROT:Q01484, EMBL:Z26634, NID:G406287, PIDN:CAA81387.1; PID:G406287
 R:Otto, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.
 J. Cell Biol. 114, 241-253, 1991
 A:Title: Isolation and characterization of cDNAs encoding human brain ankylrins reveal a
 A:Reference number: A39643; MUID:91302466, PMID:1830053
 A:Accession: A39643
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2077 <OT1>
 A:Cross-references: GB:X56957
 A:Accession: B39643
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1443,3585-3924 <OTT>
 A:Cross-references: EMBL:X56958
 R:Te, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
 Genomics 10, 858-866, 1991
 A:Title: Isolation and chromosomal localization of a novel nonerythroid ankylrin gene.
 A:Reference number: A40334; MUID:92009921; PMID:1833308
 A:Accession: A40334
 A:Molecule type: DNA
 A:Residues: 463-474, 'PE', 477-495 <TSE>
 A:Cross-references: GB:M37123, NID:G178647; PIDN:AAA62828.1; PID:G178648
 R:Chan, W.; Kordeli, E.; Bennett, V.
 J. Cell Biol. 123, 1463-1473, 1993
 A:Title: 440-kD ankylrinB: structure of the major developmentally regulated domain and se
 A:Reference number: A49462; MUID:94075409; PMID:8253844
 A:Accession: A49462
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-3924 <RES>
 A:Cross-references: EMBL:Z26634; NID:G406287; PIDN:CAA81387.1; PID:G406288
 C:Genetics:
 A:Gene: GDB:ANK2
 A:Cross-references: GDB:127607; OMIM:106410
 A:Map position: 4q25-4q27
 C:Superfamily: ankylrin; ankylrin repeat homology
 C:Keywords: alternative splicing
 F:2-3924/Product: ankylrin 2, long form #status predicted <M>
 F:12-1443,3585-3924/Product: ankylrin 2, short form #status predicted <M>
 F:63-95/Domain: ankylrin repeat homology <AN01>
 F:96-128/Domain: ankylrin repeat homology <AN02>
 F:129-161/Domain: ankylrin repeat homology <AN03>
 F:162-190/Domain: ankylrin repeat homology <AN04>
 F:191-223/Domain: ankylrin repeat homology <AN05>
 F:232-264/Domain: ankylrin repeat homology <AN06>
 F:265-297/Domain: ankylrin repeat homology <AN07>
 F:298-330/Domain: ankylrin repeat homology <AN08>
 F:331-363/Domain: ankylrin repeat homology <AN09>
 F:364-396/Domain: ankylrin repeat homology <AN10>
 F:397-429/Domain: ankylrin repeat homology <AN11>
 F:430-462/Domain: ankylrin repeat homology <AN12>
 F:463-495/Domain: ankylrin repeat homology <AN13>
 F:496-528/Domain: ankylrin repeat homology <AN14>
 F:529-561/Domain: ankylrin repeat homology <AN15>
 F:562-594/Domain: ankylrin repeat homology <AN16>
 F:595-627/Domain: ankylrin repeat homology <AN17>
 F:628-660/Domain: ankylrin repeat homology <AN18>
 F:661-693/Domain: ankylrin repeat homology <AN19>

F:694-726/Domain: ankyrin repeat homology <AN20>
F:727-759/Domain: ankyrin repeat homology <AN21>
F:760-792/Domain: ankyrin repeat homology <AN22>
F:793-825/Domain: ankyrin repeat homology <AN23>

| | | | | |
|---------------------------|-------|--------------------|------------|--------------|
| Query Match | 15.9% | Score 332; | DB 2; | Length 3924; |
| Best Local Similarity | 27.3% | Pred. No. 4.8e-19; | | |
| Matches 100; Conservative | 62; | Mismatches 127; | Indels 77; | Gaps 9; |

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OY      103 HTEVLQHLTD-----LIRNHPWSVAHLNVELGIRCFNH-----SKII 141
          |:::| |:::| |
DB      311 HDQVVELLERGARPLARTKNGLSPLMAAQGDHVECVKHLIQKARVDVTLDYLTALH 370

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QY      142 SCANC-----AENEGCTPLHLACRKGDSITVELVQY-----174
          ||| | | | | | | | | | | | | | | | | | | | | |
Db      371 VAAHCGHYRVTLLIDKRANPNARALNGFTPLHIACKNRIRKIMELLVKYGASIQAITES 430

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QY 175 -----CH-----TQMDVYDYKGETVFHVAVGQSDNSQLDQLGRNAVAG 212

 | |||::||| | : :||| | |

Dd 431 GLTFPIHVAAFMGHLINIVLLILLQNGASPDVTNIRGETALHHMARAGQVEVVRCLLRNG-AL 489

Dy 213 LNNQNNGGITPLHLACQLGQEWFRVLLCNARCINMGPNFY-PHISAMKRSQGCAEMI 271
:: : |||.:|||.:||| :||| : :
Db 490 VDARAREEQTPLHIASRLGTEIVOLLQHMAHPDAATTNGYTPLHISAREQVDVASVL 549

QY 212 ISMDSQIHSKDPRYGASPLHWAK---NAEARMMLTKRGCVNVSSTSGAGNTLHVGVNRN 328
::: || : | : ||| | : : : ||| : : | : ||| :
Db 550 --LEAGAAHSLATYKGFPLVHAARYGSLDVAKLQRRAAADSAGCNGLTFLVHAAYHD 6077

DQ 329 RPDCAIVLLTHGANADARGHGNTPLHLANSKDNIEMIKALIVFGAEVDTPDHFGEITPTF 388
::|||::|::|::|::|::|::|::|::|::|
Db 608 NOKALLLEKGA SPHATAKNGYTPLHLIAAKKNQIQIASTLNLYGAEFTNIVTKQGVIPLH 667

| | | | |
|----|-----|--------|-----|
| Qy | 389 | LASKIG | 394 |
| | | : | |
| Db | 668 | LASQEG | 673 |

RESULT 3
T15347
murkin-related unc-44 - Caenorhabditis elegans

C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282
R:Gathering: S

A:Accession: T15347
A:Reference number: Z18332
A:Description: The sequence of *C. elegans* cosmid B0350.
submitted to the EMBL Data Library, February 1996

A:status: preliminary; translated from GR/EMBL/DDBJ
A:Residues: 1-2039 <GAT>
A:Molecule type: DNA
A:Cross-references: UNIPROT:O17489; EMBL:U50071; NID:q1208871; PID:q1208873; E

A;Accession: Y15346
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1000, 'SKYOHRT', 1003-1718, 'KWEENRL', 1727, 'D', 'ES', 1942, 'ESPAORS'

A/Cross-references: EMBL:U50071, NID:g1208871, PID:g1208875, PIDN:AAA93445.1
A/Accession: T15344
!Status: pre|inary; translated from GB/EMBL/DDBT
32, 'S', /2034-2035, GSSTKRSVEPEEHKHSQHEDEGSI <GA2>
A/Cross-references: EMBL:U50071, NID:g1208871, PID:g1208875, PIDN:AAA93445.1

<CA3>
A:Residues: 1-1718, 'KW', 1903-1905, 'NRLEDESSPS', 1916-1917, 'QNSTVAESTSEQVE', 1918-1919, 'QNSTVAESTSEQVE', 1920-1921, 'QNSTVAESTSEQVE', 1922-1923, 'QNSTVAESTSEQVE', 1924-1925, 'QNSTVAESTSEQVE', 1926-1927, 'QNSTVAESTSEQVE', 1928-1929, 'QNSTVAESTSEQVE', 1930-1931, 'QNSTVAESTSEQVE', 1932-1933, 'QNSTVAESTSEQVE', 1934-1935, 'QNSTVAESTSEQVE', 1936-1937, 'QNSTVAESTSEQVE', 1938-1939, 'QNSTVAESTSEQVE', 1940-1941, 'QNSTVAESTSEQVE', 1942-1943, 'QNSTVAESTSEQVE', 1944-1945, 'QNSTVAESTSEQVE', 1946-1947, 'QNSTVAESTSEQVE', 1948-1949, 'QNSTVAESTSEQVE', 1950-1951, 'QNSTVAESTSEQVE', 1952-1953, 'QNSTVAESTSEQVE', 1954-1955, 'QNSTVAESTSEQVE', 1956-1957, 'QNSTVAESTSEQVE', 1958-1959, 'QNSTVAESTSEQVE', 1960-1961, 'QNSTVAESTSEQVE', 1962-1963, 'QNSTVAESTSEQVE', 1964-1965, 'QNSTVAESTSEQVE', 1966-1967, 'QNSTVAESTSEQVE', 1968-1969, 'QNSTVAESTSEQVE', 1970-1971, 'QNSTVAESTSEQVE', 1972-1973, 'QNSTVAESTSEQVE', 1974-1975, 'QNSTVAESTSEQVE', 1976-1977, 'QNSTVAESTSEQVE', 1978-1979, 'QNSTVAESTSEQVE', 1980-1981, 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A:Accession: J15345
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KMEELNRL', 1727, 'D', 'ES', 1942, 'PSPAORS', 1950, 'IVAES', 1956-1

PIRKSVEPBEHRHSHOHDEHSI? <GA4>
A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208876; PIDN:AAA93446.1
R;Otsuka, A.U.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Booc
T;Celt, B. *129.1081-1093*, 1995

A; Cross-references: ENBL:U50071; NID:G1208871; PID:G1208876; PIND:AAA933446.1
R; Otsuka, A.T.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontarakulpo
Cell Biol. 129, 1081-1092, 1995

A>Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in *Cad*
A/Reference number: A57282; MUID:95263663; PMID:7744957
A/Accession: A57282
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-852; 'GGG', 856-1000, 'SKLQHR', 1002-1119, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEH
'SHRD', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
A/Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
A/Accession: B57282
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEHNR', 1727, 1799, 'E
V', 1945-1947, 'VW', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPRRSVEBEHNHS', 1984-1985, 'EDHES', 1
A/Cross-references: GB:U21731
A/Accession: C57282
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 194, 'P', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, '
4, 'TIV', 1828, 'ESHS', 1833, 'OV', 1836, 'E', 1934-1935, 'EOS', 1939, 'ESHS', 1944, 'REDDGTVTT', 194
A/Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604
C/Genetics:
A/Gene: CESP:unc-44
A/Intons: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979
C/Superfamily: ankyrin; ankyrin repeat homology
F:164-192/Domain: ankyrin repeat homology <AN04>
F:358-390/Domain: ankyrin repeat homology <AN1>
F:391-423/Domain: ankyrin repeat homology <AN11>
Query Match 15.3%; Score 318; DB 2; Length 2039;
Best Local Similarity 33.6%; Pred. No. 3, 1e-18;
Matches 86; Conservative 49; Mismatches 105; Indels 16; Gaps 6;
Qy 147 AEENEECTPLHACRGDEIGELVELVQYCHTQMDVTDYKGETVPHYAVGQDNGSQTQLLG 206
Db 420 ATTESGELPLHVAAPGAIIVYLLQ-Q-GANPDVETRGETPLHAAANQTDVVRVLI 478
Qy 207 RANVAGLQNNQGLTPPLHACQLGQEMVRVLLCNARCNIMGNGY-PIHSAMKFSOK 265
Db 479 RKG-ANVDQARELOTPPLHASKRGNTDIYLLQGANSNATTRDYSPLHTAAEGOE 537
Qy 266 GCAEMTISDSSQIHSKD---PRYGASPLHMAK--NAEMAMLLKKGCVNSTSAGN 318
Db 538 EVAGILLD-----HNADKTLTKKGTPLHLSKKGNEVLVLLERGPVPIBGNQV 591
Qy 319 TALHVGWNRNRCALVLTGKANADARGHGTPLHLSKKNVETKALIVFGAEVDT 378
Db 592 TPLHVAHYVNDKVMILLENGASAKAAKNGYTPPLHIAKKQMETASTLQFKADPNA 651
Qy 379 PNDGFTPTPLASKIG 394
Db 652 KSRAGFTPLHLSAQEG 667
RESULT 4
T13940
ankyrin - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T13940
R:Hubreull, R.R.; Yu, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
A>Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in *Drosoph*
A/Reference number: Z17820; MUID:95024098; PMID:7937942
A/Accession: T13940
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1549 <DUB>
A/Cross-references: UNIPROT:Q24241; EMBL:L35601; NID:9557083; PID:9557084; PIDN:AAQ37208
C/Genetics:
A/Cross-references: FlyBase:FBgn0011747
Query Match 15.0%; Score 313.5; DB 2; Length 1549;
Best Local Similarity 23.9%; Pred. No. 5, 1e-18;

Matches 114; Conservative 68; Mismatches 144; Indels 151; Gaps 16;
Qy 45 ILFQNTPTWCULVNPNSGGRFLFQLEBADLVNPHQSSQL-----PFRESSP 99
Db 319 LLOQNP-----ILKTRNGLSALHM-----AAQGEHEAALLDNRAPVDEVTV 364
Qy 100 QVL-----HTEVLQHTDLIRNHS-----WSVAHLA-----VELGIECPH 136
Db 365 DVLTAHVAAHCGHYKVALLDYKANPAPALNGFTPLHIAKCKRIRIGVELLIK--H 421
Qy 137 HSRISCANCAENBECTPLHACRGDEIGELVELVQYCHTQMDVTDYKGETVPHYAVG 196
Db 422 GANI-----GATTESGLTPHVASFMGCINIVYLLQ-H-EASADLPTRIGETPLHAA 475
Qy 197 DNSQVQLLGRNAV-----AGLNQVNNQGLTPPLHACQLGQEMVRVLLCNARCNIMGNGY 535
Db 476 NQADIRILLRSKAKDAIVREGQTPHVASRLGNINIIMLLQHGAEINAQNDKXSALH 535
Qy 211 -----AGLNQVNNQGLTPPLHACQLGQEMVRVLLCNARCNIMGNGY 252
Db 536 IAAKGEENIVQVLENGAENNAVTKKGTPLHIAKCKGKQNVQVQLLQNGASIDPQGN 595
Qy 253 GY-PIHSAMKFSOKGCAEMTISDSS-----QI-HSKD- 283
Db 596 DVTPLHVAHYVNDKVMILLENGASAKAAKNGYTPPLHIAKCKRIRIGVELLIK--H 655
Qy 284 ---PRYGASPLHMAK--NAEMAMLLKKGCVNSTSAGNTALHVGWNRNRCALVLT 337
Db 656 NIISKSGFPLHIAAGGVNDVQVLENGV-ISAARKGLTPHVAOEGHVLVQVQLL 714
Qy 338 THGANADARGHGTPLHLSKKNVETKALIVFGAEVDTPTPLASKIG 394
Db 715 EHGANSERTRNGYTPPLHVAHYGHLDLVKFTENDADIEMSNGYTPPLHQAQOG 771
RESULT 5
A55575
ankyrin 3, long splice form - human
N/Alternate names: ankyrin G
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C/Accession: A55575
R:Kordeli, R.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A>Title: Ankyrin-G, A new ankyrin gene with neural-specific isoforms localized at the ax
A/Reference number: A55575; MUID:95138209; PMID:7836469
A/Accession: A55575
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-4377 <KOR>
A/Cross-references: UNIPROT:Q12955; GB:U13616; NID:9608024; PIDN:AAA64834.1; PID:9608025
C/Genetics:
A/Gene: GDB:ANK3
A/Cross-references: GDB:424503; OMIM:600465
A/Map position: 10q21-10q21
C/Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C/Keywords: alternative splicing; periplasmic membrane protein
F:106-138/Domain: ankyrin repeat homology <AN01>
F:139-171/Domain: ankyrin repeat homology <AN02>
F:172-200/Domain: ankyrin repeat homology <AN03>
F:201-233/Domain: ankyrin repeat homology <AN05>
F:234-266/Domain: ankyrin repeat homology <AN06>
F:267-299/Domain: ankyrin repeat homology <AN07>
F:300-332/Domain: ankyrin repeat homology <AN08>
F:333-365/Domain: ankyrin repeat homology <AN09>
F:366-398/Domain: ankyrin repeat homology <AN10>
F:399-431/Domain: ankyrin repeat homology <AN11>
F:432-464/Domain: ankyrin repeat homology <AN12>
F:465-497/Domain: ankyrin repeat homology <AN13>
F:498-530/Domain: ankyrin repeat homology <AN14>
F:531-563/Domain: ankyrin repeat homology <AN15>
F:564-596/Domain: ankyrin repeat homology <AN16>

F:597-629/Domain: ankyrin repeat homology <AN17>
 F:630-662/Domain: ankyrin repeat homology <AN18>
 F:633-666/Domain: ankyrin repeat homology <AN19>
 F:696-728/Domain: ankyrin repeat homology <AN20>
 F:729-761/Domain: ankyrin repeat homology <AN21>
 F:762-794/Domain: ankyrin repeat homology <AN22>
 F:795-827/Domain: ankyrin repeat homology <AN23>

Query Match 14.2%; Score 296; DB 2; Length 4377;
 Best Local Similarity 29.2%; Pred. No. 6, Se-16;
 Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;

QY 124 HLAVELGIRECFHRSRIISCAENEBEGCTPLHLCRKGDELVELVOYCHTQMDVTD 183
 Db HISARLGKADIVQQLQGGASPMNATTSYTPPLHSRBEHEDVAARLDDH-GASLSITT 562
 QY 184 YKEEYFHVAVQGDNSQYLQGLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLLCN 243
 Db KKGFPLHVAAKYQKLELVANLLQKS-ASPDAAKSGSLTPHLVAAHYDNKVALLLDDG 621
 QY 244 ARGNMGPNQY-PIHSAMKFSQKCAEMII--SMDSQHSKDPYVSGASPLHNAK--NA 297
 Db ASHRAAAKNGYTPPLHIAKKNQMDIATTLLEGADANAV----TROGIAVHLAAQEGHV 677
 QY 298 EMARMLKRGCVNSTSSAGNTALHVGVMKRPDCALVLLTHGANDARGEHNTPLHLA 357
 Db DWSLLGLGRNAVNLNKSGLTPHLHAAQEDRVAVVAVQGAHVDAQTKMGYTPPLHVG 737
 QY 358 MSKDNVEMIKALIVFGAEVDPNDPFGFTPTFLASKIG 394
 Db CHYGNKIVNVLLOHSAKNAKTKNGYTPHLQAQOG 774

RESULT 6

B35049
 ankyrin 1, erythrocyte splice form 3 - human

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N:Contains: ankyrin 2.2, erythrocyte
 C:Species: Homo sapiens (man)

C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998

C/Accession: B35049
 R/Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A>Title: cDNA sequence for human erythrocyte ankyrin.
 A/Reference number: A35049; MUID:90175370; PMID:1689849

A/Accession: B35049

A>Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1856 <LAM>

C/Genetics:

A/Gene: GDB:ANK1; ANK

A/Cross-references: GDB:118737; OMIM:182900

A/Map position: 8p11.2-8p11.2

C/Superfamily: ankyrin; ankyrin repeat homology

C/Keywords: alternative splicing; erythrocyte form 3 #status predicted <MAT>

F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>

F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

F:77-109/Domain: ankyrin repeat homology <AN02>

F:110-142/Domain: ankyrin repeat homology <AN03>

F:143-171/Domain: ankyrin repeat homology <AN04>

F:172-204/Domain: ankyrin repeat homology <AN05>

F:205-237/Domain: ankyrin repeat homology <AN06>

F:238-270/Domain: ankyrin repeat homology <AN07>

F:271-303/Domain: ankyrin repeat homology <AN08>

F:304-336/Domain: ankyrin repeat homology <AN09>

F:337-369/Domain: ankyrin repeat homology <AN10>

F:370-402/Domain: ankyrin repeat homology <AN11>

F:403-435/Domain: ankyrin repeat homology <AN12>

F:436-468/Domain: ankyrin repeat homology <AN13>

F:469-501/Domain: ankyrin repeat homology <AN14>

F:502-534/Domain: ankyrin repeat homology <AN15>

F:535-567/Domain: ankyrin repeat homology <AN16>

F:568-600/Domain: ankyrin repeat homology <AN17>
 F:601-633/Domain: ankyrin repeat homology <AN18>
 F:634-666/Domain: ankyrin repeat homology <AN19>
 F:667-699/Domain: ankyrin repeat homology <AN20>
 F:700-732/Domain: ankyrin repeat homology <AN21>
 F:733-765/Domain: ankyrin repeat homology <AN22>
 F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 14.1%; Score 294; DB 2; Length 1856;
 Best Local Similarity 25.6%; Pred. No. 3e-16;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LQHLTDLIRNHSWSVAHLAVELGIRECFHH--SRIISCAENENE--EGCTPLHLACR 161
 Db LDHLTLPL-----HVA-----HCGHHRVAKYLLDKAKPNSRALNGFTPLHIACK 380
 QY 162 KKGDELVELVOYCHTQMD-----VTQKGET 188
 Db KKHVRVW-BELLKTGASIDAVTESGLTPHLVASFWGHLPIVKNLORGASPNVSVKVEI 439
 QY 189 VFHYAVQGDNSQYLQGLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLLCNARCN 248
 Db PLHMAARAGHTVAKYLLQNK-AKVAKAKADQDTPHCAARIGHTMVTLLLENNAPML 498
 QY 249 MGENGY-----PIHSAMKFSQKCAEMITSN 274
 Db ATTAGTTPHLIAREGHVETVALLLEKASQACMTKKGFTPLHVAKYKRVAVELLER 558
 QY 275 DSSQHSKDPYVSGASPLHNA---KNAEMARMLKRGCVNSTSSAGNTALHVGVMKRPD 331
 Db DHP--NAAGKNLTPHLVAVHNNNDIVKLLPRGSGPHSPAMNGYTPPLHIAKKNQV 616
 QY 332 CAIVLLTHGANDARGEHNTPLHLSKDNVEMIKALIVFGAEVDPNDPFGFTPTFLAS 391
 Db VARSLLQYGSANAEVQGTTPHLHAAQGAHEMVALLSKQANGSLGKSGTTPHLVA 676
 QY 392 KIG 394
 Db 677 QEG 679

RESULT 7

A35049
 ankyrin 1, erythrocyte splice form 2 - human

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N:Contains: ankyrin 2.2, erythrocyte
 C:Species: Homo sapiens (man)

C>Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004

C/Accession: A35049

R/Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A>Title: cDNA sequence for human erythrocyte ankyrin.

A/Reference number: A35049; MUID:90175370; PMID:1689849

A/Accession: A35049

A>Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1880 <LAM>

A/Cross-references: UNIPROT:P16157; GB:M28880

C/Genetics:

A/Gene: GDB:ANK1; ANK

A/Cross-references: GDB:118737; OMIM:182900

A/Map position: 8p11.2-8p11.2

C/Superfamily: ankyrin; ankyrin repeat homology

C/Keywords: alternative splicing; cytoskeleton

F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>

F:2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

F:77-109/Domain: ankyrin repeat homology <AN01>

F:110-142/Domain: ankyrin repeat homology <AN02>

F:143-171/Domain: ankyrin repeat homology <AN03>

F:172-204/Domain: ankyrin repeat homology <AN04>

F:205-237/Domain: ankyrin repeat homology <AN05>

F:238-270/Domain: ankyrin repeat homology <AN06>

F:271-303/Domain: ankryn repeat homology <AN08>
 F:304-336/Domain: ankryn repeat homology <AN09>
 F:337-369/Domain: ankryn repeat homology <AN10>
 F:370-402/Domain: ankryn repeat homology <AN11>
 F:403-435/Domain: ankryn repeat homology <AN12>
 F:436-468/Domain: ankryn repeat homology <AN13>
 F:469-501/Domain: ankryn repeat homology <AN14>
 F:502-534/Domain: ankryn repeat homology <AN15>
 F:535-567/Domain: ankryn repeat homology <AN16>
 F:568-600/Domain: ankryn repeat homology <AN17>
 F:601-633/Domain: ankryn repeat homology <AN18>
 F:634-666/Domain: ankryn repeat homology <AN19>
 F:667-699/Domain: ankryn repeat homology <AN20>
 F:700-732/Domain: ankryn repeat homology <AN21>
 F:733-765/Domain: ankryn repeat homology <AN22>
 F:766-798/Domain: ankryn repeat homology <AN23>

Query Match 14.1%; Score 294; DB 2; Length 1880;
 Best Local Similarity 25.6%; Pred. No. 3e-16;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LOHLDLIRNHPWSVAHLAVELGIRECFHH--SRIISCANCAENE---EGCTPLHLACR 161
 DB 336 LDHLTP-----HVA-----HCGHRAVAKVLLDKGAKPNSBALNGFTPLHIACK 380
 QY 162 KGDGELIVELYOYCHTQMD-----VTDYKGET 188
 DB 381 KHNVRW-ELLKGTASIDAVTESGLTPPLVASFMGHLPVKNLDRGASPNVSNKVEET 439
 QY 189 VFHYAVQDNGSOYQLLGRNVAAGLNQVNNQGLTPPLHACOLGKOEKVRVLLCNARCNI 248
 DB 440 PLHMAARAGHTVEAKVILQNK-AKVNAKAKADDPPLHCAARIGHTMVKLLNNANPNL 498
 QY 249 MGENGY-----PIHSAMKFSQKCAEMITISM 274
 DB 499 ATTAGHTPLHIAAREGHVETVALLLEKESQAQCTKKGFPLHVAAYGKVAELLLER 558
 QY 275 DSSQHSKDPRYGASPLHMA---KNAEMAMLLKRCGNVNSTSSAGNTALHVGWENRFD 331
 DB 559 DAHP--NAAGKGLTPPLHVAVHNHNDIVKLLPRGSPHSPPMNGYTPPLHIAKONQVE 616
 QY 332 CAIVLTGAGNADARGHGNTPLHAMSNDVENIKALIVFGABVDTPNDFGCTPTFLAS 391
 DB 617 VASLIQYGGSSANABESVQVTPPLHIAQGBAEMVALLLSKQANGNLGNKSGILTPPLHVA 676
 QY 392 KIG 394
 DB 677 QEG 679

RESULT 8

ankryn 1, erythrocyte splice form 1 - human

N:Alternate names: ankryn 2.1, erythrocyte; ankryn-R
 N:Contains: ankryn 2.2

C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1991 #sequence, revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: S08275; A33219; PC2220; A35443

R:Lux, S.E.; John, K.M.; Bennett, V.
 Nature 344, 36-42, 1990

A:Title: Analysis of cDNA for human erythrocyte ankryn indicates a repeated structure
 A:Reference number: S08275; MUID:90158830; PMID:2137557

A:Accession: S08275
 A:Molecule type: mRNA

A:Residues: 1-1881 <UNI>
 A:Cross-references: UNIPROT:P16157; EMBL:X16609; NID:G28701; PIDN:CAA34610.1; PID:G28702

A:Accession: A33219
 A:Molecule type: protein

A:Residues: 2-7, 'X', '9-11', 'X', '19-20', 'T', '22-30', '733-749', 'A', '751-753', '828-833', 'X', '835-855', 'X', 'X', '1367', '1383-1442', '1501-1530', '1686-1698', 'D', '1700', '1763-1772 <LUX>
 A:Note: 845-Arg and 1392-Thr were also found

R:Hermann, J.; Barel, M.; Frade, R.
 Biochem. Biophys. Res. Commun. 204, 453-460, 1994

A:Title: Human erythrocyte ankryn, a cytoskeleton component, generates the p57 membrane
 A:Reference number: PC2220; MUID:95071348; PMID:7526850
 A:Accession: PC2220
 A:Molecule type: protein
 A:Residues: 910-929 <HER>
 R:Davis, L.H.; Bennett, V.
 J. Biol. Chem. 265, 10589-10596, 1990
 A:Title: Mapping the binding sites of human erythrocyte ankryn for the anion exchanger
 A:Reference number: A35443; MUID:90285190; PMID:214135
 A:Accession: A35443
 A:Molecule type: protein
 A:Residues: 'X', '5', 'X', '7-12', '403-417', 'X', '419-422', 'H', '424', 'LQ', '797-800', 'L', '802-814', '862-863', 'C:Genetics:
 A:Gene: GDB:ANK1; ANK
 A:Cross-references: GDB:118737; OMIM:182900
 A:Map position: 8p11.2-8p11.2
 C:Superfamily: ankryn; ankryn repeat homology
 C:Keywords: alternative splicing; phosphoprotein
 F:2-1881/Product: ankryn 1, erythrocyte form 1 #status predicted <MAT1>
 F:2-1512,1675-1881/Product: ankryn 2.2, erythrocyte #status predicted <MAT2>
 F:2-827/Domain: 89K #status predicted <DOM1>
 F:4-76/Region: anion exchange protein binding
 F:77-109/Domain: ankryn repeat homology <AN01>
 F:110-142/Domain: ankryn repeat homology <AN02>
 F:143-171/Domain: ankryn repeat homology <AN03>
 F:172-204/Domain: ankryn repeat homology <AN04>
 F:205-237/Domain: ankryn repeat homology <AN05>
 F:238-270/Domain: ankryn repeat homology <AN06>
 F:271-303/Domain: ankryn repeat homology <AN07>
 F:304-336/Domain: ankryn repeat homology <AN08>
 F:337-369/Domain: ankryn repeat homology <AN09>
 F:370-402/Domain: ankryn repeat homology <AN10>
 F:403-435/Domain: ankryn repeat homology <AN11>
 F:436-468/Domain: ankryn repeat homology <AN12>
 F:469-501/Domain: ankryn repeat homology <AN13>
 F:502-534/Domain: ankryn repeat homology <AN14>
 F:535-567/Domain: ankryn repeat homology <AN15>
 F:568-600/Domain: ankryn repeat homology <AN16>
 F:601-633/Domain: ankryn repeat homology <AN17>
 F:634-666/Domain: ankryn repeat homology <AN18>
 F:667-699/Domain: ankryn repeat homology <AN19>
 F:700-732/Domain: ankryn repeat homology <AN20>
 F:733-765/Domain: ankryn repeat homology <AN21>
 F:766-798/Domain: ankryn repeat homology <AN22>
 F:828-1382/Domain: 62K #status predicted <DOM2>
 F:828-1382/Region: spectrin binding
 F:1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 14.1%; Score 294; DB 1; Length 1881;
 Best Local Similarity 25.6%; Pred. No. 3e-16;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LOHLDLIRNHPWSVAHLAVELGIRECFHH--SRIISCANCAENE---EGCTPLHLACR 161
 DB 336 LDHLTP-----HVA-----HCGHRAVAKVLLDKGAKPNSBALNGFTPLHIACK 380
 QY 162 KGDGELIVELYOYCHTQMD-----VTDYKGET 188
 DB 381 KHNVRW-ELLKGTASIDAVTESGLTPPLVASFMGHLPVKNLDRGASPNVSNKVEET 439
 QY 189 VFHYAVQDNGSOYQLLGRNVAAGLNQVNNQGLTPPLHACOLGKOEKVRVLLCNARCNI 248
 DB 440 PLHMAARAGHTVEAKVILQNK-AKVNAKAKADDPPLHCAARIGHTMVKLLNNANPNL 498
 QY 249 MGENGY-----PIHSAMKFSQKCAEMITISM 274
 DB 499 ATTAGHTPLHIAAREGHVETVALLLEKESQAQCTKKGFPLHVAAYGKVAELLLER 558
 QY 275 DSSQHSKDPRYGASPLHMA---KNAEMAMLLKRCGNVNSTSSAGNTALHVGWENRFD 331
 DB 559 DAHP--NAAGKGLTPPLHVAVHNHNDIVKLLPRGSPHSPPMNGYTPPLHIAKONQVE 616

Qy 332 CAIVLTTHGANADARGEHGTPLHLAMSKDNVEMIKALIVFGAEVDTFNDPFGETPTFLAS 391
 Db 617 VARSLIYOGGSANASBVQVTTPLHLAAGEHAEVALLLSKQANGNILGNKSGLTPLHLVA 676
 Qy 392 KIG 394
 Db 677 QEG 679

RESULT 9

T42714
 ankyrin 3, splice form 2 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42714
 R:Peterson, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A:Reference number: Z22237; PMID:95340633; PMID:7615634
 A:Accession: T42714
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1765 <PEP>
 A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:G710548; PID:G710551; PIDN:AA01605
 A:Experimental source: strain C57BL/6J; kidney
 C:Genetics:
 A:Gene: Ank3
 A:Map position: 10
 A:Introns: 1587/1
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing

Query Match 14.1%; Score 293; DB 2; Length 1765;
 Best Local Similarity 29.2%; Pred. No. 3.4e-16;
 Matches 81; Conservative 55; Mismatches 125; Indels 16; Gaps 7;

Qy 124 HLAVELG---IRECFHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQM 179
 Db 421 HVAAFGHVNIYSQLMNH---GASPTNTVNGETALHMAARSGQAEVRYLVQ-DGAV 475
 Qy 180 DVTDYKGEVTFHVAVGNDNSQVQLLGRNVAAGLNQVNOGTLPLHLAQLGQKQEMRV 239
 Db 476 EKAAXDDQTPHLISARLGKADIVQQLQOG-ASPNAATTSGYTTPHLAAREGHEVDVAFL 534
 Qy 240 LNCNARCNIMGPGY-PIHSAMKFSQKCAEMIISMSQIHSKDPRYGASPLHMA--K 295
 Db 535 LDHGASLSTTKKGFPLHVAAKYKLEVASLLQKSAP--DAAGKSLTPLHVAAND 592
 Qy 296 NEMAMRLKRGCVNSTSGAGNTALHVGMRNRFCAIVLTTHGANADARGEHGTPLH 355
 Db 593 NQKVALLLLDQGSPPHAAKNGYTPHLIAKKQMDIATSLLEYGADANAATVROGIASVH 652
 Qy 356 LAMSKDNVEMIKALIVFGAEVDTFNDPFGETPTFLASK 392
 Db 653 LAAQEGHVDVMSLLSRNANVNLNKSGLTPLHLAAQ 689

RESULT 10

T42715
 ankyrin 3, splice form 3 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42715
 R:Peterson, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A:Reference number: Z22237; PMID:95340633; PMID:7615634
 A:Accession: T42715
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1940 <PEP>

A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:G710548; PID:G710551; PIDN:AA01604.
 A:Experimental source: strain C57BL/6J; kidney
 C:Genetics:
 A:Gene: Ank3
 A:Map position: 10
 A:Introns: 834/1
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing

Query Match 14.1%; Score 293; DB 2; Length 1940;
 Best Local Similarity 29.2%; Pred. No. 3.8e-16;
 Matches 81; Conservative 55; Mismatches 125; Indels 16; Gaps 7;

Qy 124 HLAVELG---IRECFHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQM 179
 Db 421 HVAAFGHVNIYSQLMNH---GASPTNTVNGETALHMAARSGQAEVRYLVQ-DGAV 475
 Qy 180 DVTDYKGEVTFHVAVGNDNSQVQLLGRNVAAGLNQVNOGTLPLHLAQLGQKQEMRV 239
 Db 476 EKAAXDDQTPHLISARLGKADIVQQLQOG-ASPNAATTSGYTTPHLAAREGHEVDVAFL 534
 Qy 240 LNCNARCNIMGPGY-PIHSAMKFSQKCAEMIISMSQIHSKDPRYGASPLHMA--K 295
 Db 535 LDHGASLSTTKKGFPLHVAAKYKLEVASLLQKSAP--DAAGKSLTPLHVAAND 592
 Qy 296 NEMAMRLKRGCVNSTSGAGNTALHVGMRNRFCAIVLTTHGANADARGEHGTPLH 355
 Db 593 NQKVALLLLDQGSPPHAAKNGYTPHLIAKKQMDIATSLLEYGADANAATVROGIASVH 652
 Qy 356 LAMSKDNVEMIKALIVFGAEVDTFNDPFGETPTFLASK 392
 Db 653 LAAQEGHVDVMSLLSRNANVNLNKSGLTPLHLAAQ 689

RESULT 11

T42713
 ankyrin 3, splice form 1 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42713
 R:Peterson, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A:Reference number: Z22237; PMID:95340633; PMID:7615634
 A:Accession: T42713
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1943 <PEP>
 A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:G710548; PID:G710550; PIDN:AA01606.
 A:Experimental source: strain C57BL/6J; kidney
 C:Genetics:
 A:Gene: Ank3
 A:Map position: 10
 A:Introns: 855/1
 C:Function:
 A:Description: supposed to play an important role in the polarized distribution of many
 A>Note: major kidney ankyrin
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing

Query Match 14.1%; Score 293; DB 2; Length 1943;
 Best Local Similarity 29.2%; Pred. No. 3.8e-16;
 Matches 81; Conservative 55; Mismatches 125; Indels 16; Gaps 7;

Qy 124 HLAVELG---IRECFHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQM 179
 Db 421 HVAAFGHVNIYSQLMNH---GASPTNTVNGETALHMAARSGQAEVRYLVQ-DGAV 475
 Qy 180 DVTDYKGEVTFHVAVGNDNSQVQLLGRNVAAGLNQVNOGTLPLHLAQLGQKQEMRV 239
 Db 476 EKAAXDDQTPHLISARLGKADIVQQLQOG-ASPNAATTSGYTTPHLAAREGHEVDVAFL 534

RESULT 13
S37771
ankyrin, erythrocyte - mouse
C.Species: Mus musculus (house mouse)
C.Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
Accession: S37771
R.Bitkemeier, C.S.; White, R.A.; Peters, L.T.; Hall, B.J.; Lux, S.B.; Barker, J.E.
J. Biol. Chem. 268, 9533-9540, 1993
A.Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found at
A.Reference number: S37771; MUID:93252825; PMID:8486643
A.Accession: S37771
A.Status: preliminary

RESULT 14
149502
ankyrin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession:149502
R:White, R.A.; Birkmeier, C.S.; Peters, L.L.; Barker, J.B.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A>Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory domain
A:Reference number: 149502; MUID:92345717; PMID:1386265
A:Accession: 149502

A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-1662 <RES>
A/Cross-references: UNIPROT:Q02357; GB:M84756; NID:gl191939; PDB:AAA37236.1; PID:gl191940
C/Genetics:
A/Gene: Ank-1
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keyword: alternative splicing
F/40-72/Domain: ankyrin repeat homology <AN01>
F/73-105/Domain: ankyrin repeat homology <AN02>
F/106-138/Domain: ankyrin repeat homology <AN03>
F/139-167/Domain: ankyrin repeat homology <AN04>
F/168-200/Domain: ankyrin repeat homology <AN05>
F/201-233/Domain: ankyrin repeat homology <AN06>
F/234-266/Domain: ankyrin repeat homology <AN07>
F/267-299/Domain: ankyrin repeat homology <AN08>
F/300-332/Domain: ankyrin repeat homology <AN09>
F/333-365/Domain: ankyrin repeat homology <AN10>
F/366-398/Domain: ankyrin repeat homology <AN11>
F/399-431/Domain: ankyrin repeat homology <AN12>
F/432-464/Domain: ankyrin repeat homology <AN13>
F/465-497/Domain: ankyrin repeat homology <AN14>
F/498-530/Domain: ankyrin repeat homology <AN15>
F/531-563/Domain: ankyrin repeat homology <AN16>
F/564-596/Domain: ankyrin repeat homology <AN17>
F/597-629/Domain: ankyrin repeat homology <AN18>
F/630-662/Domain: ankyrin repeat homology <AN19>
F/663-695/Domain: ankyrin repeat homology <AN20>
F/696-728/Domain: ankyrin repeat homology <AN21>
F/729-761/Domain: ankyrin repeat homology <AN22>
F/762-794/Domain: ankyrin repeat homology <AN23>

Query Match 13.7%; Score 285; DB 2; Length 1662;
Best Local Similarity 25.6%; Pred. No. 1.7e-15;
Matches 93; Conservative 55; Mismatches 121; Indels 94; Gaps 10;

QY 107 LQHLIDLNNHPSVAHLAVELGIRECFHH--SRIISCANCAENE--EGCTPLHLACR 161
DB 332 LDHLTPPL-----HVA-----HCGHRAVAKYLLDKAKPNSRALNGFTPLHIACK 376
QY 162 KGDGELVELVQYCHTQM-----VTDYKGET 188
DB 377 KQHIRMW-ELLKTAGSIDAVTESGLTPLHVASFMGHLPIVKLLQFGASPNVSNKVER 435
QY 189 VFHYAVQGNISQYLQILGRNNAVGLNQVNNQGLTPLHLACQLGKQEMVRLICNARCI 248
DB 436 PLHMAARAGHTBVAKYLQNK--AKANAKAKDDOTPLHCAARIGHTGMVKLLLENGASPNL 494
QY 249 MGENGY-----PIHSAMKFSQKCAEMIISM 274
DB 495 ATTAGHTPLHTAAREGHVDLTALLLEKEASQACMTKKGFTPLHVAAYGKVRLLAEILLH 554
QY 275 DSSQIHSKDPRYGASPLHMA---KNAEMARMLKGCNVNSTSSAGNTALHVGVMNRPD 331
DB 555 DHP--NAAGKGLTPLHVAVHNHNDIYKLLPRGSGPSHPMNGYTPHLIAKONQIE 612
QY 332 CAIVLLTHGANPDARGEHTPLHLMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLAS 391
DB 613 VARSLQYGSANAEVQGTPLHLAAGSHTEMVALLLSKQANGNLGNKSGITPLHIVS 672
QY 392 KTG 394
DB 673 QEG 675

RESULT 15

T46445
Hypothetical protein DKFp434B2328.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T46445
R/Bloeker, H.; Boeher, M.; Brandt, P.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, January 2000

A/Reference number: Z23032
A/Accession: T46445
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-397 <AAA>
A/Cross-references: UNIPROT:Q0NTA1; EMBL:AL137448
A/Experimental source: adult testis; clone DKFp434B2328
C/Genetics:
A/Note: DKFp434B2328.1

Query Match 13.5%; Score 281.5; DB 2; Length 397;
Best Local Similarity 30.7%; Pred. No. 4.2e-16;
Matches 86; Conservative 48; Mismatches 135; Indels 11; Gaps 7;

QY 121 SVANLAVELGIRECFHSHRIISCANCAENEEGCTPLHLAC--RKGDELVELVQYCHTQM 179
DB 53 SLHLAVELVQYCHTQM-----HVA-----HCGHRAVAKYLLDKAKPNSRALNGFTPLHIACK 376
QY 180 DVTDYKGETVFHYAVQ--GNSQVLLQILGRNNAVGLNQVNNQGLTPLHLACQLGKQEMVRL 238
DB 111 NAKDEQMTALHFAQNGDESSTRLLEKX--ASVNEVDPEGRTPMNVACQHQENIVRI 168
QY 239 LILCNARCMIMPNQY--PIHSAMKFSQKCAEMIISMSSQIHSKDPRYGASPLHMAK-- 295
DB 169 LIRRGVDELQGDVAVLPLHVAAMOGHLPIVKLAKQPGVSVNAQ--TLDGRTPLHLAQR 227
QY 296 -NAEMARMLKGCNVNSTSSAGNTALHVGVMNRPDCAIVLLTHGANPDARGEHTPL 354
DB 228 GHYRVARILLIDCSDVNVGSLAQTPHVAABETGHTSTARRLLHRRGAKGKAVTSQGYTAL 287
QY 355 HLMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKTG 394
DB 288 HLAARNGHATVALLVEERADVLARGPLNQTLHLHLAAHG 327

Search completed: December 15, 2004, 13:14:15
Job time : 18.7917 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:25 ; Search time 85.8019 Seconds
(without alignments)
2642.105 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084
Sequence: 1 MGFPGRLVNTFGSVTLFNSN.....EVDTPNDPGETPTPLASKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2078 | 99.7 | 806 | 1 | PA26_HUMAN |
| 2 | 2078 | 99.7 | 806 | 1 | CAG30429 |
| 3 | 1842 | 88.4 | 752 | 1 | PA26_MOUSE |
| 4 | 1842 | 88.4 | 807 | 2 | Q9JKE1 |
| 5 | 1842 | 88.4 | 807 | 2 | AAH57209 |
| 6 | 1832 | 87.9 | 752 | 2 | Q7TPX2 |
| 7 | 1808.5 | 86.8 | 751 | 1 | PA26_RAT |
| 8 | 1176 | 56.4 | 756 | 2 | Q6DDKO |
| 9 | 1037.5 | 49.8 | 818 | 2 | Q6NMW0 |
| 10 | 1037.5 | 49.8 | 818 | 2 | AAH67375 |
| 11 | 512 | 23.6 | 879 | 2 | Q7Q2U1 |
| 12 | 494.5 | 23.7 | 877 | 2 | Q9VTE0 |
| 13 | 494.5 | 23.7 | 877 | 2 | AAFS0194 |
| 14 | 494.5 | 23.7 | 887 | 2 | Q7KDD4 |
| 15 | 494.5 | 23.7 | 887 | 2 | AAAN1936 |
| 16 | 338 | 16.2 | 843 | 2 | Q8C8R3 |
| 17 | 338 | 16.2 | 1219 | 2 | Q8C8R3 |
| 18 | 332 | 15.9 | 1863 | 2 | Q7Z315 |
| 19 | 332 | 15.9 | 3924 | 1 | ANK2_HUMAN |
| 20 | 318 | 15.3 | 1004 | 2 | Q7JUN0 |
| 21 | 318 | 15.3 | 1004 | 2 | AAQ91911 |
| 22 | 318 | 15.3 | 1786 | 2 | Q17344 |
| 23 | 318 | 15.3 | 1809 | 2 | Q17487 |
| 24 | 318 | 15.3 | 1815 | 2 | Q17488 |
| 25 | 318 | 15.3 | 1841 | 2 | Q8MOC0 |
| 26 | 318 | 15.3 | 1867 | 2 | Q17486 |
| 27 | 318 | 15.3 | 2039 | 2 | Q17489 |
| 28 | 318 | 15.3 | 6994 | 2 | Q17343 |
| 29 | 318 | 15.3 | 6994 | 2 | Q17490 |
| 30 | 313.5 | 15.0 | 1549 | 2 | Q24241 |
| 31 | 313.5 | 15.0 | 1549 | 2 | Q9V4B1 |

ALIGNMENTS

| | | | | | | |
|----|-------|------|------|---|------------|---------------------|
| 32 | 310 | 14.9 | 1009 | 2 | Q8SWY2 | Q8SWY2 drosophila |
| 33 | 310 | 14.9 | 1159 | 2 | Q9NCP8 | Q9NCP8 drosophila |
| 34 | 310 | 14.9 | 1571 | 2 | Q7KXJ2 | Q7KXJ2 drosophila |
| 35 | 310 | 14.9 | 1571 | 2 | AAFS0525 | AAFS0525 drosophila |
| 36 | 305.5 | 14.7 | 792 | 2 | Q7Q172 | Q7Q172 anopheles g |
| 37 | 304.5 | 14.6 | 820 | 2 | Q8JHU3 | Q8JHU3 brachydanio |
| 38 | 301 | 14.4 | 786 | 2 | Q9ERK0 | Q9ERK0 mus muscu |
| 39 | 301 | 14.4 | 786 | 2 | AAH57871 | AAH57871 mus muscu |
| 40 | 298 | 14.3 | 2632 | 2 | Q70511 | Q70511 rattus norv |
| 41 | 296 | 14.2 | 1088 | 2 | Q13484 | Q13484 homo sapien |
| 42 | 296 | 14.2 | 4377 | 1 | ANK3_HUMAN | Q12955 homo sapien |
| 43 | 295.5 | 14.2 | 1145 | 2 | Q7PEZ8 | Q7PEZ8 anopheles g |
| 44 | 295.5 | 14.2 | 1501 | 2 | Q7OKD3 | Q7OKD3 anopheles g |
| 45 | 295 | 14.2 | 1887 | 2 | Q7Z3G4 | Q7Z3G4 homo sapien |

RESULT 1

PA26_HUMAN STANDARD; PRT; 806 AA.
ID 060733; Q7S645; Q8N452; Q9UG29; Q9UIT0; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND
RP ANKYRIN-IPLA2-2).
RC TISSUE=Brain, and Testis;
RX MEDLINE=98079046; PubMed=9417066;
RA Larsson P.K.A., Claesson H.-E., Kennedy B.P.;
RT Multiple splice variants of the human calcium-independent
RT phospholipase A2 and their effect on enzyme activity.";
RL J. Biol. Chem. 273:207-214(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Pancreatic islets;
RX MEDLINE=99194813; PubMed=10092647;
RA Ma Z., Wang X., Nowatke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct
RT catalytically active isoforms of group VI phospholipase A2 (iPLA2)
RT that arise from an exon-skipping mechanism of alternative splicing of
RT the transcript from the iPLA2 gene on chromosome 22q13.1.";
RL J. Biol. Chem. 274:9607-9616(1999).
RN [3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=99269033; PubMed=10336645;
RA Larsson Forezell P.K.A., Kennedy B.P., Claesson H.-E.;
RT "The human calcium-independent phospholipase A2 gene. Multiple enzymes
RT with different properties from a single gene.";
RL Eur. J. Biochem. 262:575-585(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RA Ansoyge W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND
RP THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://esg.gs.washington.edu>).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR HSSP; 060778; 10Y3.
DR Genew; HGNC:9039; PLA2G6.

Query Match 99.7%; Score 2078; DB 1; Length 806;
Best Local Similarity 99.7%; Pred. No. 1.9e-162;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPFGVLVNTFGSVTLFSPNPRVKEVAVADYTSRVRREEGQLIFONTPTNTWCVLV 60
DB 1 MOPFGVLVNTFGSVTLFSPNPRVKEVAVADYTSRVRREEGQLIFONTPTNTWCVLV 60
QY 61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLTEVLOHTLDIRHPSW 120
DB 61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLTEVLOHTLDIRHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDELIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDELIVELVOYCHTQMD 180
QY 181 VVDYKGETVPHYAVOGDNSQVQLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
DB 181 VVDYKGETVPHYAVOGDNSQVQLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
QY 241 LCNARCNINGPNQYPIHSAKMFQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNINGPNQYPIHSAKMFQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVGAEVDTNPDEGTPTPLASKIG 394
DB 361 DNVEMIKALIVGAEVDTNPDEGTPTPLASKIG 394

RESULT 2

CAG30429 PRELIMINARY; PRT; 806 AA.
AC CAG30429; PRT; 806 AA.
DT 01-JUN-2004 (TREMblrel. 27, Created)
DT 01-JUN-2004 (TREMblrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMblrel. 27, Last annotation update)
DE PLA2G6 protein.
GN PLA2G6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,
RA Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J.,
RA Beare D.M., Dunham I.;
RA Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; C9455543; CAG30429.1; -; 8E55CDEB9ACAD8B CRC64;
SQ SEQUENCE 806 AA; 89902 MW; 8E55CDEB9ACAD8B CRC64;

Query Match 99.7%; Score 2078; DB 2; Length 806;
Best Local Similarity 99.7%; Pred. No. 1.9e-162;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPFGVLVNTFGSVTLFSPNPRVKEVAVADYTSRVRREEGQLIFONTPTNTWCVLV 60
DB 1 MOPFGVLVNTFGSVTLFSPNPRVKEVAVADYTSRVRREEGQLIFONTPTNTWCVLV 60
QY 61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLTEVLOHTLDIRHPSW 120
DB 61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLTEVLOHTLDIRHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDELIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDELIVELVOYCHTQMD 180

QY 181 VVDYKGETVPHYAVOGDNSQVQLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
DB 181 VVDYKGETVPHYAVOGDNSQVQLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
QY 241 LCNARCNINGPNQYPIHSAKMFQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNINGPNQYPIHSAKMFQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVGAEVDTNPDEGTPTPLASKIG 394
DB 361 DNVEMIKALIVGAEVDTNPDEGTPTPLASKIG 394

RESULT 3

PA26_MOUSE STANDARD; PRT; 752 AA.
AC P97819; Q99LA9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (PLA2) (Cal-
PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=97236816; PubMed=9079688;
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RT "Identity between the Ca2+-independent phospholipase A2 enzymes from
RT p38D1 macrophages and Chinese hamster ovary cells.";
RL J. Biol. Chem. 272:8576-8580(1997).
RN [2]
RP REVISIONS TO 2-3; 9; 11 AND 211.
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh P.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Plancke C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Contains 7 ANK repeats.

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 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; U88624; AAB48511.2; -
 DR EMBL; BC003487; AAB03487.1; -
 DR HSSP; O60778; 10Y3.
 DR MGD; MGI:1859152; Pla2g6.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ANK; 6.
 DR PRINTS; PRO1415; ANKYRIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR ANK repeat; Hydrophobic; Lipid degradation; Repeat.
 KM ANK repeat; 151 181 ANK 1.
 FT REPEAT 185 215 ANK 2.
 FT REPEAT 219 248 ANK 3.
 FT REPEAT 251 281 ANK 4.
 FT REPEAT 286 312 ANK 5.
 FT REPEAT 316 345 ANK 6.
 FT REPEAT 349 378 ANK 7.
 FT ACT SITE 465 465 Potential.
 SQ SEQUENCE 752 AA; 83702 MW; AAC3347B0E1292E9 CRC64;

Query Match 88.4%; Score 1842; DB 1; Length 752;
 Best Local Similarity 87.8%; Pred. No. 5e-143;
 Matches 345; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSGVTNLFSNPRFKVAVADYSSDRVREEGQLIFONTNRTWCVLV 60
 DB 1 MOFGRLVNTLSSVTNLFSNPRFKVAVADYSSDRVREEGQLIFONTNRTWCVLV 60
 QY 61 NPNRSGGRLFLQLEADALVNFHOYSSQLLPFYSSPOVLTAVLQHLTLIRNHPW 120
 DB 61 NPNRSGGRLFLQLEADALVNFHOYSSQLLPFYSSPOVLTAVLQHLTLIRNHPW 120
 DB 61 SPNPSGGRFLFLQLEADALVNFHOYSSQLLPFYSSPOVLTAVLQHLTLIRNHPW 120
 QY 121 SVAHALVEIGIRCFHSHRISICANCAENEGCTPLHLCKRGDGIIVELVQYCHTOMD 180
 DB 121 TYTHLAVEIGIRCFHSHRISICANCAENEGCTPLHLCKRGDGIIVELVQYCHTOMD 180
 QY 181 VTDYKGETVFNHVAQDNGSVQLQLGRNVAAGVANNQGLTPHLACQIGKQEWVYLL 240
 DB 181 VTDYKGETVFNHVAQDNGSVQLQLGRNVAAGVANNQGLTPHLACQIGKQEWVYLL 240
 QY 241 LCNARCNINGPNCYPIHSAKMSQKCAEMTISMSQIHSKDPRIYASPLHWAKNAEMA 300
 DB 241 LCNARCNINGPNCYPIHSAKMSQKCAEMTISMSQIHSKDPRIYASPLHWAKNAEMA 300
 QY 301 RMLKRGKGVNNTSSAGNTALHGVNRNRPDCAIVLTTHGANADAGEHNTPLHAKMSK 360
 DB 301 RMLKRGKGVNNTSSAGNTALHGVNRNRPDCAIVLTTHGANADAGEHNTPLHAKMSK 360
 QY 361 DNVEIMKALIVFGAEVDPNDPFGETPTFLASKI 393
 DB 361 DNVEIMKALIVFGAEVDPNDPFGETPTFLASKI 393
 DB 361 DNVEIMKALIVFGAEVDPNDPFGETPTFLASKI 393

RESULT 4
 Q9JK61 PRELIMINARY; PRT; 807 AA.

ID Q9JK61
 AC Q9JK61
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Ca2+-independent phospholipase A2 long form (Pla2g6 protein).
 GN Name:Pla2g6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NH/Swiss;
 RA Chiu C.-H., Jackowski S.;
 RU Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Stemann C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
 RA Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.O., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RA Straubeberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A0259401; AAF72651.1; -
 DR EMBL; BC057209; AAF57209.1; -
 DR HSSP; O60778; 10Y3.
 DR MGD; MGI:1859152; Pla2g6.
 DR GO; GO:0003824; F.catalytic activity; IEA.
 DR GO; GO:0045735; F.nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patacin.
 DR Pfam; PF00023; ANK; 6.
 DR Pfam; PF01734; Patacin; 1.
 DR PRINTS; PRO1415; ANKYRIN.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KM ANK repeat.
 SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 88.4%; Score 1842; DB 2; Length 807;
 Best Local Similarity 87.8%; Pred. No. 5e-143;
 Matches 345; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSGVTNLFSNPRFKVAVADYSSDRVREEGQLIFONTNRTWCVLV 60
 DB 1 MOFGRLVNTLSSVTNLFSNPRFKVAVADYSSDRVREEGQLIFONTNRTWCVLV 60
 QY 61 NPNRSGGRLFLQLEADALVNFHOYSSQLLPFYSSPOVLTAVLQHLTLIRNHPW 120
 DB 61 NPNRSGGRLFLQLEADALVNFHOYSSQLLPFYSSPOVLTAVLQHLTLIRNHPW 120
 DB 61 SPNPSGGRFLFLQLEADALVNFHOYSSQLLPFYSSPOVLTAVLQHLTLIRNHPW 120
 QY 121 SVAHALVEIGIRCFHSHRISICANCAENEGCTPLHLCKRGDGIIVELVQYCHTOMD 180
 DB 121 TYTHLAVEIGIRCFHSHRISICANCAENEGCTPLHLCKRGDGIIVELVQYCHTOMD 180
 QY 181 VTDYKGETVFNHVAQDNGSVQLQLGRNVAAGVANNQGLTPHLACQIGKQEWVYLL 240
 DB 181 VTDYKGETVFNHVAQDNGSVQLQLGRNVAAGVANNQGLTPHLACQIGKQEWVYLL 240
 QY 241 LCNARCNINGPNCYPIHSAKMSQKCAEMTISMSQIHSKDPRIYASPLHWAKNAEMA 300
 DB 241 LCNARCNINGPNCYPIHSAKMSQKCAEMTISMSQIHSKDPRIYASPLHWAKNAEMA 300

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Db      241 LCNARCINMGPGGPIHTAMKFSQKCAEMITISMSDNQHSKDPRYGASPLHAKNAEMA 300
Qy      301 RMLKKGCVNNTSSAGNTALHYGVNRNRPDCALVLTTHGANDARGEHNTPLHLSMSK 360
Db      301 RMLKKGCVNNTSSAGNTALHYGVNRNRPDCALVLTTHGANDARGEHNTPLHLSMSK 360
Qy      361 DNVEMIKALIVFGAEVDPNDPFGPTPLASKI 393
Db      361 DNVEMIKALIVFGAEVDPNDPFGPTPLASKI 393

RESULT 5
AAH57209 PRELIMINARY; PRT; 807 AA.
AC      AAH57209
DT      02-MAR-2004 (T-EMBLrel. 27, Created)
DT      02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DE      02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE      Plaz26 protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC      STRAIN=NMRI; TISSUE=Mammary tumor;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueda T.B., Yoshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RT      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC      STRAIN=NMRI; TISSUE=Mammary tumor;
RA      Strausberg R.;
RA      Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
RA      EMBL; BC057209.1;
RA      EMBL; BC057209.1;
SQ      SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match      88.4%; Score 1842; DB 2; Length 807;
Best Local Similarity 87.8%; Pred. No. 5, Se-143;
Matches 345; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

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Db      181 VTDNKGETAFHYAVOGDNPOVLQLGKNASAGLNVNNOGLTPLHLACKKQEMVAVLL 240
Qy      241 LCNARCINMGPGGPIHTAMKFSQKCAEMITISMSDNQHSKDPRYGASPLHAKNAEMA 300
Db      241 LCNARCINMGPGGPIHTAMKFSQKCAEMITISMSDNQHSKDPRYGASPLHAKNAEMA 300
Qy      301 RMLKKGCVNNTSSAGNTALHYGVNRNRPDCALVLTTHGANDARGEHNTPLHLSMSK 360
Db      301 RMLKKGCVNNTSSAGNTALHYGVNRNRPDCALVLTTHGANDARGEHNTPLHLSMSK 360
Qy      361 DNVEMIKALIVFGAEVDPNDPFGPTPLASKI 393
Db      361 DNVEMIKALIVFGAEVDPNDPFGPTPLASKI 393

RESULT 6
O7TPX2 PRELIMINARY; PRT; 752 AA.
AC      O7TPX2
DT      01-OCT-2003 (T-EMBLrel. 25, Created)
DT      01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE      01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE      Phospholipase A2, group VI.
GN      Name=Plaz26;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC      STRAIN=C3H/He; TISSUE=Osteoblast;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueda T.B., Yoshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RT      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC      STRAIN=C3H/He; TISSUE=Osteoblast;
RA      Strausberg R.;
RA      Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RA      EMBL; BC052845; AAH52845.1;
RA      GO; GO:0003824; F: catalytic activity; IEA.
RA      GO; GO:0045735; F: nutrient reservoir activity; IEA.
RA      InterPro; IPR002110; ANK.
RA      InterPro; IPR002641; Patactin.
RA      Pfam; PF00023; ANK; 6.
RA      Pfam; PF01734; Patactin; 1.
RA      SMART; SM00248; ANK; 6.
RA      PROSITE; PSS0088; ANK_REPEAT; 4.
RA      PROSITE; PSS0297; ANK_RBP_REGION; 1.
RA      ANK repeat.
SQ      SEQUENCE 752 AA; 83717 MW; DAC3347B0E14A4FC CRC64;

Query Match      87.9%; Score 1832; DB 2; Length 752;
Best Local Similarity 87.5%; Pred. No. 3, Se-142;
Matches 344; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

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QY 1 MOFFGLVNTFSQVNTLFSNPFVKEVAVADYTSDDREBEGQLIFONTNRTWCVLV 60
DB 1 MOFFGLVNTVLTSSVTNLFSNPFVKEVSLTDYVSSSERVREBEGQLILQVNSNRTWCVLV 60
QY 61 NPNRNSGGRFLFQLELEADLVNPHQYSSQLLPFEYSSQVLTETVLQHTLDIRNHP 120
DB 61 SPNRPQSDPRLFLQLESEADLVNPFQYSSQLPFEYSSQVLTETVLQHTLDIRNHP 120
QY 121 SVNHLAVEIGIRCFPHSHRIISCANCAENBEGCTPLHLAKRGDGEILVELVOYCHTOMD 180
DB 121 TVNHLAVEIGIRCFPHSHRIISCANCAENBEGCTPLHLAKRGDGEILVELVOYCHTOMD 180
QY 181 VTDYKGETVFNHVAVOGDNSQVLTQLGRNAVAGINQVNNQGLTPHLACQKQEMRVLL 240
DB 181 VTDNKEBETAFNHVAVOGDNPQVLTQLGRNAVAGINQVNNQGLTPHLACQKQEMRVLL 240
QY 241 LCNARCNINGPNGYPIHSAKMFQKCAEMITISMDSSQHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNINGMGLGFPPIHTAMKFSQKCAEMITISMDSSQHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLKRGCVNNTSSAGNTALHGVNRNRPDCAIVLITGANGADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVDDSTSSAGNTALHVAVMNRNRPDCVMVLTITGANGARGEHNTPLHLAMSK 360
QY 361 DNVEMLKALIVFGAEVDTPNDFGETPTPLASKI 393
DB 361 DNMEVWKALIVFGAEVDTPNDFGETPTPLASKI 393

RESULT 7
PA26 RAT STANDARD; PRT; 751 AA.
AC P97570;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (PLA2) (Cat-
GN Name=PLA2g6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic Islets;
RX MEDLINE=97269008; PubMed=9111008;
RA Ma Z., Ramachandram S., Kempe K., Chi X.S., Ladenson J., Turk J.;
RT "Pancreatic Islets express a Ca2+-independent phospholipase A2 enzyme
RT that contains a repeated structural homologous to the integral
RT membrane protein binding domain of ankyrin.";
RL J. Biol. Chem. 272:11118-11127(1997).
CC -1- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
CC It has been implicated in normal phospholipid remodeling, nitric
CC oxide-induced or vasopressin-induced arachidonic acid release and
CC in leukotriene and prostaglandin production. May participate in
CC fas mediated apoptosis and in regulating transmembrane ion flux in
CC glucose-stimulated B-cells.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver,
CC heart and skeletal muscle.
CC -1- SIMILARITY: Contains 7 ANK repeats.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

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CC -----
DR EMBL: U51898; AAC3136.1; -
DR HSSP: Q60778; 10Y3.
DR RGD: 628867; pla2g6.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ANK_6.
DR PRINTS: PR01415; ANKTRIN.
DR SMART: SM00248; ANK_6.
DR PROSITE: PS50297; ANK_REPEAT_4.
DR PROSITE: PS50297; ANK_REPEAT_REGION_1.
KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 150 180 ANK 1.
FT REPEAT 184 214 ANK 2.
FT REPEAT 218 247 ANK 3.
FT REPEAT 250 280 ANK 4.
FT REPEAT 285 311 ANK 5.
FT REPEAT 315 344 ANK 6.
FT REPEAT 348 377 ANK 7.
FT ACT_SITE 464 464 Potential.
SQ SEQUENCE 751 AA; 83582 MW; 393BBADAVFC99B CRC64;

Query Match 86.8%; Score 1808.5; DB 1; Length 751;
Best Local Similarity 86.8%; Pred. No. 2,9e-140;
Matches 341; Conservative 20; Mismatches 31; Indels 1; Gaps 1;

QY 1 MOFFGLVNTFSQVNTLFSNPFVKEVAVADYTSDDREBEGQLIFONTNRTWCVLV 60
DB 1 MOFFGLVNTVLTSSVTNLFSNPFVKEVSLTDYVSSSERVREBEGQLILQVNSNRTWCVLV 60
QY 61 NPNRNSGGRFLFQLELEADLVNPHQYSSQLLPFEYSSQVLTETVLQHTLDIRNHP 120
DB 61 SPNRPQSDPRLFLQLESEADLVNPFQYSSQLPFEYSSQVLTETVLQHTLDIRNHP 119
QY 121 SVNHLAVEIGIRCFPHSHRIISCANCAENBEGCTPLHLAKRGDGEILVELVOYCHTOMD 180
DB 121 TVNHLAVEIGIRCFPHSHRIISCANCAENBEGCTPLHLAKRGDGEILVELVOYCHTOMD 179
QY 181 VTDYKGETVFNHVAVOGDNSQVLTQLGRNAVAGINQVNNQGLTPHLACQKQEMRVLL 240
DB 181 VTDNKEBETAFNHVAVOGDNPQVLTQLGRNAVAGINQVNNQGLTPHLACQKQEMRVLL 239
QY 241 LCNARCNINGPNGYPIHSAKMFQKCAEMITISMDSSQHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNINGPNGYPIHSAKMFQKCAEMITISMDSSQHSKDPRYGASPLHAKNAEMA 299
QY 301 RMLKRGCVNNTSSAGNTALHGVNRNRPDCAIVLITGANGADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVDDSTSSAGNTALHVAVMNRNRPDCVMVLTITGANGARGEHNTPLHLAMSK 359
QY 361 DNVEMLKALIVFGAEVDTPNDFGETPTPLASKI 393
DB 361 DNMEVWKALIVFGAEVDTPNDFGETPTPLASKI 392

RESULT 8
Q6DDKO PRELIMINARY; PRT; 756 AA.
AC Q6DDKO;
DT 01-OCT-2004 (T-REMBLrel. 28, Created)
DT 01-OCT-2004 (T-REMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (T-REMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson F.;

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RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RT Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shmolen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC077558; AAH77558.1; -.
KW Hypothetical protein.
SQ SEQUENCE 756 AA; 84303 MW; C0278741CA52A2A71 CRC64;

Query Match 56.4%; Score 1176; DB 2; Length 756;
Best Local Similarity 54.3%; Pred. No. 4,3e-88;
Matches 213; Conservative 86; Mismatches 93; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFGSVTLFSPNPRVKEVAVADYTSRVRBEGQLLFQNTPRMTDCLV 60
DB 1 MDLFGRLVNTFVAVTLFSPNPRVKEVAVADYTSRVRBEGQLLFQNTPRMTDCLV 60
QY 61 NPNSQSGRFLFQLEADLVNPHQYSSQLPFYESSPOVLADEVQLTDLIRNHPM 120
DB 61 NPSSPQNAVRLFQLEBEPALCFQEVAVLRFPESSRKLCLFETLQQLTDLIRSHPM 120
QY 121 SVNLAVELGIRCFHSHRIISGANCANEBEGCTPLHACRGDGLIVELVOYCHTMD 180
DB 121 SLNLAVELGIRCFHSHRIISGANCANEBEGCTPLHACRGDGLIVELVOYCHTMD 180
QY 181 VTDYKEVTFHYAVQDNSQVQLQGRNAVAGLNVNNGQLTPHLACQLGKQEMRVLL 240
DB 181 IDQNGEIVYHHAQONPRVIELCSVPISGVNHNKSNMNETPLHVAICRLGKTELVALL 240
QY 241 LCNARCNINPNCYPIHSAKPFQKGCAMIISMDSQIHSKDPKRGASPLHAKRAEVA 300
DB 241 RCHARDIIGDKDYPHTAKYQKCEVEALIDVSAQQLHAEDPRYQATPIHAKRAEVA 300
QY 301 RMLKSGCNVNTSSAGNTALHGVNRNRPDCAIVLLTHGANADARGHNTPLHAKMSK 360
DB 301 RLIIERGCNVNTSKLIDPLHIMVYKDRPEALMVLITVADNVNGEHNTPLHAKMSK 360
QY 361 DNEMIKALIVGAEDVTPNDPSETPTFLASK 392
DB 361 DQLELIKALMVFGADVQHNDFETPGLIAR 392

RESULT 9
Q6NMWYO PRELIMINARY; PRT; 818 AA.
AC Q6NMWYO;

DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Zgc:77476.
GN Name=zgc:77476;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shmolen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC067375; AAH67375.1; -.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; Ank_6.
DR Pfam: PF01734; Patatin; 1.
DR PRINTS: PR01415; ANKTRIN.
DR SMART: SM00248; ANK_6.
DR PROSITE: PS50088; ANK_REPEAT; 4.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8BA9 CRC64;

Query Match 49.8%; Score 1037.5; DB 2; Length 818;
Best Local Similarity 48.7%; Pred. No. 1.2e-76;
Matches 191; Conservative 87; Mismatches 113; Indels 1; Gaps 1;

QY 1 MOFGRLVNTFGSVTLFSPNPRVKEVAVADYTSRVRBEGQLLFQNTPRMTDCLV 60
DB 1 MDLGRILDTVSLSVSSLFSPNPRVKEVAVADYTSRVRBEGQLLFQNTPRMTDCLV 60
QY 61 NPNSQSGRFLFQLEADLVNPHQYSSQLPFYESSPOVLADEVQLTDLIRNHPM 120
DB 61 CPSPSPVALRMQVASEEDAMNMFQYALKLPFYEMLRPLKPEMLQPTVDCVNRHPM 120
QY 121 SVNLAVELGIRCFHSHRIISGANCANEBEGCTPLHACRGDGLIVELVOYCHTMD 180
DB 121 SSNHLIVVDGLRDLCLGNVYILSQM-SRDAQOCTPLHLACERGDVGCARELLEBCQARD 179
QY 181 VTDYKEVTFHYAVQDNSQVQLQGRNAVAGLNVNNGQLTPHLACQLGKQEMRVLL 240
DB 181 VKDKNGETPMHCAKQDSALITVLCALQACAGVNEINAAAGETPMHACLGAVVVKGL 239
QY 241 LCNARCNINPNCYPIHSAKPFQKGCAMIISMDSQIHSKDPKRGASPLHAKRAEVA 300
DB 241 LCNARCNINPNCYPIHSAKPFQKGCAMIISMDSQIHSKDPKRGASPLHAKRAEVA 300


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DB 240 AGGACDINGNNNGPFIHTAMKFSKSCAAEAILSSSPNQLADBPYGGTGPLHMAKTAEMS 299
QY 301 RMLLKGCNVNSTSSAGNTALHGVNRRNRPDCAIVLITHGANDARGHGNTPLHLAMSK 360
DB 300 RLLDRCNVNYSKSGESPLHLITKRGFEAAMTLITHGADANIRGQDGNTHLHAKML 359
QY 361 DNVEMIKALIVGAEDVTPNDFGTEPTFLASK 392
DB 360 DNMDLIKALMVFAGADVEVNDVGETFGLIAR 391

RESULT 10
AAH67375 PRELIMINARY; PRT; 818 AA.
AC AAH67375;
DT 24-MAY-2004 (T-EMBLrel. 27, Created)
DT 24-MAY-2004 (T-EMBLrel. 27, Last sequence update)
DT 24-MAY-2004 (T-EMBLrel. 27, Last annotation update)
DE Zgc:77476.
GN Zgc:77476.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
(1)
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richarde S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Holton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalka U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC067375; AAH67375.1;
SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;

Query Match 49.8%; Score 1037.5; DB 2; Length 818;
Best Local Similarity 48.7%; Pred. No. 1.2e-76;
Matches 191; Conservative 87; Mismatches 113; Indels 1; Gaps 1;
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QY 181 VTDYKGEIVFHYAVQDNSQVILQLGRNAVAGLNOVNNQGLTPHLACQLGQEMVRVLL 240
DB 180 VQDKNETBPHCAAKQDSSALILEVLCAQLCAGVINEINAGETPMHILACLGVEVVKGLL 239
QY 241 LCNARCNINPGVPRPHSAMKFSKSCAAEAILSSSPNQLADBPYGGTGPLHMAKTAEMS 300
DB 240 AGGACDINGNNNGPFIHTAMKFSKSCAAEAILSSSPNQLADBPYGGTGPLHMAKTAEMS 299
QY 301 RMLLKGCNVNSTSSAGNTALHGVNRRNRPDCAIVLITHGANDARGHGNTPLHLAMSK 360
DB 300 RLLDRCNVNYSKSGESPLHLITKRGFEAAMTLITHGADANIRGQDGNTHLHAKML 359

RESULT 11
Q7Q2U1 PRELIMINARY; PRT; 879 AA.
AC Q7Q2U1;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE BdiF359 (Fragment).
GN Name=ebiG3359; ORFNames=ENSANG000000026398;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
(1)
RN SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AAB01008968; EAA13225.1;
DR GO; GO:0003824; F.catalytic activity; IEA.
DR GO; GO:0045735; F.nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000560; H1Ac.phsphee.
DR InterPro; IPR002641; Patactin.
DR Pfam; PF00023; ANK; 6.
DR Pfam; PF01724; Patactin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50086; ANK_REPEAT; 3.
DR PROSITE; PS50287; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW ANK repeat.
FT NON_TER 1 1
FT NON_TER 879 879
SQ SEQUENCE 879 AA; 96484 MW; 3491E003CF637188 CRC64;

Query Match 24.6%; Score 512; DB 2; Length 879;
Best Local Similarity 29.8%; Pred. No. 3e-33;
Matches 113; Conservative 81; Mismatches 175; Indels 10; Gaps 5;
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DB 196 TTKEIINLIIDKSTVNLHNSDGYTPPLHVAACIADKEENVKALLAGANVNL--NAKDI 252
QY 257 HSAMKFSQKCAEMITISMSDSQIHSKDPYRGASPLHMAKNAEMARMLTKRGCVNNTSSA 316
DB 253 RKYYKTSAPTTVSSFLRTNVSFKLYTQDMKYGTPHMCSSRETLLHALINGCDVANNATND 312
QY 317 GNTALHVGWNRNPFDCALVLLTHGANADARGEHNTPLHLANSKDNVEMIKALIVGAEV 376
DB 313 GRTALHVGWNRNPFECVTVLLAHDAEIDVLDKQGNAAHLIAIEKKLVPIVQCLVVGCDI 372
QY 377 DTENDGETP 386
DB 373 NLKNKDGKTP 382
RESULT 13
ID AAF50194 PRELIMINARY; PRT; 877 AA.
AC AAF50194;
DT 01-APR-2004 (TrEMBLrel. 27, Created)
DT 01-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE CG6718-PA.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RX [1]
RP MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abri J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadelis E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA Fodor K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Hartveit K.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Jaitani M., Kalish J., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,
RA Jermal B.E., Koditz C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazotto M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sanders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RA "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537572;
RA Mista S., Crosby M.A., Mungall C.J., Mathews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminck J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminck J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RP SEQUENCE FROM N.A.
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AEO03550; AAF50194.3; -;
DR FlyBase: FBgn0036053; CG6718.
SQ SEQUENCE 877 AA; 96863 MW; C9DC2CD6C282869B CR664;
Query Match 23.7%; Score 494.5; DB 2; Length 877;
Best Local Similarity 29.2%; Pred. No. 8, 2e-32;
Matches 108; Conservative 81; Mismatches 154; Indels 27; Gaps 5;
QY 17 LPSNPRVXEVAVADYTSDDRYREBQGLLPQNTPKRTDVCVLPNRSQSGFRLEQL 76
DB 40 LFAPEP-----NSSENKRAVAYEILQRPSTSD-----SWTTSFSLYRSPV 78
QY 77 EADALVNFQYSSQLPFPFESSPOVLTEVLTDLINHPSSVLAHLVGLIRECPH 136
DB 79 QGEAEERFNAFLORLPVPFISYKEYVNNVNGLOKACDALADNRSWTLSHLIAFNLDVYS 138
QY 137 HSRITSCANCAENBEGCTPLHACRKGDELIVELVOYCHTOMDYTGKTFVHYAVOG 196
DB 139 NPKMLCQVQADAAATLMSFPQALIKQGHMEWYKALLPL--SKLEHIDINSVVFHYAA-S 195
QY 197 DNSQVQLLGRNAVAGLNVNNOGLTPLHLACQOLQKQEWVRVLLCNARCNIMGNGVYI 256
DB 196 TTKEIINLIIDKSTVNLHNSDGYTPPLHVAACIADKEENVKALLAGANVNL--NAKDI 252
QY 257 HSAMKFSQKCAEMITISMSDSQIHSKDPYRGASPLHMAKNAEMARMLTKRGCVNNTSSA 316
DB 253 RKYYKTSAPTTVSSFLRTNVSFKLYTQDMKYGTPHMCSSRETLLHALINGCDVANNATND 312
QY 317 GNTALHVGWNRNPFDCALVLLTHGANADARGEHNTPLHLANSKDNVEMIKALIVGAEV 376
DB 313 GRTALHVGWNRNPFECVTVLLAHDAEIDVLDKQGNAAHLIAIEKKLVPIVQCLVVGCDI 372
QY 377 DTENDGETP 386
DB 373 NLKNKDGKTP 382

DB 373 NLNKGKTP 382

RESULT 14

AC 07KUD4 PRELIMINARY; PRT; 887 AA.

DT 05-JUL-2004 (TEMBLrel. 27, Created)

DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

GN ORFNames=CG6718;

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxId=7227;

[1]

SEQUENCE FROM N.A.

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazer R.G., Champ M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,

RA Adl J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,

RA Burris K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K.J., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,

RA Fioder C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Mei M.H., Ibbegan C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kamei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Sinden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Slater E., Spradling A.C., Stapleton M., Strong R., Sun B.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster";

RT Science 287:2185-2195(2000).

[2]

SEQUENCE FROM N.A.

RA MEDLINE=22426065; PubMed=12537556;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

melanogaster euchromatic genome sequence";

RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[3]

SEQUENCE FROM N.A.

RA MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective";

RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

[4]

SEQUENCE FROM N.A.

RA MEDLINE=22426069; PubMed=12537572;

RA Maira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review";

RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

[5]

SEQUENCE FROM N.A.

RA MEDLINE=22426070; PubMed=12537573;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

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RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

melanogaster euchromatic genome sequence";

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[6]

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[8]

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RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

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[9]

SEQUENCE FROM N.A.

RA MEDLINE=22426070; PubMed=12537573;

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RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

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[10]

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RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[11]

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RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

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RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[12]

SEQUENCE FROM N.A.

RA MEDLINE=22426070; PubMed=12537573;

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RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

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RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

melanogaster euchromatic genome sequence";

RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[13]

SEQUENCE FROM N.A.

RA MEDLINE=22426070; PubMed=12537573;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

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RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

melanogaster euchromatic genome sequence";

RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[14]

SEQUENCE FROM N.A.

RA MEDLINE=22426070; PubMed=12537573;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

melanogaster euchromatic genome sequence";

RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[15]

SEQUENCE FROM N.A.

RA MEDLINE=22426070; PubMed=12537573;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

melanogaster euchromatic genome sequence";

RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[16]

SEQUENCE FROM N.A.

RA MEDLINE=22426070; PubMed=12537573;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:51:45 ; Search time 79.7757 Seconds
(without alignments) 1771.710 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

Sequence: 1 MQPFRRLVNTFSGVTNLPFN.....EVDTRNDGRTPTPLASKIG 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_238ep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------|
| 1 | 2084 | 100.0 | 394 | 2 | AAW17845 Cytochrome |
| 2 | 2084 | 100.0 | 394 | 5 | ABB82229 Calcium i |
| 3 | 2084 | 100.0 | 687 | 2 | AAW17847 Cytochrome |
| 4 | 2084 | 100.0 | 687 | 5 | ABB82231 Human cPL |
| 5 | 2084 | 100.0 | 688 | 2 | AAW17848 Cytochrome |
| 6 | 2084 | 100.0 | 688 | 5 | ABB82232 Human cPL |
| 7 | 2078 | 99.7 | 784 | 7 | ADDP3407 Human lrp |
| 8 | 2078 | 99.7 | 806 | 5 | AAE25968 Human P1A |
| 9 | 2078 | 99.7 | 806 | 8 | AD019776 Human PRO |
| 10 | 1837 | 88.1 | 752 | 2 | AAAR3018 Calcium-1 |
| 11 | 1837 | 88.1 | 752 | 2 | AAW01479 Calcium-1 |
| 12 | 1837 | 88.1 | 752 | 2 | AAW13163 Ca-indepe |
| 13 | 1837 | 88.1 | 752 | 2 | AAW17849 Hamster c |
| 14 | 1837 | 88.1 | 752 | 2 | AAW1825 Chinese h |
| 15 | 1837 | 88.1 | 752 | 5 | ABB82215 Calcium i |
| 16 | 1808.5 | 86.8 | 751 | 7 | ADDE6244 Rat Prote |
| 17 | 1808.5 | 86.8 | 751 | 7 | ADDE6032 Rat Prote |
| 18 | 1808.5 | 86.8 | 751 | 7 | ADDE6032 Rat Prote |
| 19 | 1808.5 | 86.8 | 751 | 7 | ADDE6032 Rat Prote |
| 20 | 1234.5 | 59.2 | 667 | 7 | ADM05093 Human pro |
| 21 | 836 | 40.1 | 401 | 4 | AAAB92811 Human pro |
| 22 | 494.5 | 23.7 | 877 | 4 | ABB62624 Drosophila |
| 23 | 338 | 16.2 | 843 | 7 | ADD27861 Rat ankyr |
| 24 | 332 | 15.9 | 1839 | 7 | ADD27862 Human bra |
| 25 | 332 | 15.9 | 1872 | 4 | AAW79160 Human pro |

| | | | | | |
|----|-------|------|------|---|---------------------|
| 26 | 324 | 15.5 | 1330 | 7 | ADM04552 Human pro |
| 27 | 313.5 | 15.0 | 1549 | 4 | ABB67412 Drosophila |
| 28 | 313.5 | 15.0 | 1549 | 4 | ABB58328 Drosophila |
| 29 | 305.5 | 14.7 | 1745 | 2 | AAW76776 D. immiti |
| 30 | 305.5 | 14.7 | 1745 | 2 | AAW70608 Full leng |
| 31 | 305.5 | 14.7 | 1745 | 3 | AAW11589 D. immiti |
| 32 | 305.5 | 14.7 | 1745 | 5 | AAO21368 Ankyrin P |
| 33 | 302.5 | 14.5 | 2443 | 5 | ABB60521 Drosophila |
| 34 | 301 | 14.4 | 763 | 3 | AAW79154 Mouse pro |
| 35 | 301 | 14.4 | 786 | 3 | AAW69163 Amino aci |
| 36 | 301 | 14.4 | 786 | 6 | ABP58149 Mouse dea |
| 37 | 301 | 14.4 | 786 | 7 | ABW02414 Mouse pro |
| 38 | 301 | 14.4 | 786 | 7 | ABW02422 Human PKK |
| 39 | 301 | 14.4 | 786 | 7 | ABW02423 Human PKK |
| 40 | 301 | 14.4 | 786 | 7 | ABW02424 Human PKK |
| 41 | 301 | 14.4 | 787 | 3 | AAW76079 Murine pr |
| 42 | 301 | 14.4 | 787 | 4 | AAW56018 Skin cell |
| 43 | 301 | 14.4 | 787 | 5 | ABW72218 Murine pr |
| 44 | 300.5 | 14.4 | 347 | 7 | ABW02421 Human PKK |
| 45 | 300.5 | 14.4 | 1724 | 5 | AAO20513 Protein o |

ALIGNMENTS

RESULT 1
AAW17845
AAW17845 standard; protein; 394 AA.
XX
XX
AC AAW17845;
XX
DT 07-AUG-1997 (first entry)
XX
XX
DE Cytosolic phospholipase A2/B (clone 19a product).
XX
XX
KM Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
XX
XX
OS Inflammation; inhibitor; antiinflammatory.
XX
XX
XX Homo sapiens.
XX
XX
XX MO9717448-A2.
XX
XX
PD 15-MAY-1997.
XX
XX
XX 07-NOV-1996; 96WO-US017794.
XX
XX
XX 08-NOV-1995; 95US-0055568.
XX
XX
XX (GENEY) GENETICS INST INC.
XX
XX Jones S, Tang J;
XX
XX WPI; 1997-281037/25.
XX
XX DR N-PSDB; AAT68823.
XX
XX
XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
XX
XX mammalian subject.
XX
XX
XX Claim 12; Page 43-44; 74pp; English.
XX
XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17845) is
XX
XX characterized by activity in the absence of calcium, by activity in a
XX
XX mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-
XX
XX phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
XX
XX lack of stimulation by ATP, and by including in its sequence at least one
XX
XX of the amino acid sequences given in AAW17839- 44). It is encoded by
XX
XX partial cDNA clone 19a (AAT68823), derived from Burkitt's lymphoma Raji
XX
XX (ATCC CRU86) cells. Other PLA2/B enzymes (AAW17846-48) have also been
XX
XX identified. sPLA2/B enzymes are thought to be involved in the release of
XX
XX arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides
XX
XX produced in transformed host cells can be used to screen for sPLA2/B
XX
XX inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic
XX
XX acid cascade

| Seq | Sequence | 394 AA; | 100.0%; | Score 2084; | DB 2; | Length 394; |
|----------|---|---|---------------|---------------------|---------|-------------|
| QY | Query Match | | 100.0%; | Score 2084; | DB 2; | Length 394; |
| Db | Best Local Similarity | | 100.0%; | Pred. No. 2.66-229; | | |
| Db | Matches 394; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; | |
| QY | 1 | MOFFGRLVNTEGGVNTLFSNPRVKEVAVADYTSDDRVREBQQLLFOPTPRMTDVCVYL | 60 | | | |
| Db | 1 | MOFFGRLVNTEGGVNTLFSNPRVKEVAVADYTSDDRVREBQQLLFOPTPRMTDVCVYL | 60 | | | |
| QY | 61 | NPRNSQSGRFLQLELEADALVNFHQYSQQLPFYESSPOVLATEVLTQHTDLINHPSM | 120 | | | |
| Db | 61 | NPRNSQSGRFLQLELEADALVNFHQYSQQLPFYESSPOVLATEVLTQHTDLINHPSM | 120 | | | |
| QY | 121 | SVAHHLAVELGIRECHTHSRITISCANCAENEBCCTPLHLACRGDGEILVELVQYCHTQMD | 180 | | | |
| Db | 121 | SVAHHLAVELGIRECHTHSRITISCANCAENEBCCTPLHLACRGDGEILVELVQYCHTQMD | 180 | | | |
| QY | 181 | VTDYGETVFHYAVQDINSQVQLLGRNVAVALQNVNNGTLPTLHLACQLGKQEWVRVYL | 240 | | | |
| Db | 181 | VTDYGETVFHYAVQDINSQVQLLGRNVAVALQNVNNGTLPTLHLACQLGKQEWVRVYL | 240 | | | |
| QY | 241 | LCNACNCTMGPNQYPIYHSAMKFSQGCAMITISMSQCHSDPPRYGASPLHMAKNAEVA | 300 | | | |
| Db | 241 | LCNACNCTMGPNQYPIYHSAMKFSQGCAMITISMSQCHSDPPRYGASPLHMAKNAEVA | 300 | | | |
| QY | 301 | RMLLRGCGVNSTSAGNLTALHVGVMRNRFPDCAIYLLTHGANADARGEHNTPLHLAMSK | 360 | | | |
| Db | 301 | RMLLRGCGVNSTSAGNLTALHVGVMRNRFPDCAIYLLTHGANADARGEHNTPLHLAMSK | 360 | | | |
| QY | 361 | DNVEMIKALIVFGAEVDTPNDGFTPTFLASKIG | 394 | | | |
| Db | 361 | DNVEMIKALIVFGAEVDTPNDGFTPTFLASKIG | 394 | | | |
| RESULT 2 | | | | | | |
| AB882229 | | | | | | |
| ID | AB882229 | standard; | protein; | 394 AA. | | |
| AC | AB882229; | | | | | |
| DT | 08-JAN-2003 | (first entry) | | | | |
| DE | Calcium independent phospholipase A2/B (cPLA2/B) (clone 19a). | | | | | |
| KW | Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme; antiinflammatory; antiarthritic; antiprosclerotic; antineumatic; cytosolic; antiaesthetic; human. | | | | | |
| OS | Homo sapiens. | | | | | |
| PN | US2002106364-A1. | | | | | |
| PD | 08-AUG-2002. | | | | | |
| PF | 09-AUG-2001; | 2001US-00927180. | | | | |
| PR | 27-JUL-1994; | 94US-00281193. | | | | |
| PR | 14-APR-1995; | 95US-00422106. | | | | |
| PR | 26-JUN-1995; | 95WO-US008069. | | | | |
| PR | 08-NOV-1995; | 95US-00555568. | | | | |
| PR | 09-SEP-1998; | 98US-00149988. | | | | |
| PR | 06-MAR-2000; | 2000US-00519223. | | | | |
| PA | (GENY) | GENETICS INST INC. | | | | |
| PI | Jones S, | Tang J; | | | | |
| DR | WPI, 2002-739923/80. | | | | | |
| DR | N-PSDB; ABV73008. | | | | | |

| Query Match | 100.0% | Score 2084 | DB 5 | Length 394 |
|-----------------------|---|--------------------|----------|------------|
| Beat Local Similarity | 100.0% | Pred. No. 2.6e-219 | | |
| Matches 394 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| PS | Claim 6; Page 18-19; 41pp; English. | | | |
| XX | The invention relates to a purified mammalian calcium independent | | | |
| XX | cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is | | | |
| CC | characterized by activity in the absence of calcium and has a molecular | | | |
| CC | weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified | | | |
| CC | calcium independent phospholipase enzyme is useful for identifying an | | | |
| CC | inhibitor of phospholipase activity which involves combining (1), | | | |
| CC | phospholipid and candidate inhibitor compound, and observing whether the | | | |
| CC | enzyme cleaves the phospholipid and releases fatty acid from it. A | | | |
| CC | pharmaceutical composition (PC) comprising a therapeutically effective | | | |
| CC | amount of the inhibitor is useful for reducing inflammation and for | | | |
| CC | treating inflammatory conditions including rheumatoid arthritis, | | | |
| CC | psoriasis, asthma, inflammatory bowel disease and other diseases mediated | | | |
| CC | by increased levels of prostaglandins, leukotriene or platelet activating | | | |
| CC | factor. A composition comprising an antibody which binds to (I) is useful | | | |
| CC | as research and diagnostic tool, and is also useful in the study of | | | |
| CC | phospholipase A2 activity and inflammatory conditions. The present | | | |
| CC | sequence represents a human cPLA2/B enzyme (clone 19a) | | | |
| XX | Sequence 394 AA: | | | |
| SO | | | | |
| QY | 1 MQFGRGLVNTSSGTTNLFNSNFRKVEAVADVYTSSDRVREGQILLPONTNRRMTDCLV 60 | | | |
| DB | 1 MQFGRGLVNTSSGTTNLFNSNFRKVEAVADVYTSSDRVREGQILLPONTNRRMTDCLV 60 | | | |
| QY | 61 NPNRSQSGFRFLFOLELEADALVNFHOYSSQLPEYESSPQVLAHTVEVLQHTLDLIRNPSW 120 | | | |
| DB | 61 NPNRSQSGFRFLFOLELEADALVNFHOYSSQLPEYESSPQVLAHTVEVLQHTLDLIRNPSW 120 | | | |
| QY | 121 SVAHLAVELGIRECFPHSHRIISCANCAENBEGCTPLHLACKGGEIVLVELVOYCHTOMD 180 | | | |
| DB | 121 SVAHLAVELGIRECFPHSHRIISCANCAENBEGCTPLHLACKGGEIVLVELVOYCHTOMD 180 | | | |
| QY | 181 VTDDKGEIVFHYAVQGDNSQVLDLGRNVAAGLVNQNQGLTPHLACQGLKQKQEMRVLL 240 | | | |
| DB | 181 VTDDKGEIVFHYAVQGDNSQVLDLGRNVAAGLVNQNQGLTPHLACQGLKQKQEMRVLL 240 | | | |
| QY | 241 LCNARCNIMGNGPYPIHSAMKFSQKGCAMIIISDSSQISHKDRPYGASPLHMAKNEMA 300 | | | |
| DB | 241 LCNARCNIMGNGPYPIHSAMKFSQKGCAMIIISDSSQISHKDRPYGASPLHMAKNEMA 300 | | | |
| QY | 301 RMLAKRGNNVSTSSAGNTALHNGVMNRFPICALVLLTHGANADARGHGTPLHLMASK 360 | | | |
| DB | 301 RMLAKRGNNVSTSSAGNTALHNGVMNRFPICALVLLTHGANADARGHGTPLHLMASK 360 | | | |
| QY | 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394 | | | |
| DB | 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394 | | | |
| RESULT 3 | | | | |
| AAWI17847 | | | | |
| ID | AAWI17847 standard; protein; 687 AA. | | | |
| AC | AAWI17847; | | | |
| XX | | | | |
| DT | 07-AUG-1997 (first entry) | | | |
| XX | | | | |
| DE | Cycosolic phospholipase A2/B (alternatively spliced clone 19a). | | | |
| XX | | | | |
| KM | Cycosolic phospholipase A2/B; sPLA2/B; arachidonic acid caseade; | | | |
| XX | inflammation; inhibitor; antiinflammatory. | | | |
| OS | Homo sapiens | | | |

XX
 PN MO9717446-A2.
 XX
 PD 15-MAY-1997.
 XX
 PF 07-NOV-1996; 96WO-US017794.
 XX
 PR 08-NOV-1995; 95US-00555568.
 XX
 PA (GENM) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 DR WPI, 1997-281037/25.
 DR N-PSDB; AAT68825.
 XX
 PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PT mammalian subject.
 PS
 PS Claim 12; Page 49-51; 74pp; English.
 XX
 XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
 CC characterized by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
 CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAW17839-44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17845)
 CC and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes are
 CC (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
 CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade
 CC
 SQ Sequence 687 AA;

Query Match 100.0%; Score 2084; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 6,5e-219; Indels 0; Gaps 0;
 Matches 394; Conservative 0; Mismatches 0;

QY 1 MOFGRLVNTFSGVTLFNSNPRVKEVAADYTSDDRVREEGQLIFONTPNRTMPCVLY 60
 DB 1 MOFGRLVNTFSGVTLFNSNPRVKEVAADYTSDDRVREEGQLIFONTPNRTMPCVLY 60
 QY 61 NPNRSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPQVLTTEVLQHLTDLIRNHPSW 120
 DB 61 NPNRSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPQVLTTEVLQHLTDLIRNHPSW 120
 QY 121 SVANLAVELGIRECFHHSRIISCANCAENEGCTPLILACRKDGDELIVELVOYCHTQMD 180
 DB 121 SVANLAVELGIRECFHHSRIISCANCAENEGCTPLILACRKDGDELIVELVOYCHTQMD 180
 QY 181 VVDYKETVPHVAVOGDNSQVLLQGNNAVAGLNQVNNQGLTPLHLACQIGKEMRVLL 240
 DB 181 VVDYKETVPHVAVOGDNSQVLLQGNNAVAGLNQVNNQGLTPLHLACQIGKEMRVLL 240
 QY 241 LCNARCNINGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNINGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLLKRGCVNVTSSAGNTALAVGMNRNFDCAIVLLITGKANADARGEHNTPLHLSMSK 360
 DB 301 RMLLKRGCVNVTSSAGNTALAVGMNRNFDCAIVLLITGKANADARGEHNTPLHLSMSK 360
 QY 361 DNVEMLKALIVFGAEVDTPNDFGEPTEFLASKIG 394
 DB 361 DNVEMLKALIVFGAEVDTPNDFGEPTEFLASKIG 394

RESULT 4
 ABB82231
 ID ABB82231 standard; protein; 687 AA.

XX
 AC ABB82231;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Human cPLA2/B splice variant (clone 19a).
 XX
 KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antirheumatic; antipsoriatic; antineumatic; cytosolic;
 KW antiasthmatic; human.
 XX
 OS Homo sapiens.
 XX
 PN US2002106364-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 09-AUG-2001; 2001US-00927180.
 XX
 PR 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422420.
 PR 26-JUN-1995; 95WO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SRP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GENM) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 DR WPI, 2002-739923/80.
 DR N-PSDB; ABV73010.
 XX
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX
 PS Claim 6; Page 23-25; 41pp; English.

Query Match 100.0%; Score 2084; DB 5; Length 687;
 Best Local Similarity 100.0%; Pred. No. 6,5e-219; Indels 0; Gaps 0;
 Matches 394; Conservative 0; Mismatches 0;

QY 1 MOFGRLVNTFSGVTLFNSNPRVKEVAADYTSDDRVREEGQLIFONTPNRTMPCVLY 60
 DB 1 MOFGRLVNTFSGVTLFNSNPRVKEVAADYTSDDRVREEGQLIFONTPNRTMPCVLY 60
 QY 61 NPNRSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPQVLTTEVLQHLTDLIRNHPSW 120
 DB 61 NPNRSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPQVLTTEVLQHLTDLIRNHPSW 120

```

QY 121 SVANHLAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
DB 121 SVANHLAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
QY 181 VTDYKEETVPHYAVQGDNSQVQLLGRNNAVAGLNQVNNQGLTPLHLACQKGKQEMVRVLL 240
DB 181 VTDYKEETVPHYAVQGDNSQVQLLGRNNAVAGLNQVNNQGLTPLHLACQKGKQEMVRVLL 240
QY 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNPDEGETPTPLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNPDEGETPTPLASKIG 394

RESULT 5
AAW17848
ID AAW17848 standard; protein; 688 AA.
AC AAW17848;
XX
XX 07-AUG-1997 (first entry)
DT
DT Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
DE Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
XX
XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KW inflammation; inhibitor; antiinflammatory.
XX
XX Homo sapiens.
OS
XX
XX WO9717448-A2.
PN
XX
XX 15-MAY-1997.
PD
XX
XX 07-NOV-1996; 96WO-US017794.
PF
XX
XX 08-NOV-1995; 95US-00555568.
PR
XX
XX (GEMV ) GENETICS INST INC.
PA
XX
XX Jones S, Tang J;
PI
XX
XX WPI; 1997-281037/25.
DR
XX
XX N-PSDB; AAT68826.
DR
XX
XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
PT mammalian subject.
PT
XX
XX Claim 12; Page 54-56; 74pp; English.
XX
XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is
CC characterized by activity in the absence of calcium, by activity in a
CC mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-
CC phosphatidylcholine by ATP, and by including in its sequence at least one
CC of the amino acid sequences given in AAW17839- 44). It is an
CC alternatively spliced variant of another isolated polypeptide (AAW17846)
CC and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes
CC (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are
CC thought to be involved in the release of arachidonic acid in specific
CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
CC drugs which inhibit the arachidonic acid cascade
XX
XX Sequence 688 AA;
SQ
Query Match 100.0%; Score 2084; DB 2; Length 688;

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Best Local Similarity 100.0%; Pred. No. 6,5e-219;
Matches 394; Conservative 0; Mismatch 0; Indels 0; Gaps 0;
QY 1 MOPFGRVNTFGSVTLFSPNPRVKEVAADVTSSDRVBEQGLIFONTPTPTMPCVLV 60
DB 1 MOPFGRVNTFGSVTLFSPNPRVKEVAADVTSSDRVBEQGLIFONTPTPTMPCVLV 60
QY 61 NPNRSQSGFRFLQLEADALVNFQYSQQLPFYESSPOVLHTEVLOHITDLIRNHPGM 120
DB 61 NPNRSQSGFRFLQLEADALVNFQYSQQLPFYESSPOVLHTEVLOHITDLIRNHPGM 120
QY 121 SVANHLAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
DB 121 SVANHLAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
QY 181 VTDYKEETVPHYAVQGDNSQVQLLGRNNAVAGLNQVNNQGLTPLHLACQKGKQEMVRVLL 240
DB 181 VTDYKEETVPHYAVQGDNSQVQLLGRNNAVAGLNQVNNQGLTPLHLACQKGKQEMVRVLL 240
QY 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNPDEGETPTPLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNPDEGETPTPLASKIG 394

RESULT 6
ABB82232
ID ABB82232 standard; protein; 688 AA.
AC ABB82232;
XX
XX 08-JAN-2003 (first entry)
DT
DT Human cPLA2/B splice variant (clone 19b).
DE
XX
XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
XX antiaesthetic; human.
XX
XX Homo sapiens.
OS
XX
XX US2002106364-A1.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 09-AUG-2001; 2001US-00927180.
PF
XX
XX 27-UTL-1994; 94US-00281193.
PR
XX
XX 14-APR-1995; 95US-00422106.
PR
XX
XX 26-JUN-1995; 95US-00422420.
PR
XX
XX 08-NOV-1995; 95WO-US008069.
PR
XX
XX 09-SEP-1998; 98US-00149988.
PR
XX
XX 06-MAR-2000; 2000US-00519223.
PA
XX
XX (GEMV ) GENETICS INST INC.
XX
XX Jones S, Tang J;
PI
XX
XX WPI; 2002-739923/80.
DR
XX
XX N-PSDB; ABV73011.
DR
XX
XX Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
XX
XX

```


PS Claim 6; Page 28-30; 41pp; English.

XX The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (II),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
CC 19b)

XX Sequence 688 AA;

Query Match 100.0%; Score 2084; DB 5; Length 688;
Best Local Similarity 100.0%; Pred. No. 6.5e-219;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFGVNTLFSNPFPRKVAVAADYSSDRVREBGLILFQNTPRNTMDCVLY 60
DB 1 MOFGRLVNTFGVNTLFSNPFPRKVAVAADYSSDRVREBGLILFQNTPRNTMDCVLY 60
QY 61 NPNSSGGRFLFQLELEADALVNFHOYSQQLPFYESSQVLAHTVLQHLTLIRNHPBW 120
DB 61 NPNSSGGRFLFQLELEADALVNFHOYSQQLPFYESSQVLAHTVLQHLTLIRNHPBW 120
QY 121 SVANHLAVEGIRCECFHSHRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQMD 180
DB 121 SVANHLAVEGIRCECFHSHRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQMD 180
QY 181 VTDYKGETVFNHVAVGQDNSQVTLQLGRNAVAGINQVNNQGLTPPLHLACQLGKQEMRVLL 240
DB 181 VTDYKGETVFNHVAVGQDNSQVTLQLGRNAVAGINQVNNQGLTPPLHLACQLGKQEMRVLL 240
QY 241 LCNARININGPNQYPIHSAKFSQKCAEMTISMDSSQIHSKDPKRGASPLHAKNAEMA 300
DB 241 LCNARININGPNQYPIHSAKFSQKCAEMTISMDSSQIHSKDPKRGASPLHAKNAEMA 300
QY 301 RMLLKRCGVNSTSSAGNTALHGVWNRNRPDCAIVLLTHGANADARGHGTPLHLAMSK 360
DB 301 RMLLKRCGVNSTSSAGNTALHGVWNRNRPDCAIVLLTHGANADARGHGTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTPEDEETPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTPEDEETPTFLASKIG 394

RESULT 7

ID ADD93407 standard; protein; 784 AA.

AC ADD93407;

XX 29-JUN-2004 (first entry)

XX Human lipid-associated molecule LIPAM-14 polypeptide.

KM Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;
KM antihypoid; antidiabetic; cytostatic; dermatological; immunosuppressive;
KM antiinflammatory; chrysothymic; antiallergic; cerebroprotective;
KM gastroinestinal; hepatotropic; nephrotoxic; anticonvulsant;
KM antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
KM virucide; uterogonic; antirheumatic; cardiant; cardiovascular; anti-HIV;
KM nootropic.

XX Homo sapiens.

XX WO2003083081-A2.

XX 09-OCT-2003.

XX 27-MAR-2003; 2003WO-US009755.

XX 29-MAR-2002; 2002US-0368722P.

XX 03-MAY-2002; 2002US-037576P.

XX 05-JUL-2002; 2002US-0393934P.

XX 27-SEP-2002; 2002US-0414269P.

XX (INCYTE) INCYTE CORP.

XX Emerling BM, Margulis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;

XX Baughn MR, Lee EA, Griffin JA, Kabie AE, Elliott VS, Chang H;

XX Lee S, Ramkumar J, Bulloch SA, Hafalia AWA, Khare R, Jiang X;

XX Jackson AA;

XX WPI, 2003-788347/74.

XX N-PSDB; ADD93426.

XX Claim 69; Page 206-207; 238pp; English.

XX The present sequence is the protein sequence of human lipid-associated

XX molecule LIPAM-14 (Incyte polypeptide 751266CD), a protein that shows

XX homology to human Ca2+-independent phospholipase A2 short isoform. This

XX is one of 19 LIPAM polypeptides of the invention. The invention relates

XX to these novel LIPAMs and the nucleic acids encoding them, and to the use

XX of nucleic acids and proteins in the diagnosis, treatment and prevention

XX of disorders associated with abnormal expression or activity of LIPAM

XX such as neurodegenerative disorders (e.g. Parkinson's disease,

XX Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,

XX catatonias), endocrine disorders (e.g. diabetes, Grave's disease), cancers

XX (e.g. leukemia, cervical or breast cancers), immunological disorders

XX (e.g. scleroderma, systemic lupus erythematosus, allergies),

XX gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.

XX Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,

XX parasitic, protozoal, helminthic), cardiovascular disorders (e.g.

XX atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention

XX also relates to the assessment of the effects of exogenous compounds on

XX the expression of nucleic acids and LIPAMs. The invention provides

XX expression vectors, host cells, antibodies, agonists and antagonists,

XX transgenic organisms, and arrays and microarrays of the polynucleotides.

XX Sequence 784 AA;

Query Match 99.7%; Score 2078; DB 7; Length 784;
Best Local Similarity 99.7%; Pred. No. 3.6e-218;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFGVNTLFSNPFPRKVAVAADYSSDRVREBGLILFQNTPRNTMDCVLY 60
DB 33 MOFGRLVNTFGVNTLFSNPFPRKVAVAADYSSDRVREBGLILFQNTPRNTMDCVLY 92
QY 61 NPNSSGGRFLFQLELEADALVNFHOYSQQLPFYESSQVLAHTVLQHLTLIRNHPBW 120
DB 93 NPNSSGGRFLFQLELEADALVNFHOYSQQLPFYESSQVLAHTVLQHLTLIRNHPBW 152
QY 121 SVANHLAVEGIRCECFHSHRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQMD 180
DB 153 SVANHLAVEGIRCECFHSHRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQMD 212
QY 181 VTDYKGETVFNHVAVGQDNSQVTLQLGRNAVAGINQVNNQGLTPPLHLACQLGKQEMRVLL 240
DB 213 VTDYKGETVFNHVAVGQDNSQVTLQLGRNAVAGINQVNNQGLTPPLHLACQLGKQEMRVLL 272

QY 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRIYASPLHWAKNAEA 300
 DB 273 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRIYASPLHWAKNAEA 332
 QY 301 RMLKRGCVNSTSSAGNTALHVGVRNRPDCAIVLTTGANAADARGEHNTPLHLAMSK 360
 DB 333 RMLKRGCVNSTSSAGNTALHVGVRNRPDCAIVLTTGANAADARGEHNTPLHLAMSK 392
 QY 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
 DB 393 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 426

RESULT 8
 AAE25968
 ID AAE25968 standard; protein; 806 AA.
 XX AAE25968;
 AC AAE25968;
 DT 15-NOV-2002 (first entry)
 XX
 DE Human PLA2 group VI (Ca2+-independent) protein.
 XX
 KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
 KW antisense therapy; PLA2 protein.
 XX
 OS Homo sapiens.
 XX
 PN US6410325-B1.
 PD 25-JUN-2002.
 XX
 PF 09-MAY-2001; 2001US-00851896.
 XX
 PR 09-MAY-2001; 2001US-00851896.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Freiler SM, Watt AT;
 XX
 DR WPI; 2002-616513/66.
 DR N-PSDB; AAD42941.
 XX
 PT Novel antisense compounds useful for inhibiting gene expression of human
 PT phospholipase A2, group VI and for treating diseases associated with
 PT expression of phospholipase A2, group VI.
 XX
 PS Disclosure; Col 109-116; 72pp; English.
 XX
 CC The present invention relates to novel antisense compounds which inhibit
 CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 CC (Ca2+-independent) in human cells or tissues and for treating an animal,
 CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnostics, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) protein
 CC
 XX
 SQ Sequence 806 AA;

Query Match 99.7%; Score 2078; DB 5; Length 806;
 Best Local Similarity 99.7%; Pred. No. 3.8e-218;
 Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQFGRLVNTFGSVTLFNSNPRFVKEVAVADYSSDRVREBQGLIFONTPNRTMDCVLY 60
 DB 1 MQFGRLVNTFGSVTLFNSNPRFVKEVAVADYSSDRVREBQGLIFONTPNRTMDCVLY 60
 QY 61 NRRNSGSGRLQLLEADALVNFHOYSQQLPFYSSQVLTTEVLQHLTDLIRNHPW 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 61 NRRNSGSGRLQLLEADALVNFHOYSQQLPFYSSQVLTTEVLQHLTDLIRNHPW 120
 QY 121 SVAAHLAVELGIRECFPHSRRIISCANCAENEBGCTPLHLACRGDEILVELVOYCHTQMD 180
 DB 121 SVAAHLAVELGIRECFPHSRRIISCANCAENEBGCTPLHLACRGDEILVELVOYCHTQMD 180
 QY 181 VTDYKGETVFHYAVOGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGQENVRVLL 240
 DB 181 VTDYKGETVFHYAVOGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGQENVRVLL 240
 QY 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRIYASPLHWAKNAEA 300
 DB 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRIYASPLHWAKNAEA 300
 QY 301 RMLKRGCVNSTSSAGNTALHVGVRNRPDCAIVLTTGANAADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNSTSSAGNTALHVGVRNRPDCAIVLTTGANAADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
 DB 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

RESULT 9
 ADO19776
 ID ADO19776 standard; protein; 806 AA.
 XX ADO19776;
 AC ADO19776;
 DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polypeptide #350.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004043361-A2.
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WJ, Wu TD;
 XX
 DR WPI; 2004-420067/39.
 DR N-PSDB; ADO19775.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7, SEQ ID NO 700; 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune

CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.

XX Sequence 806 AA;

Query Match 99.7%; Score 2078; DB 8; Length 806;
 Best Local Similarity 99.7%; Pred. No. 3,8e-218;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPFGLVNTFSGVTNLFSPNPRVKEVAVADYTSDDVREBQGLIFONTPNRTWCVLV 60
 DB 1 MOPFGLVNTFSGVTNLFSPNPRVKEVAVADYTSDDVREBQGLIFONTPNRTWCVLV 60
 QY 61 NPNNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLHTEVLOHITDLIRNHP 120
 DB 61 NPNNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLHTEVLOHITDLIRNHP 120
 QY 121 SVNHLAVEIGIRCFHHSRIISCANCAENEBGCTPLHLACRKDGSELVLEVOYCHTQMD 180
 DB 121 SVNHLAVEIGIRCFHHSRIISCANCAENEBGCTPLHLACRKDGSELVLEVOYCHTQMD 180
 QY 181 VTDYKGETVPHYAVQDQNSQVQLLGRNAVAGLNQVNOGLTPHLACOLGKQEMRVLL 240
 DB 181 VTDYKGETVPHYAVQDQNSQVQLLGRNAVAGLNQVNOGLTPHLACOLGKQEMRVLL 240
 QY 241 LCNARCNIMGPNKYPIHSAKPFQKCAEMIISMDSQIHSKDPRIYASPLHAKNAEMA 300
 DB 241 LCNARCNIMGPNKYPIHSAKPFQKCAEMIISMDSQIHSKDPRIYASPLHAKNAEMA 300
 QY 301 RMLKRGCVNVTSSAGNTALHVGVMNRPFDCAILITGAGNADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNVTSSAGNTALHVGVMNRPFDCAILITGAGNADARGEHNTPLHLAMSK 360
 QY 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
 DB 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

RESULT 10
 AAR83018
 ID AAR83018 standard; protein; 752 AA.

XX AAR83018;
 DT 15-JUN-1996 (first entry)

XX Calcium-independent cytosolic phospholipase-A2/B enzyme.

XX CHO; calcium-independent cytosolic phospholipase-A2/B; enzyme;
 KM phospholipase-A2; phospholipase-B; drug screening; antiinflammatory;
 KW antibody.

XX Cricetus griseus.

XX US5466595-A.

XX 14-NOV-1995.

XX 27-JUL-1994; 94US-00281193.

XX 27-JUL-1994; 94US-00281193.

XX (GEMV) GENETICS INST INC.

XX Tang J, Jones S;

XX WPI; 1996-009526/01.

XX DR N-PSDB; AAT05842.

PT Isolated polynucleotide encoding cytosolic phospholipase A2/8 - for
 PT producing enzyme for use in screening anti-inflammatory agents and prodn.
 PT of antibodies.

XX Claim 5; Col 15-22; 24pp; English.

CC The enzyme may be produced recombinantly in host cells such as animal
 CC cells, insect cells, eukaryotes, prokaryotes, etc. The protein may also
 CC be expressed in transgenic animals (e.g. milk of transgenic cow). The
 CC protein is used to screen for agents which inhibit phospholipase activity
 CC for use as antiinflammatory agents. These agents can be used to treat
 CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
 CC and other disease mediated by increased levels of prostaglandins,
 CC leukotriene or platelet activating factor. The enzyme can also be used
 CC for the production of antibodies for use as research or diagnostic tools

XX Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752;
 Best Local Similarity 87.3%; Pred. No. 1e-191;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOPFGLVNTFSGVTNLFSPNPRVKEVAVADYTSDDVREBQGLIFONTPNRTWCVLV 60
 DB 1 MOPFGLVNTFSGVTNLFSPNPRVKEVAVADYTSDDVREBQGLIFONTPNRTWCVLV 60
 QY 61 NPNNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLHTEVLOHITDLIRNHP 120
 DB 61 NPNNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLHTEVLOHITDLIRNHP 120
 QY 121 SVNHLAVEIGIRCFHHSRIISCANCAENEBGCTPLHLACRKDGSELVLEVOYCHTQMD 180
 DB 121 SVNHLAVEIGIRCFHHSRIISCANCAENEBGCTPLHLACRKDGSELVLEVOYCHTQMD 180
 QY 181 VTDYKGETVPHYAVQDQNSQVQLLGRNAVAGLNQVNOGLTPHLACOLGKQEMRVLL 240
 DB 181 VTDYKGETVPHYAVQDQNSQVQLLGRNAVAGLNQVNOGLTPHLACOLGKQEMRVLL 240
 QY 241 LCNARCNIMGPNKYPIHSAKPFQKCAEMIISMDSQIHSKDPRIYASPLHAKNAEMA 300
 DB 241 LCNARCNIMGPNKYPIHSAKPFQKCAEMIISMDSQIHSKDPRIYASPLHAKNAEMA 300
 QY 301 RMLKRGCVNVTSSAGNTALHVGVMNRPFDCAILITGAGNADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNVTSSAGNTALHVGVMNRPFDCAILITGAGNADARGEHNTPLHLAMSK 360
 QY 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKI 393
 DB 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKI 393

RESULT 11
 AAW01479
 ID AAW01479 standard; protein; 752 AA.

XX AAW01479;

XX 25-MAR-2003 (revised)

XX 12-FEB-1997 (first entry)

XX Calcium-independent cytosolic phospholipase A2/B.

XX cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
 KW arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;
 XX anti-inflammatory; screen; rheumatoid arthritis.

XX Synthetic.

XX US5554511-A.

XX 10-SEP-1996.

XX 14-APR-1995; 95US-00422420.

Db 301 RMLKRGCDVDSAGNTALHVAWRNFDCEMVLITGANAAGTGEHGNTPHLAIISK 360

Qy 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKI 393
Db 361 DNMEMIKALIVFGAEVDTPNDFGETPTAFMAISKI 393

RESULT 13

AAW17849 standard; protein; 752 AA.

AAW17849;

27-AUG-2003 (revised)
07-AUG-1997 (first entry)

Hamster cytosolic phospholipase A2/B.

Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory; CHO.

Cricetus.

Key Location/Qualifiers
Active-site 465 /note="mutagenesis of Ser-465 results in loss of activity"

WO9717448-A2.

15-MAY-1997.

07-NOV-1996; 96WO-US017794.

08-NOV-1995; 95US-00555568.

(GENY) GENETICS INST INC.

Jones S, Tang J;

WPI; 1997-281037/25.

N-PSDB; AAT68827.

Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.

Example 4; Page 33-36; 74pp; English.

A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is thought to be involved in the arachidonic acid cascade. Its amino acid sequence was deduced from a cDNA clone (AAT68827) obtd. from a CHO-DUX cDNA library. The recombinant enzyme has been expressed in CHO and COS host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also been isolated. These can be used to screen for inhibitors useful as antiinflammatory agents that block the arachidonic acid cascade in mammals. (Updated on 27-AUG-2003 to correct OS field.)

Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752;
Best Local Similarity 87.3%; Pred. No. 1e-191;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

1 MOFFGLVNTFSGVTNLFSNPFVKVAVADYTSDDRVEEGQLIFONTNRTMDCVAV 60

1 MOFFGLVNTLSSVTNLFSNPFVKVAVADYTSDDRVEEGQLIFONASNRMTDCLIV 60

61 NPNNSGSGRLPQLEADALVNFHQSGLLPFYESSPOVLAHTEVLAQHITDLIRNHP 120

61 SPNPNPSGRLPQLEADALVNFHQSGLLPFYESSPOVLAHTEVLAQHITDLIRNHP 120

121 SVNHLAVELGIRCFHHSRIISCANCAENBEGCTPLHLACRKGDSILVELVQYCHTQMD 180

Db 121 TVTHLAVELGIRCFHHSRIISCANSTENBEGCTPLHLACRKGDSILVELVQYCHTQMD 180

Qy 181 VTDYKGEIVFHYAVOGDNSQVQLIGRNAVAGLNQVNNQGLTPHLACQLGQEMRVLL 240

181 VTDNKGETAHYAVOGDNSQVQLIGKNASAGLNQVNNQGLTPHLACQMGQEMRVLL 240

241 LCNARCNIMPGNPGPIHSAKFSQKGCAMETISMSOSIHSKDPYGAELHMAKXAEMA 300

241 LCNARCNVMPGPGPIHSMKFSQKGCAMETISMSOSIHSKDPYGAELHMAKXAEMA 300

301 RMLKRGCDVDSAGNTALHVAWRNFDCAIYLLTGANADAGEHGNTPHLAIISK 360

301 RMLKRGCDVDSAGNTALHVAWRNFDCEMVLITGANAAGTGEHGNTPHLAIISK 360

361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKI 393

361 DNMEMIKALIVFGAEVDTPNDFGETPTAFMAISKI 393

RESULT 14

AAW81825 standard; protein; 752 AA.

AAW81825;

02-FEB-1999 (first entry)

Chinese hamster calcium independent cPLA2/B protein.

Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening; anti-inflammatory; arachidonic acid cascade; chinese hamster.

Cricetulus griseus.

US5840511-A.

24-NOV-1998.

23-OCT-1996; 96US-00735716.

27-JUL-1994; 94US-00281193.

14-APR-1995; 95US-00422106.

(GENY) GENETICS INST INC.

Tang J, Jones S;

WPI; 1999-034032/03.

N-PSDB; AAV64840.

Screening assay for phospholipase inhibitors - using specified phospholipase polypeptide.

Claim 1b; Col 21-24; 24pp; English.

This sequence represents a novel calcium independent cytosolic phospholipase A2/B enzyme isolated from chinese hamster ovary cells. This protein can be used for screening unknown compounds for anti-inflammatory activity mediated by the arachidonic acid cascade

Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752;
Best Local Similarity 87.3%; Pred. No. 1e-191;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

1 MOFFGLVNTFSGVTNLFSNPFVKVAVADYTSDDRVEEGQLIFONTNRTMDCVAV 60

1 MOFFGLVNTLSSVTNLFSNPFVKVAVADYTSDDRVEEGQLIFONASNRMTDCLIV 60

61 NPNNSGSGRLPQLEADALVNFHQSGLLPFYESSPOVLAHTEVLAQHITDLIRNHP 120

61 SPNPNPSGRLPQLEADALVNFHQSGLLPFYESSPOVLAHTEVLAQHITDLIRNHP 120

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Db      61 SPKPHSGFRLFQLESEADALVNFQPSQLPPFYESSVQVLAHVEVLQHLSDLIRHPSM 120
Qy      121 SYAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Db      121 TVTHLAVELGIRECFHSHRIISCANSTENEBEGCTPLHLACRKGDSILVELVOYCHTOMD 180
Qy      181 VTDYKGETVFAHVAQDQNSQVQLQLGRNAVAGLNQVNNQGLTPHLACQGLKQEMVRVLL 240
Db      181 VTDNKGETAFHYAVQDQNSQVQLQLGRNAVAGLNQVNNQGLTPHLACQGLKQEMVRVLL 240
Qy      241 LCNARCNINPGNYPHSAAMKPSQKCAEMIISMDSQHSKDPRYGASPLHMAKNAEMA 300
Db      241 LCNARCNINPGNYPHSAAMKPSQKCAEMIISMDSQHSKDPRYGASPLHMAKNAEMA 300
Qy      301 RMLLRKGCNVNSTSSAGNTALHVGVRNRFDCALVLTGANAADARGEHNTPLHLAMSK 360
Db      301 RMLLRKGCNVNSTSSAGNTALHVGVRNRFDCALVLTGANAADARGEHNTPLHLAMSK 360
Qy      361 DNVEMIKALIVFGAEVDTPNDFGETPFLASKI 393
Db      361 DNVEMIKALIVFGAEVDTPNDFGETPFLASKI 393

```

RESULT 15

AB82215 ABB82215 standard; protein; 752 AA.

AC ABB82215;

DT 08-JAN-2003 (first entry)

DE Calcium independent phospholipase A2/B (cPLA2/B) (clone 9).

KM Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;

KM antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytotoxic;

KM antiaesthetic.

OS Unidentified.

PN US2002106364-A1.

PF 08-AUG-2002.

PR 09-AUG-2001; 2001US-00927180.

PR 27-JUL-1994; 94US-00281193.

PR 14-APR-1995; 95US-00422106.

PR 26-JUN-1995; 95US-00422420.

PR 08-NOV-1995; 95US-00555568.

PR 09-SEP-1998; 98US-00149988.

PR 06-MAR-2000; 2000US-00519223.

PA (GENY) GENETICS INST INC.

PI Jones S. Tang J;

DR N-PSDB; ABV73007.

PT Novel composition comprising purified mammalian calcium independent

PT phospholipase enzyme, useful for the screening of inhibitors of

PT phospholipase activity, is active in the absence of calcium.

PS Example 4; Page 10-12; 41pp; English.

CC The invention relates to a purified mammalian calcium independent

CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is

CC characterized by activity in the absence of calcium and has a molecular

CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified

CC calcium independent phospholipase enzyme is useful for identifying an

CC inhibitor of phospholipase activity which involves combining (I),

CC phospholipid and candidate inhibitor compound, and observing whether the

CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a cPLA2/B enzyme (clone 9)

CC Sequence 752 AA;

CC Query Match 88.1%; Score 1837; DB 5; Length 752;

CC Best Local Similarity 87.3%; Pred. No. 16-191;

CC Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

CC 1 MOFPGRLVNTSEGVNTLNFSPNPRVKEVAVADYTSRVRVEGQLIFONTPTMDCLV 60

CC 1 MOFPGRLVNTLSSVNTLNFSPNPRVKEISVADYTSRVRVEGQLIFONASRRTMDCLV 60

CC 61 SPKPHSGFRLFQLESEADALVNFQPSQLPPFYESSVQVLAHVEVLQHLSDLIRHPSM 120

CC 61 SPKPHSGFRLFQLESEADALVNFQPSQLPPFYESSVQVLAHVEVLQHLSDLIRHPSM 120

CC 121 SYAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180

CC 121 TVTHLAVELGIRECFHSHRIISCANSTENEBEGCTPLHLACRKGDSILVELVOYCHTOMD 180

CC 181 VTDYKGETVFAHVAQDQNSQVQLQLGRNAVAGLNQVNNQGLTPHLACQGLKQEMVRVLL 240

CC 181 VTDNKGETAFHYAVQDQNSQVQLQLGRNAVAGLNQVNNQGLTPHLACQGLKQEMVRVLL 240

CC 241 LCNARCNINPGNYPHSAAMKPSQKCAEMIISMDSQHSKDPRYGASPLHMAKNAEMA 300

CC 241 LCNARCNINPGNYPHSAAMKPSQKCAEMIISMDSQHSKDPRYGASPLHMAKNAEMA 300

CC 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRFDCALVLTGANAADARGEHNTPLHLAMSK 360

CC 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRFDCALVLTGANAADARGEHNTPLHLAMSK 360

CC 361 DNVEMIKALIVFGAEVDTPNDFGETPFLASKI 393

CC 361 DNVEMIKALIVFGAEVDTPNDFGETPFLASKI 393

Search completed: December 15, 2004, 13:08:03

Job time : 82.7757 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 13:01:00 ; Search time 20.0874 Seconds
(Without alignments)
1300.780 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084
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Scoring table: BLOSUM62
Gapop 10.0, Gapept 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
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6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|---------------------------|-------------------|
| 1 | 2084 | 100.0 | 394 2 US-08-555-568B-17 | Sequence 17, Appl |
| 2 | 2084 | 100.0 | 394 3 US-09-519-223-17 | Sequence 17, Appl |
| 3 | 2084 | 100.0 | 394 4 US-09-927-180-17 | Sequence 17, Appl |
| 4 | 2084 | 100.0 | 687 2 US-08-555-568B-21 | Sequence 21, Appl |
| 5 | 2084 | 100.0 | 687 3 US-09-519-223-21 | Sequence 21, Appl |
| 6 | 2084 | 100.0 | 687 4 US-09-927-180-21 | Sequence 21, Appl |
| 7 | 2084 | 100.0 | 688 2 US-08-555-568B-23 | Sequence 23, Appl |
| 8 | 2084 | 100.0 | 688 3 US-09-519-223-23 | Sequence 23, Appl |
| 9 | 2084 | 100.0 | 688 4 US-09-927-180-23 | Sequence 23, Appl |
| 10 | 1837 | 88.1 | 752 1 US-08-281-193-2 | Sequence 2, Appl |
| 11 | 1837 | 88.1 | 752 2 US-08-422-106-2 | Sequence 2, Appl |
| 12 | 1837 | 88.1 | 752 3 US-08-735-716-2 | Sequence 2, Appl |
| 13 | 1837 | 88.1 | 752 4 US-08-555-568B-2 | Sequence 2, Appl |
| 14 | 1837 | 88.1 | 752 5 US-09-519-223-2 | Sequence 2, Appl |
| 15 | 1837 | 88.1 | 752 6 US-09-927-180-2 | Sequence 2, Appl |
| 16 | 1837 | 88.1 | 752 7 PCT-US95-08069-2 | Sequence 2, Appl |
| 17 | 494.5 | 17.3 | 896 4 US-09-270-767-46130 | Sequence 46130, A |
| 18 | 359.5 | 12.7 | 545 4 US-09-270-767-46184 | Sequence 46184, A |
| 19 | 338 | 16.2 | 843 2 US-09-172-977-3 | Sequence 3, Appl |
| 20 | 338 | 16.2 | 843 3 US-09-404-108-3 | Sequence 3, Appl |
| 21 | 332 | 15.9 | 1839 2 US-09-172-977-4 | Sequence 4, Appl |
| 22 | 332 | 15.9 | 1839 3 US-09-404-108-4 | Sequence 4, Appl |
| 23 | 332 | 15.9 | 3924 4 US-09-538-092-1246 | Sequence 1246, Ap |
| 24 | 305.5 | 14.7 | 1745 2 US-09-031-485-33 | Sequence 33, Appl |
| 25 | 305.5 | 14.7 | 1745 3 US-08-847-429A-33 | Sequence 33, Appl |
| 26 | 305.5 | 14.7 | 1745 4 US-09-065-474-33 | Sequence 33, Appl |
| 27 | 305.5 | 14.7 | 1745 5 US-09-557-034-33 | Sequence 33, Appl |

| | | | | |
|----|-------|------|--------------------------|--------------------|
| 28 | 301 | 14.4 | 786 4 US-09-509-802-2 | Sequence 2, Appl |
| 29 | 301 | 14.4 | 787 3 US-09-188-930-334 | Sequence 334, App |
| 30 | 301 | 14.4 | 787 4 US-09-312-283C-334 | Sequence 334, App |
| 31 | 296 | 14.2 | 1088 3 US-09-082-059-2 | Sequence 2, Appl |
| 32 | 282.5 | 13.6 | 303 2 US-09-031-485-23 | Sequence 23, Appl |
| 33 | 282.5 | 13.6 | 303 3 US-08-847-429A-23 | Sequence 23, Appl |
| 34 | 282.5 | 13.6 | 303 4 US-09-065-474-23 | Sequence 23, Appl |
| 35 | 282.5 | 13.6 | 303 5 US-09-557-034-23 | Sequence 23, Appl |
| 36 | 281.5 | 13.5 | 784 4 US-09-781-882-2 | Sequence 2, Appl |
| 37 | 272 | 13.1 | 994 4 US-10-164-595-38 | Sequence 38, Appl |
| 38 | 271 | 13.0 | 352 3 US-09-065-474-139 | Sequence 139, Appl |
| 39 | 271 | 13.0 | 352 4 US-09-557-034-139 | Sequence 139, Appl |
| 40 | 270.5 | 13.0 | 302 2 US-09-031-485-38 | Sequence 38, Appl |
| 41 | 270.5 | 13.0 | 302 3 US-08-847-429A-38 | Sequence 38, Appl |
| 42 | 270.5 | 13.0 | 302 4 US-09-065-474-38 | Sequence 38, Appl |
| 43 | 270.5 | 13.0 | 302 5 US-09-557-034-38 | Sequence 38, Appl |
| 44 | 253.5 | 12.2 | 1619 4 US-09-392-812A-4 | Sequence 4, Appl |
| 45 | 252.5 | 12.1 | 348 2 US-09-031-485-28 | Sequence 28, Appl |

ALIGNMENTS

```

RESULT 1
US-08-555-568B-17
Sequence 17, Application US/08555568B
Patent No. 597854
GENERAL INFORMATION:
APPLICANT: Jones, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
City: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 498-8224
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-555-568B-17

Query Match 100.0%; Score 2084; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 4.4e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MOPFGLVNTFSGVTNLFSNPPRKEVAADYSSDRVREBGLIFONTPNRTMDCVY 60
Db 1 MOPFGLVNTFSGVTNLFSNPPRKEVAADYSSDRVREBGLIFONTPNRTMDCVY 60
Cy 61 NPNSGSGFLFQLELEADALVNFQYSSQLPFYESSPOVLTEVLOHITDRIHNP 120
Db 61 NPNSGSGFLFQLELEADALVNFQYSSQLPFYESSPOVLTEVLOHITDRIHNP 120

```

QY 121 SVANLAVELGIRCEPHHSRIISCANCAENEBGCTPLHLACRKGDELIVELVOYCHTOMD 180
DB 121 SVANLAVELGIRCEPHHSRIISCANCAENEBGCTPLHLACRKGDELIVELVOYCHTOMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVPHYAVQGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNINPNGYPIHSAMKFSQKGCAMETISMDSSQHSKDPYRGASPLHWAKAEMA 300
DB 241 LCNARCNINPNGYPIHSAMKFSQKGCAMETISMDSSQHSKDPYRGASPLHWAKAEMA 300
QY 301 RMLKRGCVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
DB 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

RESULT 2

US-09-519-223-17
; Sequence 17, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-519-223-17

Query Match 100.0%; Score 2084; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 4,4e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSQVTLFNSNPRKVEYAVADYTSRDVREBQGLIFONTPNTWCVLV 60
DB 1 MOFGRLVNTFSQVTLFNSNPRKVEYAVADYTSRDVREBQGLIFONTPNTWCVLV 60
QY 61 NPNSSQGRFLFQLELEADALVNFHOYSQQLLPYESSPOVLTHTVLQHLTDLIRNHPSW 120

DB 61 NPNSSQGRFLFQLELEADALVNFHOYSQQLLPYESSPOVLTHTVLQHLTDLIRNHPSW 120
QY 121 SVANLAVELGIRCEPHHSRIISCANCAENEBGCTPLHLACRKGDELIVELVOYCHTOMD 180
DB 121 SVANLAVELGIRCEPHHSRIISCANCAENEBGCTPLHLACRKGDELIVELVOYCHTOMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVPHYAVQGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNINPNGYPIHSAMKFSQKGCAMETISMDSSQHSKDPYRGASPLHWAKAEMA 300
DB 241 LCNARCNINPNGYPIHSAMKFSQKGCAMETISMDSSQHSKDPYRGASPLHWAKAEMA 300
QY 301 RMLKRGCVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
DB 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

RESULT 3

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
; US-09-927-180-17

Query Match 100.0%; Score 2084; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 4,4e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSQVTLFNSNPRKVEYAVADYTSRDVREBQGLIFONTPNTWCVLV 60

Db 1 MGFGRGLVNTFSGVTNLFSNPFRVKEVAVADYTSDDRVRBEGQLILFQNTPNRTMDCVLV 60
 QY 61 NPNRSGSGRLFLQLELEADALVNFHOYSQQLPFYESSPOVLATEYLQHLTDLIRNHPSM 120
 Db 61 NPNRSGSGRLFLQLELEADALVNFHOYSQQLPFYESSPOVLATEYLQHLTDLIRNHPSM 120
 QY 121 SVANLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEILVELVOYCHTQMD 180
 Db 121 SVANLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEILVELVOYCHTQMD 180
 QY 181 VTDYKGETVFNHVAOGDNSQVLIQLGRNAVAGLNQVNNQGLTPHLACQLGKQEWVRVLL 240
 Db 181 VTDYKGETVFNHVAOGDNSQVLIQLGRNAVAGLNQVNNQGLTPHLACQLGKQEWVRVLL 240
 QY 241 LCNARCNIMGPNPGYPIHSAKMFQKCAEMIIISMDSQHSKDPRIYGASPLHMAKNAEVA 300
 Db 241 LCNARCNIMGPNPGYPIHSAKMFQKCAEMIIISMDSQHSKDPRIYGASPLHMAKNAEVA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHGVNRNRPDCAIYLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLRKGCNVNSTSSAGNTALHGVNRNRPDCAIYLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
 Db 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

RESULT 4

US-08-555-568B-21
 ; Sequence 21, Application US/08555568B
 ; Patent No. 5976854
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 687 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-555-568B-21

Query Match 100.0%; Score 2084; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1,1e-222;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGFGRGLVNTFSGVTNLFSNPFRVKEVAVADYTSDDRVRBEGQLILFQNTPNRTMDCVLV 60
 Db 1 MGFGRGLVNTFSGVTNLFSNPFRVKEVAVADYTSDDRVRBEGQLILFQNTPNRTMDCVLV 60

QY 61 NPNRSGSGRLFLQLELEADALVNFHOYSQQLPFYESSPOVLATEYLQHLTDLIRNHPSM 120
 Db 61 NPNRSGSGRLFLQLELEADALVNFHOYSQQLPFYESSPOVLATEYLQHLTDLIRNHPSM 120
 QY 121 SVANLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEILVELVOYCHTQMD 180
 Db 121 SVANLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEILVELVOYCHTQMD 180
 QY 181 VTDYKGETVFNHVAOGDNSQVLIQLGRNAVAGLNQVNNQGLTPHLACQLGKQEWVRVLL 240
 Db 181 VTDYKGETVFNHVAOGDNSQVLIQLGRNAVAGLNQVNNQGLTPHLACQLGKQEWVRVLL 240
 QY 241 LCNARCNIMGPNPGYPIHSAKMFQKCAEMIIISMDSQHSKDPRIYGASPLHMAKNAEVA 300
 Db 241 LCNARCNIMGPNPGYPIHSAKMFQKCAEMIIISMDSQHSKDPRIYGASPLHMAKNAEVA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHGVNRNRPDCAIYLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLRKGCNVNSTSSAGNTALHGVNRNRPDCAIYLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
 Db 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

RESULT 5

US-09-519-223-21
 ; Sequence 21, Application US/09519223
 ; Patent No. 6274140
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/519,223
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 687 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-519-223-21

Query Match 100.0%; Score 2084; DB 3; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1,1e-222;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGFGRGLVNTFSGVTNLFSNPFRVKEVAVADYTSDDRVRBEGQLILFQNTPNRTMDCVLV 60
 Db 1 MGFGRGLVNTFSGVTNLFSNPFRVKEVAVADYTSDDRVRBEGQLILFQNTPNRTMDCVLV 60

Db 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYSSDSVREBQGLIFQNTPNRTWDCVLV 60
Qy 61 NPNRSQSGFRLFOLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHPSW 120
Db 61 NPNRSQSGFRLFOLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHPSW 120
Qy 121 SVHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
Db 121 SVHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
Qy 181 VTDYKGETVHYAVQDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVHYAVQDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Qy 241 LCNARCNIMGPNPGYPHSAKFSQKCAEMIIISMDSQHSKDPYRGASPLHMAKNAEMA 300
Db 241 LCNARCNIMGPNPGYPHSAKFSQKCAEMIIISMDSQHSKDPYRGASPLHMAKNAEMA 300
Qy 301 RMLLRKGCNVNSTSSAGNTALHGVWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHGVWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Qy 361 DNVEMIKALIVFGAEVDTNPDPFGETPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNPDPFGETPTFLASKIG 394

RESULT 6
US-09-927-180-21
Sequence 21, Application US/09927180
Patent No. 6645736

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-927-180-21

Query Match 100.0%; Score 2084; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYSSDSVREBQGLIFQNTPNRTWDCVLV 60
Db 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYSSDSVREBQGLIFQNTPNRTWDCVLV 60
Qy 61 NPNRSQSGFRLFOLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHPSW 120
Db 61 NPNRSQSGFRLFOLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHPSW 120
Qy 121 SVHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
Db 121 SVHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
Qy 181 VTDYKGETVHYAVQDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVHYAVQDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Qy 241 LCNARCNIMGPNPGYPHSAKFSQKCAEMIIISMDSQHSKDPYRGASPLHMAKNAEMA 300
Db 241 LCNARCNIMGPNPGYPHSAKFSQKCAEMIIISMDSQHSKDPYRGASPLHMAKNAEMA 300
Qy 301 RMLLRKGCNVNSTSSAGNTALHGVWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHGVWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Qy 361 DNVEMIKALIVFGAEVDTNPDPFGETPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNPDPFGETPTFLASKIG 394

RESULT 7
US-08-555-568B-23
Sequence 23, Application US/08555568B
Patent No. 5976854

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-555-568B-23

Query Match 100.0%; Score 2084; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOPFRLVNTFSGVNTLFSNPPRVKAVAVADYTSSDRVREBQTLIFONTPNRTMDCVY 60
 DB 1 MOPFRLVNTFSGVNTLFSNPPRVKAVAVADYTSSDRVREBQTLIFONTPNRTMDCVY 60
 QY 61 NPNRSQSGRFLPOLLEADALVNFHOYSQQLPFYSSQVLTETVLQHLTDLIRNHPM 120
 DB 61 NPNRSQSGRFLPOLLEADALVNFHOYSQQLPFYSSQVLTETVLQHLTDLIRNHPM 120
 QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECPPLHLACRGDGEILVELVOYCHTQMD 180
 DB 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECPPLHLACRGDGEILVELVOYCHTQMD 180
 QY 181 VTDYGEVTFHYAVOGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
 DB 181 VTDYGEVTFHYAVOGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
 QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQHSKDPYRGASPLHMAKNAEMA 300
 DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQHSKDPYRGASPLHMAKNAEMA 300
 QY 301 RMLLRGCVNSTSSAGNTALHVGVRNRFDCALVLLTGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLRGCVNSTSSAGNTALHVGVRNRFDCALVLLTGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVGAEVDTPNDFGETPTPLASKIG 394
 DB 361 DNVEMIKALIVGAEVDTPNDFGETPTPLASKIG 394

RESULT 8

US-09-519-223-23
 ; Sequence 23, Application US/09519223
 ; Patent No. 6274140

GENERAL INFORMATION:

APPLICANT: Jones, Simon

APPLICANT: Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/519,223

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELEPHONE: (617) 498-8224

TELEPHONE: (617) 876-5851

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-519-223-23

Best Local Similarity 100.0%; Pred. No. 1,1e-222;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MOPFRLVNTFSGVNTLFSNPPRVKAVAVADYTSSDRVREBQTLIFONTPNRTMDCVY 60
 DB 1 MOPFRLVNTFSGVNTLFSNPPRVKAVAVADYTSSDRVREBQTLIFONTPNRTMDCVY 60
 QY 61 NPNRSQSGRFLPOLLEADALVNFHOYSQQLPFYSSQVLTETVLQHLTDLIRNHPM 120
 DB 61 NPNRSQSGRFLPOLLEADALVNFHOYSQQLPFYSSQVLTETVLQHLTDLIRNHPM 120
 QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECPPLHLACRGDGEILVELVOYCHTQMD 180
 DB 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECPPLHLACRGDGEILVELVOYCHTQMD 180
 QY 181 VTDYGEVTFHYAVOGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
 DB 181 VTDYGEVTFHYAVOGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
 QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQHSKDPYRGASPLHMAKNAEMA 300
 DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQHSKDPYRGASPLHMAKNAEMA 300
 QY 301 RMLLRGCVNSTSSAGNTALHVGVRNRFDCALVLLTGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLRGCVNSTSSAGNTALHVGVRNRFDCALVLLTGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVGAEVDTPNDFGETPTPLASKIG 394
 DB 361 DNVEMIKALIVGAEVDTPNDFGETPTPLASKIG 394

RESULT 9

US-09-927-180-23

; Sequence 23, Application US/09927180

; Patent No. 6645736

GENERAL INFORMATION:

APPLICANT: Jones, Simon

APPLICANT: Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE:

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELEPHONE: (617) 498-8224

TELEPHONE: (617) 876-5851

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Query Match 100.0%; Score 2084; DB 3; Length 688;

US-09-927-180-23

Query Match 100.0%; Score 2084; DB 4; Length 688;
 Best Local Similarity 100.0%; Pred. No. 1,1e-222;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSW 120
 DB 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSW 120
 QY 121 SVNHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGDELVELVOYCHTQMD 180
 DB 121 SVNHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGDELVELVOYCHTQMD 180
 QY 121 VTDYKGETVFNHVAVOGDSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 DB 121 VTDYKGETVFNHVAVOGDSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 QY 181 VTDYKGETVFNHVAVOGDSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFNHVAVOGDSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 QY 241 LCNARCNMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLKKGCVNNTSSAGNTALHGVWNRNRPDCALVLTTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLKKGCVNNTSSAGNTALHGVWNRNRPDCALVLTTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNEMIKALIVFGAEVDPNDPGEPTPLASKIG 394
 DB 361 DNEMIKALIVFGAEVDPNDPGEPTPLASKIG 394

RESULT 10
 US-08-281-193-2
 / Sequence 2, Application US/08281193
 / Patent No. 5466595
 / GENERAL INFORMATION:
 / APPLICANT: Jones, Simon
 / APPLICANT: Tang, Jim
 / TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 / NUMBER OF SEQUENCES: 15
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/281,193
 / FILING DATE:
 / CLASSIFICATION: 435
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 752 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-281-193-2

Query Match 88.1%; Score 1837; DB 1; Length 752;
 Best Local Similarity 87.3%; Pred. No. 3.9e-195;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSW 120
 DB 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSW 120

QY 121 SVNHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGDELVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRCFHHSRIISCANSTENEGCTPLHLACRKDGDELVELVOYCHTQMD 180
 QY 181 VTDYKGETVFNHVAVOGDSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFNHVAVOGDSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 QY 241 LCNARCNMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLKKGCVNNTSSAGNTALHGVWNRNRPDCALVLTTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLKKGCVNNTSSAGNTALHGVWNRNRPDCALVLTTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNEMIKALIVFGAEVDPNDPGEPTPLASKI 393
 DB 361 DNEMIKALIVFGAEVDPNDPGEPTPLASKI 393

RESULT 11
 US-08-422-106-2
 / Sequence 2, Application US/08422106
 / Patent No. 558170
 / GENERAL INFORMATION:
 / APPLICANT: Jones, Simon
 / APPLICANT: Tang, Jim
 / TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 / NUMBER OF SEQUENCES: 15
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/422,106
 / FILING DATE: 14-APR-1995
 / CLASSIFICATION: 435
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 752 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-422-106-2

Query Match 88.1%; Score 1837; DB 1; Length 752;
 Best Local Similarity 87.3%; Pred. No. 3.9e-195;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSW 120
 DB 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSW 120
 QY 121 SVNHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGDELVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRCFHHSRIISCANSTENEGCTPLHLACRKDGDELVELVOYCHTQMD 180
 QY 181 VTDYKGETVFNHVAVOGDSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFNHVAVOGDSQVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
 QY 241 LCNARCNMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300

QY 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADAGEHNTPLHAKSK 360
 DB 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADAGEHNTPLHAKSK 360
 QY 361 DNMEMIKALIVFGAEVDTNPDPGERTPLASKI 393
 DB 361 DNMEMIKALIVFGAEVDTNPDPGERTPLASKI 393

RESULT 12
 US-08-735-716-2
 ; Sequence 2, Application US/08735716
 ; Patent No. 5840511
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/735,716
 ; FILING DATE: 23-OCT-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/281,193
 ; FILING DATE: 27-JUL-1994
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-735-716-2

Query Match 88.1%; Score 1837; DB 2; Length 752;
 Best Local Similarity 87.3%; Pred. No. 3.9e-195;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;
 QY 1 MOPFGRLVNTFSGVNTLFSNPRKVEAVADYTSRVRBEGQLIFONTPRRTMDCVLY 60
 DB 1 MOPFGRLVNTLSSVNTLFSNPRKVEAVADYTSRVRBEGQLIFONTASRTMDCVLY 60
 QY 61 NPNRSQSGRFLFQLEADALVNFHQSQQLPFYESSPOVLTATEVLOHLDLIRNHPSM 120
 DB 61 SPRNPHSGRFLFQLEADALVNFHQSQQLPFYESSPOVLTATEVLOHLDLIRNHPSM 120
 QY 121 SYAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
 DB 121 TYTHLAVELGIRECFHHSRIISCANSTENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
 QY 181 VTDYKGETVFNHVAVOGDSNQVLOLGRNAVAGLNQNNQGLTPHLACOLGKQEMRVLL 240
 DB 181 VTDNKEETAFHVAVOGDSNQVLOLGRNAVAGLNQNNQGLTPHLACOLGKQEMRVLL 240
 QY 241 LCNARCNMGPNPGYPHSAAMKFSQKCAEMIISMDSQHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNMGPNPGYPHSAAMKFSQKCAEMIISMDSQHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADAGEHNTPLHAKSK 360
 DB 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADAGEHNTPLHAKSK 360
 QY 361 DNMEMIKALIVFGAEVDTNPDPGERTPLASKI 393
 DB 361 DNMEMIKALIVFGAEVDTNPDPGERTPLASKI 393

RESULT 13

US-08-555-568B-2
 ; Sequence 2, Application US/08555568B
 ; Patent No. 5976854
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-555-568B-2

Query Match 88.1%; Score 1837; DB 2; Length 752;
 Best Local Similarity 87.3%; Pred. No. 3.9e-195;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;
 QY 1 MOPFGRLVNTFSGVNTLFSNPRKVEAVADYTSRVRBEGQLIFONTPRRTMDCVLY 60
 DB 1 MOPFGRLVNTLSSVNTLFSNPRKVEAVADYTSRVRBEGQLIFONTASRTMDCVLY 60
 QY 61 NPNRSQSGRFLFQLEADALVNFHQSQQLPFYESSPOVLTATEVLOHLDLIRNHPSM 120
 DB 61 SPRNPHSGRFLFQLEADALVNFHQSQQLPFYESSPOVLTATEVLOHLDLIRNHPSM 120
 QY 121 SYAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
 DB 121 TYTHLAVELGIRECFHHSRIISCANSTENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
 QY 181 VTDYKGETVFNHVAVOGDSNQVLOLGRNAVAGLNQNNQGLTPHLACOLGKQEMRVLL 240
 DB 181 VTDNKEETAFHVAVOGDSNQVLOLGRNAVAGLNQNNQGLTPHLACOLGKQEMRVLL 240
 QY 241 LCNARCNMGPNPGYPHSAAMKFSQKCAEMIISMDSQHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNMGPNPGYPHSAAMKFSQKCAEMIISMDSQHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADAGEHNTPLHAKSK 360
 DB 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADAGEHNTPLHAKSK 360
 QY 361 DNMEMIKALIVFGAEVDTNPDPGERTPLASKI 393
 DB 361 DNMEMIKALIVFGAEVDTNPDPGERTPLASKI 393

RESULT 14
 US-09-519-223-2

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; Sequence 2, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-519-223-2

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Query Match      88.1%; Score 1837; DB 3; Length 752;
Best Local Similarity 87.3%; Pred. No. 3.9e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

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DB 1 MOFGGLVNTLSSVTNLFSPNPRVKEISVADYTSHERVREEGQLIFQNASNRMTDCILY 60
QY 61 NPNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLAHTEVLAQHLDLIRNHP 120
DB 61 SPNPHSGRFLFQLESEADALVNFQFSSQLPFYESSVQVLAHVEVLQHLSDLRSHPSV 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRGDGEIVELVQYCHTQND 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEBEGCTPLHLACRGDSEIVELVQYCHQND 180
QY 181 VTDYKGETVFHYAVQDNGSOVLQLGKNAVAGLNQVNNQGLTPHLACQLGKQEMRVLYL 240
DB 181 VTDNKEITAFHYAVQDNGSOVLQLGKNASAGLNQVNNQGLTPHLACQMGKQEMRVLYL 240
QY 241 LCNARCNINPGNPGYPHISAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHAKNAEVA 300
DB 241 LCNARCNVWGPSPFPIHTAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHAKNAEVA 300
QY 301 RMLLRKGCNVNSTSSAGNTALTALHGVNMRNRPDCAIYLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSSAGNTALTALHVAVMNRNRPDCAIYLLTHGANAGTGEHNTPLHLATISK 360
QY 361 DNVEIMKALIVFGAEVDTNPDGERTPTFLASKI 393
DB 361 DNMEIMKALIVFGAEVDTNPDGERTPAFMSKI 393

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RESULT 15
US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

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Query Match      88.1%; Score 1837; DB 4; Length 752;
Best Local Similarity 87.3%; Pred. No. 3.9e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFGGLVNTFSGVTNLFSPNPRVKEVAVADYTSSDRVREEGQLIFONTPTMTDCVLY 60
DB 1 MOFGGLVNTLSSVTNLFSPNPRVKEISVADYTSHERVREEGQLIFQNASNRMTDCILY 60
QY 61 NPNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLAHTEVLAQHLDLIRNHP 120
DB 61 SPNPHSGRFLFQLESEADALVNFQFSSQLPFYESSVQVLAHVEVLQHLSDLRSHPSV 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRGDGEIVELVQYCHTQND 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEBEGCTPLHLACRGDSEIVELVQYCHQND 180
QY 181 VTDYKGETVFHYAVQDNGSOVLQLGKNAVAGLNQVNNQGLTPHLACQLGKQEMRVLYL 240
DB 181 VTDNKEITAFHYAVQDNGSOVLQLGKNASAGLNQVNNQGLTPHLACQMGKQEMRVLYL 240
QY 241 LCNARCNINPGNPGYPHISAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHAKNAEVA 300
DB 241 LCNARCNVWGPSPFPIHTAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHAKNAEVA 300
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DB 301 RMLLRKGCVDVSTSSAGNTALTALHVAVMNRNRPDCAIYLLTHGANAGTGEHNTPLHLATISK 360
QY 361 DNVEIMKALIVFGAEVDTNPDGERTPTFLASKI 393
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' Thu Dec 16 19:13:23 2004

us-10-612-668-17.ra1

Page 9

Db 361 DNMEMIKALIVGAEVDTPNDFGSTPAFMASKI 393

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 15, 2004, 13:13:21 ; Search time 69.158 Seconds
(without alignments)
2034.879 Million cell updates/sec

Title: US-10-612-668-17
Perfect score: 2084
Sequence: 1 MGFPGRLVNTFGVTLFNSN.....EVDTPNDPGETPTPLSKITG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues
Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|--------------------|
| 1 | 2084 | 100.0 | 394 | US-09-927-180-17 | Sequence 17, Appl |
| 2 | 2084 | 100.0 | 687 | US-09-927-180-21 | Sequence 21, Appl |
| 3 | 2084 | 100.0 | 688 | US-09-927-180-23 | Sequence 23, Appl |
| 4 | 1837 | 88.1 | 752 | US-09-927-180-2 | Sequence 2, Appl |
| 5 | 1234.5 | 59.2 | 667 | US-10-108-260A-3778 | Sequence 3778, Ap |
| 6 | 324 | 15.5 | 1330 | US-10-108-260A-3237 | Sequence 3237, Ap |
| 7 | 301 | 14.4 | 786 | US-10-164-080-2 | Sequence 2, Appl |
| 8 | 301 | 14.4 | 786 | US-10-299-327-2 | Sequence 2, Appl |
| 9 | 301 | 14.4 | 786 | US-10-128-174-13 | Sequence 13, Appl |
| 10 | 301 | 14.4 | 786 | US-10-128-174-31 | Sequence 31, Appl |
| 11 | 301 | 14.4 | 786 | US-10-128-174-32 | Sequence 32, Appl |
| 12 | 301 | 14.4 | 786 | US-10-128-174-33 | Sequence 33, Appl |
| 13 | 301 | 14.4 | 787 | US-09-866-050A-334 | Sequence 334, Appl |

| | | | | | | |
|----|-------|------|------|----|---------------------|-------------------|
| 14 | 300.5 | 14.4 | 347 | 14 | US-10-128-174-30 | Sequence 30, Appl |
| 15 | 300.5 | 14.4 | 1724 | 9 | US-09-964-899-43 | Sequence 43, Appl |
| 16 | 286 | 14.2 | 3913 | 15 | US-10-334-193-45 | Sequence 45, Appl |
| 17 | 288 | 13.8 | 1762 | 14 | US-10-205-194-17 | Sequence 117, App |
| 18 | 283.5 | 13.6 | 784 | 14 | US-10-164-080-7 | Sequence 7, Appl |
| 19 | 283.5 | 13.6 | 784 | 14 | US-10-258-951-70 | Sequence 70, Appl |
| 20 | 281.5 | 13.5 | 784 | 14 | US-10-354-358-38 | Sequence 38, Appl |
| 21 | 281.5 | 13.5 | 784 | 14 | US-10-128-174-12 | Sequence 12, Appl |
| 22 | 281.5 | 13.5 | 784 | 15 | US-10-659-904-2 | Sequence 2, Appl |
| 23 | 280.5 | 13.5 | 720 | 15 | US-10-433-794-20 | Sequence 20, Appl |
| 24 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-3 | Sequence 3, Appl |
| 25 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-34 | Sequence 34, Appl |
| 26 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-35 | Sequence 35, Appl |
| 27 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-36 | Sequence 36, Appl |
| 28 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-37 | Sequence 37, Appl |
| 29 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-38 | Sequence 38, Appl |
| 30 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-39 | Sequence 39, Appl |
| 31 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-40 | Sequence 40, Appl |
| 32 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-41 | Sequence 41, Appl |
| 33 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-42 | Sequence 42, Appl |
| 34 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-43 | Sequence 43, Appl |
| 35 | 280.5 | 13.5 | 765 | 14 | US-10-128-174-44 | Sequence 44, Appl |
| 36 | 280.5 | 13.5 | 765 | 15 | US-10-182-243-56 | Sequence 56, Appl |
| 37 | 278.5 | 13.4 | 784 | 16 | US-10-648-593-153 | Sequence 153, App |
| 38 | 272 | 13.1 | 367 | 15 | US-10-250-613-6 | Sequence 6, Appl |
| 39 | 271.5 | 13.0 | 1053 | 14 | US-10-291-172-343 | Sequence 343, App |
| 40 | 271.5 | 13.0 | 1053 | 15 | US-10-221-278-343 | Sequence 4122, Ap |
| 41 | 267.5 | 12.8 | 919 | 15 | US-10-108-260A-4122 | Sequence 6689, Ap |
| 42 | 258 | 12.4 | 1023 | 14 | US-10-369-493-6689 | Sequence 6690, Ap |
| 43 | 258 | 12.4 | 1023 | 14 | US-10-369-493-6690 | Sequence 4, Appl |
| 44 | 253.5 | 12.2 | 1619 | 14 | US-10-369-978-4 | Sequence 2, Appl |
| 45 | 251 | 12.0 | 1704 | 14 | US-10-369-978-2 | |

ALIGNMENTS

RESULT 1
US-09-927-180-17
Sequence 17, Application US/099277180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Jim
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:

LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match 100.0%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.4e-190;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFGLVNTFSGVTLFNSNPFVKEVAVADYSSDRVREEGQLLFONTPTMTDCVLY 60
DB 1 MGFGLVNTFSGVTLFNSNPFVKEVAVADYSSDRVREEGQLLFONTPTMTDCVLY 60
QY 61 NPNNSQGRFLFQLEADALVNFHOYSQQLPFYESSPQVLHTEVLOHLDLIRNHP 120
DB 61 NPNNSQGRFLFQLEADALVNFHOYSQQLPFYESSPQVLHTEVLOHLDLIRNHP 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVOYCHTOMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVOYCHTOMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
QY 241 LCNARCNINPNGYPIHSAKFQSKCAEMIISMDSQHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNINPNGYPIHSAKFQSKCAEMIISMDSQHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKKGCVNVSSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLSK 360
DB 301 RMLKKGCVNVSSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLSK 360
QY 361 DNVEMIKALIVFGAEVDTPTNDGERTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTPTNDGERTPTFLASKIG 394

RESULT 2

US-09-927-180-21
Sequence 21, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 33,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 2084; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFGLVNTFSGVTLFNSNPFVKEVAVADYSSDRVREEGQLLFONTPTMTDCVLY 60
DB 1 MGFGLVNTFSGVTLFNSNPFVKEVAVADYSSDRVREEGQLLFONTPTMTDCVLY 60
QY 61 NPNNSQGRFLFQLEADALVNFHOYSQQLPFYESSPQVLHTEVLOHLDLIRNHP 120
DB 61 NPNNSQGRFLFQLEADALVNFHOYSQQLPFYESSPQVLHTEVLOHLDLIRNHP 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVOYCHTOMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVOYCHTOMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
QY 241 LCNARCNINPNGYPIHSAKFQSKCAEMIISMDSQHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNINPNGYPIHSAKFQSKCAEMIISMDSQHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKKGCVNVSSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLSK 360
DB 301 RMLKKGCVNVSSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLSK 360
QY 361 DNVEMIKALIVFGAEVDTPTNDGERTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTPTNDGERTPTFLASKIG 394

RESULT 3

US-09-927-180-23
Sequence 23, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 2084; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.2e-189; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSSDRVREBQGLIFONTPTNTMDCVLY 60
1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSSDRVREBQGLIFONTPTNTMDCVLY 60
61 NPNRNSGFRLLFQLEADALVNFHOYSQQLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
61 NPNRNSGFRLLFQLEADALVNFHOYSQQLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
121 SVAHLAVELGIRCFHRSRIISCANCAENEBCGTPHLACRKDGELVELVQYCHTQMD 180
121 SVAHLAVELGIRCFHRSRIISCANCAENEBCGTPHLACRKDGELVELVQYCHTQMD 180
181 VTDYKEITFHYAVQDQNSQVLOLGRNAVAGLNQVNNQGLTPHLACQKQEMRVLL 240
181 VTDYKEITFHYAVQDQNSQVLOLGRNAVAGLNQVNNQGLTPHLACQKQEMRVLL 240
241 LCNARCNMGPNQPIHSAKFQSKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
241 LCNARCNMGPNQPIHSAKFQSKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
301 RMLKRGCVNNTSSAGNTALHGVNMRNPDCAIVLLTHGANADAGEHNTPLHLAMSK 360
301 RMLKRGCVNNTSSAGNTALHGVNMRNPDCAIVLLTHGANADAGEHNTPLHLAMSK 360
361 DNEMIKALIVFGAEVDTPNDFGPTPLASKIG 394
361 DNEMIKALIVFGAEVDTPNDFGPTPLASKIG 394

RESULT 4
US-09-927-180-2
Sequence 2, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/927,180
APPLICATION NUMBER: US-AUG-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

Query Match 88.1%; Score 1837; DB 9; Length 752;
Best Local Similarity 87.3%; Pred. No. 5e-166;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSSDRVREBQGLIFONTPTNTMDCVLY 60
1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSSDRVREBQGLIFONTPTNTMDCVLY 60
61 NPNRNSGFRLLFQLEADALVNFHOYSQQLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
61 NPNRNSGFRLLFQLEADALVNFHOYSQQLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
121 SVAHLAVELGIRCFHRSRIISCANCAENEBCGTPHLACRKDGELVELVQYCHTQMD 180
121 SVAHLAVELGIRCFHRSRIISCANCAENEBCGTPHLACRKDGELVELVQYCHTQMD 180
181 VTDYKEITFHYAVQDQNSQVLOLGRNAVAGLNQVNNQGLTPHLACQKQEMRVLL 240
181 VTDYKEITFHYAVQDQNSQVLOLGRNAVAGLNQVNNQGLTPHLACQKQEMRVLL 240
241 LCNARCNMGPNQPIHSAKFQSKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
241 LCNARCNMGPNQPIHSAKFQSKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
301 RMLKRGCVNNTSSAGNTALHGVNMRNPDCAIVLLTHGANADAGEHNTPLHLAMSK 360
301 RMLKRGCVNNTSSAGNTALHGVNMRNPDCAIVLLTHGANADAGEHNTPLHLAMSK 360
361 DNEMIKALIVFGAEVDTPNDFGPTPLASKIG 393
361 DNEMIKALIVFGAEVDTPNDFGPTPLASKIG 393

RESULT 5
US-10-108-260A-3778
Sequence 3778, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3778
LENGTH: 667
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 59.2%; Score 1234.5; DB 15; Length 667;
Best Local Similarity 64.0%; Pred. No. 1.3e-108;
Matches 252; Conservative 1; Mismatches 2; Indels 139; Gaps 1;
1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSSDRVREBQGLIFONTPTNTMDCVLY 60

SEQ ID NO 2
LENGTH: 786
TYPE: PRT
ORGANISM: Mus sp.
US-10-299-327-2

Query Match 14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;

Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY 112 DLIRNPSVAVHAYELGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGELIVE 170
DB 434 DLVLD-SSASLHLAVAGQEBECVKMLLNANPNLNRKGSTPLHMAVERKRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVPHYAVQ-GDNSQVQLQGRNAVAGLNQVNOGLTPLHLACQ 229
DB 491 LLARSTSVAKEDQWTALHFAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLCNARCNINMGNGY-PIHSAMKFSQKCAEMTISMSQIHSKDPYGA 288
DB 549 HGOENIVRTLIRRGVDVGLQKDMPLHYAAMOGHLPYKLAKOPGVSVNAQ-TLDGR 607
QY 289 SPLHMAK--NAEMARMLKRGCVNSTSSAGNTALHGVWRNRPFCATVILTHGNADA 345
DB 608 TPLHLAQRGHYVARILIDLCSDVNICSLQAOPTPLHVAETGHTSTARLLHHRGAKXA 667
QY 346 RGEHGTPLHLAMSKDNVEMIKALIVFGAEVDPNDPFGETPTPLASKIG 394
DB 668 LTSEGYTALHLAQNGLATVTKLLIEBKADVMARGLNQTALHLAARG 716

RESULT 9

US-10-128-174-13
Sequence 13; Application US/10128174
Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohito
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128, 174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-13

Query Match 14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;

Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY 112 DLIRNPSVAVHAYELGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGELIVE 170
DB 434 DLVLD-SSASLHLAVAGQEBECVKMLLNANPNLNRKGSTPLHMAVERKRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVPHYAVQ-GDNSQVQLQGRNAVAGLNQVNOGLTPLHLACQ 229
DB 491 LLARSTSVAKEDQWTALHFAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLCNARCNINMGNGY-PIHSAMKFSQKCAEMTISMSQIHSKDPYGA 288
DB 549 HGOENIVRTLIRRGVDVGLQKDMPLHYAAMOGHLPYKLAKOPGVSVNAQ-TLDGR 607
QY 289 SPLHMAK--NAEMARMLKRGCVNSTSSAGNTALHGVWRNRPFCATVILTHGNADA 345
DB 608 TPLHLAQRGHYVARILIDLCSDVNICSLQAOPTPLHVAETGHTSTARLLHHRGAKXA 667
QY 346 RGEHGTPLHLAMSKDNVEMIKALIVFGAEVDPNDPFGETPTPLASKIG 394
DB 668 LTSEGYTALHLAQNGLATVTKLLIEBKADVMARGLNQTALHLAARG 716

RESULT 10

US-10-128-174-31
Sequence 31; Application US/10128174
Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohito
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128, 174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-31

Query Match 14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;

Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY 112 DLIRNPSVAVHAYELGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGELIVE 170
DB 434 DLVLD-SSASLHLAVAGQEBECVKMLLNANPNLNRKGSTPLHMAVERKRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVPHYAVQ-GDNSQVQLQGRNAVAGLNQVNOGLTPLHLACQ 229
DB 491 LLARSTSVAKEDQWTALHFAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLCNARCNINMGNGY-PIHSAMKFSQKCAEMTISMSQIHSKDPYGA 288
DB 549 HGOENIVRTLIRRGVDVGLQKDMPLHYAAMOGHLPYKLAKOPGVSVNAQ-TLDGR 607
QY 289 SPLHMAK--NAEMARMLKRGCVNSTSSAGNTALHGVWRNRPFCATVILTHGNADA 345
DB 608 TPLHLAQRGHYVARILIDLCSDVNICSLQAOPTPLHVAETGHTSTARLLHHRGAKXA 667
QY 346 RGEHGTPLHLAMSKDNVEMIKALIVFGAEVDPNDPFGETPTPLASKIG 394
DB 668 LTSEGYTALHLAQNGLATVTKLLIEBKADVMARGLNQTALHLAARG 716

RESULT 11

US-10-128-174-32
Sequence 32; Application US/10128174
Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohito
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128, 174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-32

Query Match 14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;

Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY 112 DLIRNPSVAVHAYELGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGELIVE 170
DB 434 DLVLD-SSASLHLAVAGQEBECVKMLLNANPNLNRKGSTPLHMAVERKRG--IVE 490

```

QY      171 LVQCCHTMDVTDYGEIVFHYAVO-GDMSGYLTOLLGRVAALGVNNOGQLTPFLACQ 229
        :|::||::||::||::||::||::||::||::||::||::||::||::||
Db      491 LILARKTSVNAKDEBQWTAHHPAANGDBASTRLLEKK--ASVAEVDREGATPMHYAQ 548
QY      230 LGKEEMVAVLLLCNARCINMGPNXY-PLHSAMKFESOKGCAEMIISMDSQIHSKDPRYA 288
        :|::||::||::||::||::||::||::||::||::||::||::||::||
Db      549 HGOERIVETLTLRRGVDAVLGGKDAWLPHLYAAVOGHLPVLKLAKQPGVSVAHQ--TLDR 607
QY      289 SPLHWAK---NAEMARMLLKRGCVNSTSSAGNTALTAVGVMEHRFPFCALVLTTHGANADA 345
        :||::||::||::||::||::||::||::||::||::||::||::||
Db      608 TPLHLAAQRGHYRVARRILLDCSDVNICSLQAQOTPLHVAAEEHGHNSTALLHLRGAKEA 667
QY      346 RGEHGNTPHLHAMSNDVNEMIKALIVFGAEVDPENDPGETPTFFLSKITG 394
        :||::||::||::||::||::||::||::||::||::||::||::||
Db      668 LTSEGVTALHLAANGHLATVTLTIEEKADVWARGPRLNQATALHLAAARG 716

RESULT 12
US-10-128-174-33
; Sequence 33, Application US/10128174
; Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-33
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Query Match 14.4%; Score 301; DB 14; Length 766;
Best Local Similarity 13.8%; Pred No. 2.1e-19;
Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

QY      112 DLIRNHPMSVAHLAVELGIRECFHHSRIISCANCAENEBCGTPHLAC-RKGDGEILVE 170
Db      434 DLIVD-SSASLHLHLAVEAGQEECVKMLLNANPNLTRKSGTPLHMAVERKGRG--IYE 490

QY      171 LVQYCHTQMDVTDYGETVFHYAVQ-GDNSQVLQLIGRNAVAGLQVNNQGLTPHLACQ 229
Db      491 LLLARKTSVNAKDEBQDTALHFAAONGDEASRYLLLEKN--ASVNEVDEGRTPMHVAQ 548

QY      230 LGGKEMTVVLLCNARCINMGNGV-PLHSANKFSQKGAEMIISMSDSQHSKDPRYGA 288
Db      549 HGOEIVTVTLIRGVGVGGQKDAWPLHYAAMQGHLPVTKLLAKOPGVSVNAQ--TLDR 607

QY      289 SPLHWAK--NAEMARMLLKRGCNSTSSAGNTALHVGVMENRFDCALVLLTHGCANADA 345
Db      608 TPLHLAAARGHYRVARILIDLCSDVNICSLOQOTPLHVAALRGHSTALLHLHKGKXA 667

QY      346 RGEHGNTPHLAMSKDNVEMIKALIVFGAEVDPDNDFGETPTFLASKIG 394
Db      668 LTSGYTALHLAAQNGHLATVTLLEKADVVARGPDLQNTALHLAAARG 716

RESULT 13
US-09-866-050A-334
Sequence 334, Application US/09866050A
Publication No. US20030040471A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muriison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells

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; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000..1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 334
LENGTH: 787
TYPE: PRT
ORGANISM: Mouse
US-09-866-050A-334

Query Match      14.4%; Score 301; DB 10; Length 787;
Best Local Similarity 31.8%; Pred. No. 2,1e-19;
Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8,

Qy      112 DLIRHPMSVAHLAVELGIEKRCFPHSRHIIISCANCAENEGECTPLHLAC-RKGDGEILVE 170
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      435 DVLVD-SASLILHLAVEAGQECVCXWLLNNNPNLTRKGSTPLHMVNRGRG--IYE 491

Qy      171 LVQCCHTOMDVTYDKGETVFHYAVD-GDNSOVLTLIGRNAVGLNOVNOGGLTPLHLAQ 229
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Db      492 LILARKTSIVNAKDDEDMTALHPFAONGEASTRLLEKN--ASVNEVDEGRTPMHPVAQQ 549

Qy      230 LGKQEMTVLVLLCNARCNIMGNPGY-PHISAMKFSGKKCAEMIISMDSQIHSKDPRYGA 288
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Db      550 HGOEIYATTLRGGVDVGIOGKDAMPPLHYAMOGHLPVKLIANGPQSVANAQ-TLDER 608

Qy      289 SPLHWAK--NAEMARMILLKGCNVNSTSSAGNTALHGVGMRRNPEDCAIVLLTHGANADA 345
        ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      609 TPLHLAARGHYVARILIDLCSDVNICSLQAOTPLHVAAETGHSTARLLHRGAKGA 668

Qy      346 RGEHGNTPLHAMSNDVNMFKALIVFGAEVDTPTPDGFTPTFLASKIG 394

Db      669 LTSEITLHLDAONGHLATYKLLLEEKADVNARGPDLNOTALHLAAPRG 717
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RESULT 14
US-10-128-174-30
; Sequence 30, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 347
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-30

Query Match      14.4% Score 300.5, DB 14, Length 347;
Best Local Similarity 31.9%; Pred. No. 7, 4e-20;
Matches 90; Conservative 46; Mismatches 135; Indels 11; Gaps 7;

QY    119 SMSVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLAC-RKDDGEILVELVGYCHT 177
       ||||| | : : : ||||| : ||||| : |||||
Db     1 SASLIHLAVEAGOECCVMKLILNNPNMLTKRKGSTPLHMAVERKGRG--IVELLARKT 58
       ||||| | : : : ||||| : ||||| : |||||

QY    178 QMDVTDYKGELVFPHAYO-GDNSQVLQLLGRNAVVGGLNOVNNGQLTPHLIACOLGKOENV 236
       :: ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db     59 SVNAKDDEQMTALHFAONGDBASTRLLDCKN--ASVNEVDDEGRTPMHVACOHQGENIV 116
       ||||| | : ||||| | : ||||| | : ||||| | : |||||

QY    237 RVLLLCNARCIMGNGXY-PHSAAKFSGKGAEMIISSDSQIHSDKPBGYSPLHWAK 295
       ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db     117 RTLNRGVDELQGDADWLPFLHYAMQHGLPRTVKLLAQPGVSVAHQ-TLDRGTPLHLAA 175
       ||||| | : ||||| | : ||||| | : ||||| | : |||||

QY    296 --NAEMARKLLKRCGNVSTSSAGNTALHVGVMENRFDCAILVLTTHGANADARGHGNT 352

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Db 176 QRGHYAVARLILDLCSVDNLCISLAQOTPLVAAETGHTSTARLILHRGAGKEALTSEGT 235
 QY 353 PHLIAMSNDVENIKALIVGAEVDTPNDGEPFLASKIG 394
 Db 236 ALHLAONGHILATVKKLIEKADVMARGPLNQTAHLHAAARG 277

RESULT 15

US-09-964-899-43
 ; Sequence 43, Application US/09964899
 ; Patent No. US2002017446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Dalia et al.
 ; TITLE OF INVENTION: Identification of Genes Involved in
 ; FILE REFERENCE: 4-31612 A
 ; CURRENT APPLICATION NUMBER: US/09/964,899
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,893
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/298,309
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 1724
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-09-964-899-43

Query Match 14.4%; Score 300.5; DB 9; Length 1724;
 Best Local Similarity 28.4%; Pred. No. 7e-19;
 Matches 85; Conservative 71; Mismatches 120; Indels 23; Gaps 10;
 QY 106 VLQH--LTDLRNHPMSVAHLAVELGIRECFHH--SRIISCANCAENE--GCTPLH 157
 Db 315 LLOHNPVDDVTNDY--LTALHVA--HCHYKAKVLDKKANPNKALNGFTPLH 367
 QY 158 LACRKGDEILVELVOYCHTQMDVTDYKGETVFHYAVQDGNQOVLQLRNNAVAGLNQVN 217
 Db 368 IACKKRIKVMELLKHGASIQAVTE-RGETALHMAARSGQAEVVRVLYQDG-AQVEAKA 425
 QY 218 NQGLTPLHLACQKQEMRVVLLCNARCINMGNGY-PHISAMKBSQKCAEMIISMS 276
 Db 426 KDDQTPHLHSARLGKADIVQQLQOGASPNAAATTSGYTPLHSAREGHEVAAFLLDHGA 485
 QY 277 SQHSKDPKRYGASPLHWA--KNAEMARMLLKRCNVNSTSSAGNTALHYGVNRNRPDCA 333
 Db 486 SL--SITTKSGLTPLHVAHYDNQKVALLLDDGASPHAAAKNGYTPPLHIAKKNQMDIA 543
 QY 334 IVLLTHGANADARGHGNTPLHLAMSNDVENIKALIVGAEVDTPNDGEPFLASK 392
 Db 544 TTLLEYGADANAVTRQGIASVHLAAQGHVDMVSLILGRNANVNLNYSKSGLTPLHLAAQ 602

Search completed: December 15, 2004, 13:34:52
 Job time: 70.158 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 11:36:42 ; Search time 4401 Seconds
(without alignments)
10573.401 Million cell updates/sec

Title: US-10-612-668-18
Perfect score: 1277
Sequence: 1 GAATCTTACGCCCCCAGATTC.....CAGACGGCGCGCCGGAATTC 1277

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821965908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 854.2 | 66.9 | 2259 | AY421137 | AY421137 Homo sapi |
| 2 | 818.4 | 64.1 | 2259 | AY421138 | AY421138 Pan trogl |
| 3 | 770.8 | 60.4 | 914 | BG751481 | BG751481 602730060 |
| 4 | 763.8 | 59.8 | 776 | BG746419 | BG746419 602703692 |
| 5 | 759.2 | 59.5 | 1042 | BM805376 | BM805376 AGENCOURT |
| 6 | 747.4 | 58.5 | 851 | B1819262 | B1819262 603034691 |
| 7 | 698.6 | 54.7 | 3010 | BC061866 | BC061866 Rattus no |
| 8 | 697.4 | 54.6 | 2259 | AY421139 | AY421139 Mus muscu |
| 9 | 671.6 | 52.6 | 815 | BG328183 | BG328183 602427250 |
| 10 | 653.2 | 51.2 | 910 | CA489815 | CA489815 AGENCOURT |
| 11 | 631.4 | 49.4 | 636 | BG575678 | BG575678 602598744 |
| 12 | 590.2 | 46.2 | 658 | BG752410 | BG752410 602730892 |
| 13 | 577.4 | 45.2 | 940 | BQ423546 | BQ423546 AGENCOURT |
| 14 | 544.8 | 42.7 | 741 | BG576880 | BG576880 602597576 |
| 15 | 526.8 | 41.3 | 980 | BF178544 | BF178544 601807913 |
| 16 | 514.4 | 40.3 | 1868 | BM903742 | BM903742 AGENCOURT |
| 17 | 506 | 39.6 | 1060 | BO899244 | BO899244 AGENCOURT |
| 18 | 505.4 | 39.6 | 516 | BI013478 | BI013478 RCO-ET018 |
| 19 | 505.4 | 39.6 | 732 | CK356848 | CK356848 AGENCOURT |
| 20 | 494.2 | 38.7 | 620 | BM729323 | BM729323 UT-B-E01 |
| 21 | 493 | 38.6 | 865 | CB204862 | CB204862 AGENCOURT |
| 22 | 482.6 | 37.8 | 615 | BO840333 | BO840333 mah66a10 |
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| 26 | 430.4 | 33.7 | 776 | 6 | CB948314 | CB948314 AGENCOURT |
| 27 | 425.6 | 33.3 | 544 | 6 | CB612036 | CB612036 AMGNMNC-N |
| 28 | 412 | 32.3 | 528 | 4 | BM107521 | BM107521 511770 MA |
| 29 | 393.8 | 30.8 | 600 | 5 | BU924627 | BU924627 7094-21 M |
| 30 | 393.4 | 30.8 | 570 | 2 | AW753653 | AW753653 CM0-CT027 |
| 31 | 371.2 | 29.1 | 759 | 4 | BI330667 | BI330667 602982618 |
| 32 | 368.2 | 28.6 | 565 | 7 | H10676 | H10676 Y199911.X1 |
| 33 | 357.8 | 28.0 | 648 | 2 | AM825629 | AM825629 uel1907.Y |
| 34 | 356.2 | 27.9 | 530 | 5 | BX524262 | BX524262 BX524262 |
| 35 | 352.4 | 27.6 | 361 | 6 | CF139617 | CF139617 UT-HF-CBO |
| 36 | 344.8 | 27.2 | 593 | 4 | BG917622 | BG917622 602820461 |
| 37 | 346.8 | 27.0 | 540 | 5 | BX119788 | BX119788 BX119788 |
| 38 | 343.6 | 26.9 | 566 | 1 | AI663704 | AI663704 u647a01.Y |
| 39 | 330.4 | 25.9 | 865 | 6 | CA488194 | CA488194 AGENCOURT |
| 40 | 323.8 | 25.4 | 612 | 4 | BI697743 | BI697743 603346835 |
| 41 | 323.4 | 25.3 | 769 | 7 | CO385967 | CO385967 AGENCOURT |
| 42 | 315.8 | 24.7 | 468 | 2 | BF930043 | BF930043 MR2-NT013 |
| 43 | 299.4 | 23.4 | 599 | 1 | AI568578 | AI568578 tn41a11.X |
| 44 | 291.2 | 22.8 | 682 | 5 | BX298130 | BX298130 BX298130 |
| 45 | 288.2 | 22.6 | 747 | 2 | BF178956 | BF178956 601808073 |

ALIGNMENTS

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LOCUS
DEFINITION
Homo sapiens PLA2G6 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY421137
ACCESSION
AY421137 GI:39777094
VERSION
AY421137.1 GI:39777094
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 2259)
Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Todd,M.A., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
AUTHORS
Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Todd,M.A., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="PLA2G6"
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Query Match 66.9%; Score 854.2; DB 9; Length 2259;
Best Local Similarity 99.7%; Pred. No. 4.7e-196;
Matches 856; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY 389 CACAGACTACAGATCTCATGCAATCTCCACGGCGCCGAGACCGAGCTTCACTCTGGG 448

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| Db | 1182 | CAGACAACTACAGGATCTCATGCAATCTCACGGGCCCGGAAGCCAGGGCTTCATCTGGG | 12411 |
| Qy | 449 | CTCCATGAGGGACCGAAGCGGACCCCAAGACCACTGCTGTGCTCTGATGAGAGAGAGT | 508 |
| Db | 1242 | CTCCATGAGGGACGGAAGCGGACCCCAAGACCACTGCTGTGCTCTGATGAGAGAGAGT | 13010 |
| Qy | 509 | GAAAGGCTCATCATCATCATCTCAAGCTCTCATGCGCCATCGAAGAGGCTCGGGTGTGGCCAC | 568 |
| Db | 1302 | GAAAGGCTCATCATCATCATCTCAAGCTCTCATGCGCCATCGAAGAGGCTCGGGTGTGGCCAC | 13610 |
| Qy | 569 | CAAGGACCTGTTTGACTGGGTGGCGGGGACCAAGCACTGGAGGCATCTTGCCCTTGGCCAT | 628 |
| Db | 1362 | CAAGGACCTGTTTGACTGGGTGGCGGGGACCAAGCACTGGAGGCATCTTGCCCTTGGCCAT | 14211 |
| Qy | 629 | TCCTGACAGTAAAGTTCATGAGCTTACATGACGCGGCATGTAAGTTCATGAGAGATGAGGT | 688 |
| Db | 1422 | TCCTGACAGTAAAGTTCATGAGCTTACATGAGCTTACATGAGAGATGAGGT | 14811 |
| Qy | 689 | GTTCCGGGGGCTCCAGGCCCTCAGTACGAGTCGGGGCCCTTGGAGGAGTTCTTGAACGGGAGTT | 748 |
| Db | 1482 | GTTCCGGGGGCTCCAGGCCCTCAGTACGAGTCGGGGCCCTTGGAGGAGTTCTTGAACGGGAGTT | 15411 |
| Qy | 749 | TGGGAGACACACCAAGATGACGAGAGCTCAAGAAACCCAAAGTGAATGCTGAACAGGACACT | 808 |
| Db | 1542 | TGGGAGAGACACCAAGATGACGAGAGCTCAAGAAACCCAAAGTGAATGCTGAACAGGAGCACT | 16010 |
| Qy | 809 | GTTCTGACCCGGAGCGGCTGAATCTCACTCTTCCGAACTTACGATGCTCCAGAAACTGT | 868 |
| Db | 1602 | GTTCTGACCCGGAGCGGCTGAATCTCACTCTTCCGAACTTACGATGCTCCAGAAACTGT | 16610 |
| Qy | 869 | CCGGAGGCTCTGTTTCAACACAGAAAGTTAACTCAGGCTTCAAGTCAAGCCTTCAAGACA | 928 |
| Db | 1662 | CCGGAGGCTCTGTTTCAACACAGAAAGTTAACTCAGGCTTCAAGTCAAGCCTTCAAGACA | 17211 |
| Qy | 929 | GCTGGTGTGGCGGGCGGCCCAAGGAGGAGGGGAGGCTCTTACTTACTTCCAGCCCAATGG | 988 |
| Db | 1722 | GCTGGTGTGGCGGGCGGCCCAAGGAGGAGGGGAGGCTCTTACTTACTTCCAGCCCAATGG | 17811 |
| Qy | 989 | GCGCTTCTTGACCGGTGGGCTGTTGGCCAAACAACCCACGCTGATGTCATGACCGAGAT | 10481 |
| Db | 1782 | GCGCTTCTTGACCGGTGGGCTGTTGGCCAAACAACCCACGCTGATGTCATGACCGAGAT | 18411 |
| Qy | 1049 | CCATGAGTACAAATACAGACCTGATCCGCAAGGTCAGGCTCAAAAGTGAAGAAACTCTGC | 11081 |
| Db | 1842 | CCATGAGTACAAATACAGACCTGATCCGCAAGGTCAGGCTCAAAAGTGAAGAAACTCTTC | 19010 |
| Qy | 1109 | CATCGTTGTCTCCCTGGGAGCAAGGAGGTCCCAACMAGTGCTGTGACTGTGTGATGT | 11681 |
| Db | 1902 | CATCGTTGTCTCCCTGGGAGCAAGGAGGTCCCAACMAGTGCTGTGACTGTGTGATGT | 19610 |
| Qy | 1169 | CTTCCCTGCCAGCAACCCCTGGAGCTGGCCAAAGCTTTTTTTGGGGCCAAAGAACTGGG | 12281 |
| Db | 1962 | CTTCCCTGCCAGCAACCCCTGGAGCTGGCCAAAGCTTTTTTTGGGGCCAAAGAACTGGG | 20211 |
| Qy | 1229 | CAAGATGGTGTGACTGT 1247 | |
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| RESULT 2 | | | |
| AY421138 | | | |
| LOCUS | AY421138 | 2259 bp | DNA linear GSS 17-DEC-2003 |
| DEFINITION | Pan troglodytes PLAZ6 gene, VIRUTAL TRANSCRIPT, partial sequence, | | |
| ACCESSION | AY421138 | | |
| VERSION | AY421138.1 | GI:39777095 | |
| KEYWORDS | GSS. | | |
| SOURCE | Pan troglodytes (chimpanzee) | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan. | | |
| REFERENCE | 1 (bases 1 to 2259) | | |
| AUTHORS | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejelirwal,A., | | |

| TITLE | JOURNAL | PUBMED | REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT | FEATURES | ORIGIN |
|-----------------------|--------------------------------------|---|-------------------------|---|---|---|---|---------------------|--------|
| gene titlos | Science 302 (5652), 1960-1963 (2003) | 14671302 | 2 (bases 1 to 2259) | Todd,M.A., Tanenbaum,D.M.,Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. | Interferring nonmetrical evolution from human-chimp-mouse orthologous | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | This sequence as made by sequencing genomic exons and ordering them based on alignment. | Location/Qualifiers | gene |
| source | 1..2259 | /organism="Pan troglodytes" | /mol_type="genomic DNA" | /db_xref="taxon:9598" | <1..>2259 | /gene="PLA2G6" | /locus_tag="HCOM7457" | | |
| Query Match | 64.1%; | Score 818.4; | DB 9; | Length 2259; | | | | | |
| Best Local Similarity | 95.7%; | Pred. No. 2,38-187; | | | | | | | |
| Matches 822; | Conservative 0; | Mismatches 37; | Indels 0; | Gaps 0; | | | | | |
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| Db | 1182 | CAGACNNNNNNNNNNNNCTCATGCACTCACTCCGCGGAAAGCAGGTCATCTGGG | 1241 | | | | | | |
| QY | 449 | CTCCATAGGAGGACGAGAAAGGAGACCAAGACCACTGCTGAGCTGTGATGAGAGAGAGT | 508 | | | | | | |
| Db | 1242 | CNCCATAGAGGATGAGAAAGGAGACCAAGACCACTGCTGCTGTGATGAGAGAGAGT | 1301 | | | | | | |
| QY | 509 | GAAAGGCTCATCATCATCCAGCTCCTCATGCGCATGAGAAAGGCTTGGGTGTGGCCAC | 568 | | | | | | |
| Db | 1302 | GAAAGGCTCATCATCATCCAGCTCCTCATGCGCATGAGAAAGGCTTGGGTGTGGCCAC | 1361 | | | | | | |
| QY | 569 | CAAGGACCTCTTTGACCTGGGTGGGGGACACAGACCTGAGAGCATCTCGGCTCGGCAT | 628 | | | | | | |
| Db | 1362 | CAAGGACCTCTTTGACCTGGGTGGGGGACACAGACCTGAGAGCATCTCGGCTCGGCAT | 1421 | | | | | | |
| QY | 629 | TCTGCACAGTAAGTCATGAGCTTACATGACGCGGAGTACTTTCGATGAGAGATGAGT | 688 | | | | | | |
| Db | 1422 | TCTGCACAGTAAGTCATGAGCTTACATGACGCGGAGTACTTTCGATGAGAGATGAGT | 1481 | | | | | | |
| QY | 689 | GTTCCGGGGGCTCCAGGCGCTTACGAGTGGGGGCCCCCTGAGAGATTCTTGAAGCGGAGTT | 748 | | | | | | |
| Db | 1482 | GTTCCGGGGGCTCCAGGCGCTTATGAGTGGGGGCCCCCTGAGAGATTCTTGAAGCGGAGTT | 1541 | | | | | | |
| QY | 749 | TGGGAGACCAACCAAGATGACGAGCCAGAGAACCAAGGTGATGTGACAGGAGCACT | 808 | | | | | | |
| Db | 1542 | TGGGAGACCAACCAAGATGACGAGCCAGAGAACCAAGGTGATGTGACAGGAGCACT | 1601 | | | | | | |
| QY | 809 | GTCGACCGGACGCGGCTGAATCTCACTTTCCGGAATTACGATGCTCCAGAACTGT | 868 | | | | | | |
| Db | 1602 | NNNNNACCGGACGCGGNNNNNANCTCCACTCTTCGAGANNNACATGCTCCAGAACTGT | 1661 | | | | | | |
| QY | 869 | CCGGAGGCTCTGTTTCAACAGAACTTTAATCTCAAGCTTCCACTCAGCCCTAGAGCA | 928 | | | | | | |
| Db | 1662 | CCGGAGGCTCTGTTTCAACAGAACTTTAATCTCAAGCTTCCACTCAGCCCTAGAGCA | 1721 | | | | | | |
| QY | 929 | GCTGATGTGGCGGGCGGCGCGAGACAGCGGGGAGCTCTTAATTAATCTTCGAGCCAAATG | 988 | | | | | | |
| Db | 1722 | GCTGATGTGGCGGGCGGCGCGAGAGCAAGGGGAGCTCTTAATTAATCTTCGAGCCAAATG | 1781 | | | | | | |
| QY | 989 | GCGCTTCTTGACGCTGGGCTGTTGGCCAAACACCCACGCTGATGTCATGACCGAGAT | 1048 | | | | | | |

Db 1782 GGGCTTCTGGAAGGAGGCTGCTGGCAACACCAGGCTGGATCCATGACCGAGAT 1841
 Qy 1049 CCATGATACATCAGGACCTGATCCGCAAGGCTCAGGCCCAAGGTGAAGAACTCTC 1108
 Db 1842 CCATGATACATCAGGACCTGATCCGCAAGGCTCAGGCCCAAGGTGAAGAACTCTC 1901
 Qy 1109 CATTGTTGTCCTCTGGGAGCAGGAGGATCCCAAGATGCTGTGACCTGTGTGATGT 1168
 Db 1902 CATTGTTGTCCTCTGGGAGCAGGAGGATCCCAAGATGCTGTGACCTGTGTGATGT 1961
 Qy 1169 CTTCCGTCCTCAGCAACCCCTGGAGCTGGCCCAAGACTGTTTGGGCGCAAGAACTGGG 1228
 Db 1962 CTTCCGTCCTCAGCAACCCCTGGAGCTGGCCCAAGACTGTTTGGGCGCAAGAACTGGG 2021
 Qy 1229 CAAGATGTGTGACTGT 1247
 Db 2022 CAAGATGTGTGACTGT 2040

RESULT 3

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 LOCUS 602730060F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4873766 5',
 DEFINITION mRNA sequence.

ACCESSION Bg751481 GI:14062134
 VERSION Bg751481
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 914) NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCMT752 row: g column: 15
 High quality sequence stop: 804.
 Location/Qualifiers

FEATURES

source

1..914
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4873766"
 /issue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_43"
 /note="Organ: eye; Vector: pORF7, Site_1: XhoI, Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 60.4%; Score 770.8; DB 4; Length 914;
 Best Local Similarity 97.9%; Pred. No. 6.6e-176;
 Matches 834; Conservative 0; Mismatches 12; Indels 6; Gaps 5;
 Qy 389 CACAGAACTACAGATCTCATGCACTCTCAACGGCCCGAAGCAGGTTTCATCTGGG 448
 Db 63 CAGCAACTACAGATCTCATGCACTCTCAACGGCCCGAAGCAGGTTTCATCTGGG 122

Qy 449 CTCATGAGGAGCAGAGAGCGGACCCACGACCACTGTGTGCTGATGAGAGAGAT 508
 Db 123 CTCATGAGGAGCAGAGAGCGGACCCACGACCACTGTGTGCTGATGAGAGAGAT 182
 Qy 509 GAAAGCCTCATCATCATCAAGCTCTCATTCGCAATGAGAAAGCCTCGGTTGCGCAC 568
 Db 183 GAAAGCCTCATCATCATCAAGCTCTCATTCGCAATGAGAAAGCCTCGGTTGCGCAC 242
 Qy 569 CAAGACCTGTTGATCGGTTGCGGCGCACAGCATGAGAGGATCTGAGCCCTGCGCAT 628
 Db 243 CAAGACCTGTTGATCGGTTGCGGCGCACAGCATGAGAGGATCTGAGCCCTGCGCAT 302
 Qy 629 TCGCAAGTATGATCATGAGCTTACATGCGCGCATGATCTTTCGATGAGATAGAT 688
 Db 303 TCGCAAGTATGATCATGAGCTTACATGCGCGCATGATCTTTCGATGAGATAGAT 362
 Qy 689 GTTCCGGGCTCCAGGCGCTTACAGAGTCGAGGCGCTTGAAGAGTTCTGAAGCGGAGTT 748
 Db 363 GTTCCGGGCTCCAGGCGCTTACAGAGTCGAGGCGCTTGAAGAGTTCTGAAGCGGAGTT 422
 Qy 749 TGGGAGACACCAAGATGACGAGCTCAGAGAAACCAAGTGTATCTGACAGGACACT 808
 Db 423 TGGGAGACACCAAGATGACGAGCTCAGAGAAACCAAGTGTATCTGACAGGACACT 482
 Qy 809 GTCTGACCGGACCGGCTGAACTCCACCTCTCCGGAATACAGATGCTCCAGAACTGT 868
 Db 483 GTCTGACCGGACCGGCTGAACTCCACCTCTCCGGAATACAGATGCTCCAGAACTGT 542
 Qy 869 CCGGAGCCTCGTTTCAACAGAACCTTAACTCAGGCTCCAGCTCAGGCTCAGACCA 928
 Db 543 CCGGAGCCTCGTTTCAACAGAACCTTAACTCAGGCTCCAGCTCAGGCTCAGACCA 602
 Qy 929 GCTGTGTGCGGCGCGCGCGCGGAGACGAGCGGCGAGCTCTTACTTACTTCGAGACCAATG 988
 Db 603 GCTGTGTGCGGCGCGCGCGGAGACGAGCGGCGAGCTCTTACTTACTTCGAGACCAATG 661
 Qy 989 GGGCTTCTGGAAGGAGGAGGCTGTGGCAACACCCGCTGATGCCATGACCGAGAT 1048
 Db 662 GGGCTTCTGGAAGGAGGAGGCTGTGGCAACACCCGCTGATGCCATGATGCCAGAT 721
 Qy 1049 CCATGATACATCAGGACCTGATCCGCAAGGCTCA-GGCCCAAGAGTGAAGAACTCT 1107
 Db 722 CCATGATACATCAGGACCTGATCCGCAAGGCTCAAGGCTCAAGGCTCAAGAACTCT 781
 Qy 1108 CCATGTTGTTCTCTCTGGGAGCAGGAGGTCCTCCCAAGTGTGTGATG 1167
 Db 782 CCATGTTGTTCTCTCTGGGAGCAGGAGGT-CCCAAGTGTGTGATG 840
 Qy 1168 TCTTCGTCCTCAGCAACCCCTGGAGCTGGCCAAAGCTGTTTGGGCGCAAGAACTGG 1227
 Db 841 TCTTCGTCCTCAGCAACCCCTGGAGCTGGCCAAAGCTG--GTTGGGCGCAAGAACTGG 897
 Qy 1228 GCAAGATGTGG 1239
 Db 898 GCAAGATGTGG 909

RESULT 4

Bg746419 776 bp mRNA linear EST 15-MAY-2001
 LOCUS 602703692F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4856903 5',
 DEFINITION mRNA sequence.

ACCESSION Bg746419 GI:14057072
 VERSION Bg746419
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 776) NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM1708 row: h column: 24
 High quality sequence stop: 766.
 Location/Qualifiers

FEATURES

source

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 /organism="Homo sapiens"
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 /clone="IMAGE:4856903"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 15"
 /note="Organ: colon; Vector: pORF7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 59.8%; Score 763.8; DB 4; Length 776;
 Best Local Similarity 99.7%; Pred. No. 3.2e-174;
 Matches 765; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 473 CCACGACCACTTCTGCTGTGATGAGAGAGAGTAAAGGCTCATCATCATCCAGCT 532
 DB 6 CCACGACCACTTCTGCTGTGATGAGAGAGAGTAAAGGCTCATCATCATCCAGCT 65
 QY 533 CCTCATCGCCATGAGAGAGCTCGGGTGGGCCAACCAAGACCTGTTTGACTGGGTCG 592
 DB 66 CCTCATCGCCATGAGAGAGCTCGGGTGGGCCAACCAAGACCTGTTTGACTGGGTCG 125
 QY 593 GGGCAGCAGCACTGAGAGCACTCTGGCCCTGACCATTCTGACAGTAAGTCATGAGCTTA 652
 DB 126 GGGCAGCAGCACTGAGAGCACTCTGGCCCTGACCATTCTGACAGTAAGTCATGAGCTTA 185
 QY 653 CATGCCGCGATGATCTTTCGATGAGAGATGAGTGTTCGGGGCTCCAGGCCCTTACGA 712
 DB 186 CATGCCGCGATGATCTTTCGATGAGAGATGAGTGTTCGGGGCTCCAGGCCCTTACGA 245
 QY 713 GTCCGGGCCCCCTGAGAGAGTTCCTGAAGCGGAGTTTGGGAGACACCAAGATGACGA 772
 DB 246 GTCCGGGCCCCCTGAGAGAGTTCCTGAAGCGGAGTTTGGGAGACACCAAGATGACGA 305
 QY 773 CGTCAGAGAAACCAAGGTGATGCTGACAGAGACATGTCTGACCGAGCCGCTGAAGT 832
 DB 306 CGTCAGAGAAACCAAGGTGATGCTGACAGAGACATGTCTGACCGAGCCGCTGAAGT 365
 QY 833 CCACCTCTTCCGGAATCAATGATCTCCAGAACTGTTCGGGAGCCTGTTTCAACCGAA 892
 DB 366 CCACCTCTTCCGGAATCAATGATCTCCAGAACTGTTCGGGAGCCTGTTTCAACCGAA 425
 QY 893 CGTTAAGCTCAGAGCTCAGCTCAGCCCTCAGACAGCTGATGAGCGGCGGCGGCGAAG 952
 DB 426 CGTTAAGCTCAGAGCTCAGCTCAGCCCTCAGACAGCTGATGAGCGGCGGCGGCGAAG 485
 QY 953 CAGCGGGGCACTCTTAATTCTCCAGACCAATGGGCGCTTCCTGAGCGGTGGCTGTT 1012
 DB 486 CAGCGGGGCACTCTTAATTCTCCAGACCAATGGGCGCTTCCTGAGCGGTGGCTGTT 545
 QY 1013 GGGCAACCAACCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1072
 DB 546 GGGCAACCAACCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 605

QY 1073 CCAGAGGTCAGAGCCCAAGAGTGAAGAACTCTCATCTGTTCTCCCTGGGAGCAG 1132
 DB 606 CCGCAAGGTCAGAGCCCAAGAGTGAAGAACTCTCATCTGTTCTCCCTGGGAGCAG 665
 QY 1133 GAGGTCCCAAGAGTCTGTGATCCTGTGTGATGTTCTTCCGTCAGCAACCTCTGGGA 1192
 DB 666 GAGGTCCCAAGAGTCTGTGATCCTGTGTGATGTTCTTCCGTCAGCAACCTCTGGGA 725
 QY 1193 GCTGGCCAGACATGTTTGGGGGCAAGAACTGGGCAAGATGATGATG 1239
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RESULT 5
 BM805376 1042 bp mRNA linear EST 05-MAR-2002
 LOCUS BM805376
 DEFINITION AGENCOURT_6499717 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728708
 5', mRNA sequence.
 ACCESSION BM805376
 VERSION BM805376.1 GI:19122199
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Invitrogen
 CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM12724 row: n column: 05
 High quality sequence stop: 688.
 Location/Qualifiers

FEATURES

source

1. 1042
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 /mol_type="mRNA"
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 /clone="IMAGE:5728708"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 124"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV
 (destroyed); Site 2: NotI; RNA source male hippocampus,
 age 27. Library is oligo-dT primed and directionally
 cloned (EcoRV site is destroyed upon cloning). Average
 insert size 1.4 kb. Insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."

ORIGIN

Query Match 59.5%; Score 759.2; DB 4; Length 1042;
 Best Local Similarity 99.5%; Pred. No. 4.4e-173;
 Matches 761; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 508 TGAAGGCTCATCATCATCCAGCTCCTATGCGCATTCAGAAAGGCTCGGGTGGCCA 567
 DB 1 TGAAGGCTCATCATCATCCAGCTCCTATGCGCATTCAGAAAGGCTCGGGTGGCCA 60
 QY 568 CCAAGACCTGTTGACTGGGTGGCGGACCAAGCACTGAGAGCATCTGAGCCCTGGCCA 627
 DB 61 CCAAGACCTGTTGACTGGGTGGCGGACCAAGCACTGAGAGCATCTGAGCCCTGGCCA 120
 QY 628 TTCTGACAGTAAGTCATGAGCCTTACATGCGGCGCATGTACTTTGCGATGAAGATGAGG 687

QY 1259 AGACGGCGCGCCG 1271
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 782 AGACGGCGCGCTG 794

RESULT 7
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 LOCUS
 DEFINITION Rattus norvegicus cDNA clone IMAGE:5598166, containing frame-shift errors.
 ACCESSION BC061866
 VERSION BC061866.1 GI:38511544
 KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Rahe, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richardson, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Lu, X., Gibbs, R.A., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butler, D.L., Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Scherneck, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
 JOURNAL MEDLINE
 PUBMED 12388257
 12477932
 2 (bases 1 to 3010)
 Strausberg, R.
 Direct Submission
 Submitted (05-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeff Green/Patruu Kondalah, NCI.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc.mgc@nih.gov
 Akhtar, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaapi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stancirpop, S., Thomas, P.J., Touchman, J.W., Tsurenko, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

REMARK
 COMMENT
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
 Series: IRAC Plate: 137 Row: b Column: 23

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 /clone_idb="NCI_CGAP_Pr49"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6.1"

ORIGIN

Query Match 54.7%; Score 698.6; DB 3; Length 3010;
 Best Local Similarity 86.2%; Pred. No. 2,7e-158;
 Matches 773; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 376 CTGCTCTGTGCTTCAAGAGATCTCATGATCTCTGACATCTCAAGGCGCGGAAGCCAG 435
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 Db 1340 CTTCAGAGATCAGACAGACAGCTTCAGACCTCATGCCCTTCGAGCCCGAGACG 1399

QY 436 CGTTTCCTCTGCTTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
 |||||
 Db 1400 CGTTTCCTCTGAGCTTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459

QY 496 ATGAG 555
 |||||
 Db 1460 AGGAG 1519

QY 556 CGGAGTGGCCACCAAG 615
 |||||
 Db 1520 CAGGTGGCTACCAAG 1579

QY 616 TGGCCCTGACCATTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 675
 |||||
 Db 1580 TGGCCCTGACCATTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1639

QY 676 TGAAG 735
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 Db 1640 TGAAG 1699

QY 736 TGAAG 795
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 Db 1700 TGAAG 1759

QY 796 TGAAG 855
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 Db 1760 TGAAG 1819

QY 856 CTTCAG 915
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 Db 1820 CCCAG 1879

QY 916 AGCCCTCAG 975
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 Db 1880 AGCCCTCAG 1939

QY 976 TCGAG 1035
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 Db 1940 TCGAG 1999

QY 1036 CCATGAG 1095
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 Db 2000 CCATGAG 2059

QY 1096 TGAAG 1155
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 Db 2060 TGAAG 2119

QY 1156 CCTGTGTGATGATCTTCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1215

Db 2120 CCTGTAGATGCTTTCCTCCAGCAACCTTGGAGACCTGGCCAGACATGTTTGGAG 2179

Qy 1216 CCAGAGAACTGGGCAAGATGCTGTGATCTGTTGACGAGATCCAGACGGGCGCCGG 1272

Db 2180 CCAGAGAACTGGGCAAGATGCTGTGATCTGTTGACGAGATCCAGATGAGGCGGCGCTG 2236

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DEFINITION genomic survey sequence.
ACCESSION AY421139
VERSION AY421139.1 GI:39777096
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2259)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, D.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)

JOURNAL PUBLISHED 14671302
2 (bases 1 to 2259)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, D.J.,
Adams, M.D. and Cargill, M.
Direct Submissions
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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ORIGIN
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Best Local Similarity 88.2%; Pred. No. 5e-158;
Matches 758; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 389 CACAGAACTACAGATCTCATGACATCTCAGCGGCGCCGGAAGCGCTTACCTCGGG 448

Db 1182 CAAGCAGCTTCAGATCTCATGCTCCATCTCTCAGAGCCCGAAGCCAGCTTACCTCGAG 1241

Qy 449 CTCATGAGGAGCAGAAAGCGGACCCAGACACCTGCTGTGCTGAGTGAAGAGAGT 508

Db 1242 CTCATGAGGAGCAGAAAGCGGAGTCCAGACACCTGCTGTGAGTGAAGAGAGT 1301

Qy 509 GAAAGGCTCATATCATCATGCTCCATGCGCATGAGAAAGGCTCGGGTGTGGCCAC 568

Db 1302 GAAAGGCTCGTATATATCAAGCTTCTCATGCGCATGAGAAAGGCTCGGGAGTGGCAC 1361

Qy 569 CAAGACCTGTGACTGCTGGCGGACACAGACATGAGGACATCTGCGCCCTGGCCAT 628

Db 1362 CAAGACCTTGTGACTGCTGGCGGACACAGACATGAGGACATCTGCGCCCTGGCCAT 1421

Qy 629 TCTGCAAGTAAGTCCATGCGCTTACATGCGCGGAGCATCTTTCGATGAAGATGAGT 688

Db 1422 TCTGCAAGTAAGTCCATGCGCTTACATGCGCGGAGCATCTTTCGATGAAGATGAGT 1481

Qy 689 GTTCCGGGCTCCAGGCGCTTACAGATGCTGGGCGCCCTGAGAGAGTCTCTGAGCGGAGTT 748

Db 1482 GTTTCGGGCTCCAGGCGCTTACAGATGCTGGGCGCCCTGAGAGAGTCTCTGAGCGGAGTT 1541

Qy 749 TGGGAGCACCACCAAGATGACGAGCTGACAGAAACCCAAAGTATCTGACAGGACACT 808

Db 1542 TGGGAGCACCACCAAGATGACAGATGACAGATGACAGATGACAGATGACAGATGAC 1601

Qy 809 GTCTGACCGGACGCGGCTGAACTCCACTCTTCCGGAACCTAGATGCTCCGAAACTGT 868

Db 1602 GTCTGACCGGACGCGGCTGAACTCCACTCTTCCGGAACCTAGATGCTCCGAAACTGT 1661

Qy 869 CCGGAGCGCTCGTTTCAACAGAACTTAACTCAGGCTCCAGCTCAGGCGCTCAGACCA 928

Db 1662 TCGAGAGCCCGCTGCAACCAAACTTAACTCAGGACCACTCAGGCTCAGACCA 1721

Qy 929 GCTGTGTGTGGCGGCGCGCCGGAAGCAGCGGCGGAGCTCTACTTACTTCCAGCCATG 988

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Qy 989 GCGCTTCTGAGAGGCTGTGCTGTGGCCAAACCCCAAGCTGAGATGCCATGCCAGAT 1048

Db 1782 ACCTTCTGAGATGAGGCTGTGCTGTGGCCAAACCCCAAGCTGAGATGCCATGCCAGAT 1841

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Db 1842 CCATGAGTACATCAAGACCTGATCCGCAAGGCTCAGGCAACAGGTAAGAACTCTC 1901

Qy 1109 CATGCTGTGCTCCTCGGGGACAGGAGGCTCCCAAGTGCCTGTGATCTGTGATGT 1168

Db 1902 CATGCTGTGCTCCTCGGGGACAGGAGGCTCCCAAGTGCCTGTGATCTGTGATGT 1961

Qy 1169 CTTCCTGCTCCAGAACCCCTGGGAGCTGGCCAAAGACTGTTTGGGCGCAAGAACTGG 1228

Db 1962 CTTCCTGCTCCAGAACCCCTGGGAGCTGGCCAAAGACTGTTTGGGCGCAAGAACTGG 2021

Qy 1229 CAAGATGTGTGTGAGTGT 1247

Db 2022 CAAGATGTGTGTGAGTGT 2040

RESULT 9
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VERSION BG328183.1 GI:13134621
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 815)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-rc@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
<http://image.llnl.gov>
Plate: LNCM1233 row: d column: 14
High quality sequence stop: 753.
FEATURES
Location/Qualifiers
source 1..815
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"


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/clone="IMAGE:4546525"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC.15"
/notes="Organ: Colon; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

```

ORIGIN

```

Query Match      52.6%; Score 671.6; DB 4; Length 815;
Best Local Similarity 95.6%; Pred. No. 7.4e-152;
Matches 767; Conservative 0; Mismatches 24; Indels 11; Gaps 7;

QY 473 CCAAGACCACTGCTGCTGCTGATGAGAGAGTAAAGGCTCATCATCCAGCT 532
DB 6 CCAAGACCACTGCTGCTGCTGATGAGAGAGTAAAGGCTCATCATCCAGCT 65
QY 533 CCGATGCGCATGAGAGAGGCTCGGGTGGCCACCAAGGACCTGTTGACTGGGTGGC 592
DB 66 CCGATGCGCATGAGAGAGGCTCGGGTGGCCACCAAGGACCTGTTGACTGGGTGGC 125
QY 593 GGGCACCAGCAGTGAAGGCACTGCGCTGCGCATTCGACAGTAAGTCAATGAGCTTA 652
DB 126 GGGCACCAGCAGTGAAGGCACTGCGCTGCGCATTCGACAGTAAGTCAATGAGCTTA 165
QY 653 CATGCGCGCATGTACTTTGCGATGAAGATGAGGTGTTCCGGGGCTCCAGGCTTACGA 712
DB 186 CATGCGCGCATGTACTTTGCGATGAAGATGAGGTGTTCCGGGGCTCCAGGCTTACGA 245
QY 713 GTGGGGGGCCCTGGAGAGAGTTCCTGAAGCGGGAGTTTGGGAGAGACCAAGATGAGGA 772
DB 246 GTGGGGGGCCCTGGAGAGAGTTCCTGAAGCGGGAGTTTGGGAGAGACCAAGATGAGGA 305
QY 773 CGTCAGAGAAACCAAGGTGATGCTGACAGGAGCACTGTCTGACCGGAGCGGCTGACT 832
DB 306 CGTCAGAGAAACCAAGGTGATGCTGACAGGAGCACTGTCTGACCGGAGCGGCTGACT 365
QY 833 CCACCTTTTCCGGAATCAAGATGCTCCAGAACTGTCCGGAGCTTGTTCAACCAAGAA 892
DB 366 CCACCTTTTCCGGAATCAAGATGCTCCAGAACTGTCCGGAGCTTGTTCAACCAAGAA 425
QY 893 CGTTAACCTAGAGCTCAGCTCAGGCTCAGACCAAGCTGATGAGGGGCGGCGGAG 952
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QY 953 CAGCGGGGAGCTCTACTTACTTCCAGCCCAATGGCGCTTCTGAGCGGTGGCTGTT 1012
DB 486 CAGCGGGGAGCTCTACTTACTTCCAGCCCAATGGCGCTTCTGAGCGGTGGCTGTT 545
QY 1013 GGGCAACAAACCCAGCTGATGCTGATGACCGAGATCATGATGATCAATCAAGACTGAT 1072
DB 546 GGGC-AACAACCAACCCAGCTGATGCTGATGACCGAGATCATGATGATCAATCAAGACTGAT 603
QY 1073 CCGCAAGGGTCAAGGCAAGAGTGAAGAACTCTCATGTTGTTCCCTGGGGAGAG 1132
DB 604 CCGCAAGGGTCAAGGCAAGAGTGAAGAACTCTCATGTTGTTCT-CTTGGGAGAGG 662
QY 1133 GAGGTCCCAACAAGTGTGATGCTGTGATGATGTTCTCCGTCACAGAACCTCTGGGA 1192
DB 663 GAGGT-CCCAACAAGTGTGATGCTGTGATGATGTTCTCCGTCACAGAA-CCCTGGGA 720
QY 1193 GCTGGCCAACACTGTTTGGGGCAAGAACTGGGGCAAGTGGTGTGACTGTTGCAC 1252
DB 721 GCTGGC--AGACTGTTTGGGG--CAAGAACTGGGGCAAGTGGTGTG-CCGGTGGCC 774
QY 1253 GGATCCAGAGGGGGCGCGGAA 1274
DB 775 GGTTCCAAAGGGGGGCGTGA 796

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RESULT 10
CA489815
LOCUS
DEFINITION
CA489815 910 bp mRNA linear EST 14-NOV-2002
AGENCOURT_10810716 MABCL Homo sapiens cDNA clone IMAGE:6722303 5',
mRNA sequence.
ACCESSION
CA489815
VERSION
CA489815.1 GI:24952606
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 910)
NIH-MGC http://imgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: Agencourt Bioscience Corporation (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLAM4284 row: m column: 23
High quality sequence stop: 612.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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hTERT-HMEL, LNCaP"
/lab_host="EMDH10B"
/clone_lib="MABCL"
/notes="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Straubeberg,
Bungkok Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

```

FEATURES

source

ORIGIN

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Query Match      51.3%; Score 653.2; DB 6; Length 910;
Best Local Similarity 99.3%; Pred. No. 2.2e-147;
Matches 677; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 593 GGGCACCAGCAGTGAAGGCACTCTGGCCCTGGGCATTCGCAAGTAAGTCATGGCTTA 652
DB 1 GGGCACCAGCAGTGAAGGCACTCTGGCCCTGGGCATTCGCAAGTAAGTCATGGCTTA 60
QY 653 CATGCGCGCATGTACTTTGCGATGAAGATGAGTGTCCGGGGCTCCAGGCTTACGA 712
DB 61 CATGCGCGCATGTACTTTGCGATGAAGATGAGTGTTCGGGGCTCCAGGCTTACGA 120
QY 713 GTGGGGGGCCCTGGAGAGTTCCTGAAGCGGAGTTTGGGGAGCACCAAGATGACGA 772
DB 121 GTGGGGGGCCCTGGAGAGTTCCTGAAGCGGAGTTTGGGGAGCACCAAGATGACGA 180
QY 773 CGTCAGAGAAACCAAGTGTGATGCTGACAGGAGACACTGTCTGACCGGACGCGGTAACT 832
DB 181 CGTCAGAGAAACCAAGTGTGATGCTGACAGGAGACACTGTCTGACCGGACGCGGTAACT 240
QY 833 CCACCTTTTCCGGAATCAAGATGCTCCAGAACTGTCCGGAGCTCGTTTCAACAGAA 892
DB 241 CCACCTTTTCCGGAATCAAGATGCTCCAGAACTGTCCGGAGCTCGTTTCAACAGAA 300

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QY 893 CGTTAAGCTGAGGCTTCAGCTGAGCCCTGAGCAAGCTGTGTGGGGGCGGAG 952
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 QY 953 CAGCGGGGAGCTCTACTTACTTCCGACCCAAATGGGCGCTTCGAGCGGTGGCTGT 1012
 DB 361 CAGCGGGGAGCTCTACTTACTTCCGACCCAAATGGGCGCTTCGAGCGGTGGCTGT 420
 QY 1013 GGGCAACAAACCCCAAGCTGATGATGATGATGATGATGATGATGATGATGAT 1072
 DB 421 GGGCAACAAACCCCAAGCTGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 1073 CGGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1131
 DB 481 CGGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 540
 QY 1132 GAGAGTCCCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1191
 DB 541 GAGAGTCCCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 600
 QY 1192 AGCTGGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1250
 DB 601 AGCTGGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 1251 AGGATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1272
 DB 661 AGGATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 682

RESULT 11
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 LOCUS 60259874F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4707491 5',
 DEFINITION mRNA sequence.
 ACCESSION BG575678
 VERSION BG575678.1 GI:13583331
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 636)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/BTP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLM10577 row: 9 column: 12
 High quality sequence start: 2
 High quality sequence stop: 631.
 Location/Qualifiers
 1. 636

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:4707491"
 /tissue_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1b="NIH MGC 87"
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 Site 2: Salt; Cloned unidirectionally; oligo-dt primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.4%; Score 631.4; DB 4; Length 636;
 Best Local Similarity 99.8%; Pred. No. 3.9e-142;
 Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 401 GGATCTCATGCAATCTCAAGGAGCCGGAAGCCAGGCTTCATCTGGGCTCATGAGGA 460
 DB 1 GGATCTCATGCAATCTCAAGGAGCCGGAAGCCAGGCTTCATCTGGGCTCATGAGGA 60
 QY 461 CGAAGAGCGGAGCCCAAGCACTCTGCTGTGCTGTGATGAGAGAGAGAGAGAGAG 520
 DB 61 CGAAGAGCGGAGCCCAAGCACTCTGCTGTGCTGTGATGAGAGAGAGAGAGAGAG 120
 QY 521 CATCATCAAGCTCTCATGAGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 580
 DB 121 CATCATCAAGCTCTCATGAGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 581 TGAAG 640
 DB 181 TGAAG 240
 QY 641 GTCCATGAGCTCATATGCGGAGCATGTACTTTGCGATGAGAGAGAGAGAGAGAG 700
 DB 241 GTCCATGAGCTCATATGCGGAGCATGTACTTTGCGATGAGAGAGAGAGAGAGAG 300
 QY 701 CAGGAGCTCAAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 760
 DB 301 CAGGAGCTCAAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 QY 761 CAAGATGAG 820
 DB 361 CAAGATGAG 420
 QY 821 GCGGAGTGAAGTCAAGCTCTTCCGAACTGATGATGATGATGATGATGATGATGAT 880
 DB 421 GCGGAGTGAAGTCAAGCTCTTCCGAACTGATGATGATGATGATGATGATGATGAT 480
 QY 881 TTTCAGCAAGAGAGTCAAGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 940
 DB 481 TTTCAGCAAGAGAGTCAAGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 540
 QY 941 GCGGAGCCGAG 1000
 DB 541 GCGGAGCCGAG 600
 QY 1001 CGGTGGGCTGTGGCCCAAGCAAGCCCAAGCTGGA 1033
 DB 601 CGGTGGGCTGTGGCCCAAGCAAGCCCAAGCTGGA 633

RESULT 12
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 LOCUS 602730892F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4874542 5',
 DEFINITION mRNA sequence.
 ACCESSION BG752410
 VERSION BG752410.1 GI:14063063
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 658)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:

| | | | |
|----|-----|--|-----|
| QY | 515 | CCTCATCATCATCCAGCTCTTCATCGCCATCGAAGAGCTCGGGTGTGGCCACCAAGGA | 574 |
| Db | 481 | CCTCATCATCATCCAGCTCTTCATCGCCATCGAAGAGCTCGGGTGTGGCCACCAAGGA | 540 |
| QY | 575 | CCTGTTTGACTGGGTGGGGGACCAAGCACTGGAGGCATCTGTGGCCCTGGCCATTCTGCA | 634 |
| Db | 541 | CCTGTTTGACTGGGTGGGGGACCAAGCACTGGAGGCATCTGTGGCCCTGGCCATTCTGCA | 600 |
| QY | 635 | CAGTAAGTCCATGGCCTTACATGGCGGGCATGTACTTTGCGCATGAAGATGAGGTTCGG | 694 |
| Db | 601 | CAGTAAGTCCATGGCCTTACATGGCGGGCATGTACTTTGCGCATGAAGATGAGGTTCGG | 660 |
| QY | 695 | GGGCTCCAGGCCCTTACGAGTGGGG--CCCTGGAGAGTTCCTGAAGCGGAG--TTTG | 750 |
| Db | 661 | GGGCTCCAGGCCCTTACGAGTGGGGCCCTCGAGAGAAATCCCTGAAGCGGAGTTTGG | 720 |
| QY | 751 | GGGAGCAACCAAGATGA--CGGACTGANGAAGAACCAAGGTGATCTGTACAGGGACACTG | 809 |
| Db | 721 | GGGAGCAACCAAGATGA--CGGACTGANGAAGAACCAAGGTGATCTGTACAGGGAGAA | 780 |
| QY | 810 | TCTGACGGGAGCCGGCTG | 828 |
| Db | 781 | ACTGCTTGAACCCGGCAG | 799 |

| RESULT 14 | |
|------------|--|
| LOCUS | BG576680 |
| DEFINITION | BG576680 741 bp mRNA linear EST 10-APR-2001 6025597576P1 NIH_MGC_87 Homo sapiens CDNA clone IMAGE:4705347 5', |

| | | |
|----------|----------------------|-------------|
| VERSION | BG576680.1 | GI:13584333 |
| KEYWORDS | EST. | |
| SOURCE | Homo sapiens (human) | |
| ORGANISM | Homo sapiens | |

| REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
|--------------------|---|---|--|---------|
| 1 (bases 1 to 741) | NIH-MGC | http://mgc.ncbi.nih.gov/ . | National Institutes of Health, Mammalian Gene Collection (MGC) | |
| | | Unpublished (1999) | | |
| | Contact: Robert Strausberg, Ph.D. | | | |
| | Email: cranba-remail@nih.gov | | | |

ILISBE Procurement: UCIn/DIRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plates: LNL0574 Row: 9 Column: 20
High quality sequence set: 741.

| FEATURES | Location/Qualifiers |
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| source | 1. .741 |

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/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_87"
/notes="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI,
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1,383 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC library."

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| Query | Match | Score | DB | Length |
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| Best Local Similarity | 87.3% | Pred. No. 4,1e-12; | | |
| Matches 647; | Conservative | 0; | Mismatches 3; | Indels 91; |
| | | | | Gaps 1 |
| 401 | GGATCTCATGACATCTCAGCGGCCGGAAGCAGCGTTTCATCTCTGGGCTCATGAGGA | 460 | | |

| | | | |
|----|------|--|------|
| Db | 1 | GGATCTCATGCACATCTCACGGGCGCCGGGAAGCCAGCGTTATCTGGGGCTTCATGAGGGA | 60 |
| QY | 461 | CGAAGAGCGAACCACGACCACTGTGTGTGCTTGATGAGAGAGAGTGAAGGCTTCAT | 520 |
| Db | 61 | CGAAGAGCGAACCACGACCACTGTGTGTGCTTGATGAGAGAGAGTGAAGGCTTCAT | 120 |
| QY | 521 | CATCATCGAGTCTCTCATCGGCATCGAAGAGGCTCGGGGTGTGGCCACCAAGACCTGTT | 580 |
| Db | 121 | CATCATCGAGTCTCTCATCGGCATCGAAGAGGCTCGGGGTGTGGCCACCAAGACCTGTT | 180 |
| QY | 581 | TGACGTGGGTGGCGGGGACCAAGCACTGAGAGGATCTGGGCGCTTGCCCATTCGCAAGTTAA | 640 |
| Db | 181 | TGACGTGGGTGGCGGGGACCAAGCACTGAGAGGATCTGGGCGCTTGCCCATTCGCAAGTTAA | 240 |
| QY | 641 | GTCCATGGCCCAACATGCGCGGCGCATGTACTTTCCGATGAAGGATGAGGTGTTCCGGGCTC | 700 |
| Db | 241 | GTCCATGGCCCAACATGCGCGGCGCATGTACTTTCCGATGAAGGATGAGGTGTTCCGGGCTC | 300 |
| QY | 701 | CAGGCCCTTACGAGTCGGGGGCCCTCTGAGAGATTCTGAAGCGGGAGTTTGGGAGACAC | 760 |
| Db | 301 | CAGGCCCTTACGAGTCGGGGGCCCTCTGAGAGATTCTGAAGCGGGAGTTTGGGAGACAC | 360 |
| QY | 761 | CAAGATGACGAGCGTCAAGAAACCCAA-----787 | |
| Db | 361 | CAAGATGACGAGCGTCAAGAAACCCAAATTGGAACCAATCTGACATCTCTCAGACATGACC | 420 |
| QY | 788 | -----GG789 | |
| Db | 421 | GGAGAGAGCCTGTTTTCGGGGAGTGTGCCGGGAGAAACCCACTATCCGGAACAGAGG | 480 |
| QY | 790 | TGATGCTGACAGGAGACACTGTCTGACCGGAGCGCGGCTGAACTCACTCTTCCGAACT | 849 |
| Db | 481 | TGATGCTGACAGGAGACACTGTCTGACCGGAGCGCGGCTGAACTCACTCTTCCGAACT | 540 |
| QY | 850 | ACGATGCTCCAGAAACTGTCCGGGAGCGTGTTCACCAAGACGTTAACTCAGGCGTC | 909 |
| Db | 541 | ACGATGCTCCAGAAACTGTCCGGGAGCGTGTTCACCAAGACGTTAACTCAGGCGTC | 600 |
| QY | 910 | CAGCTCAGCGCTTCAAGACCAAGTGTGTGTGGGGGCGGCCCGAAGCAGGGGCACTCTTA | 969 |
| Db | 601 | CAGCTCAGCGCTTCAAGACCAAGTGTGTGTGGGGGCGGCCCGAAGCAGGGGCACTCTTA | 660 |
| QY | 970 | CTTATCTTCCAGCCCAATATGGGCGCTTCTCTGACCGGTGGGCTTTGGCCCAACCCCAAGC | 1029 |
| Db | 661 | CTTATCTTCCAGCCCAATATGGGCGCTTCTCTGACCGGTGGGCTTCTGGCCCAACCCCAAGC | 720 |
| QY | 1030 | TGATGTCATGACCGAGATCC1050 | |
| Db | 721 | TGATGTCATGACCGAGATCC741 | |

RESULT 15
BF178544

| | | | | | |
|------------|--|--------|------|--------|-----------------|
| LOCUS | BP178544 | 980 bp | mRNA | linear | EST 31-OCT-2000 |
| DEFINITION | 601807913F1 NCI CGAP Mam5 Mus musculus cDNA clone IMAGE:4038626 5' | | | | |

| | |
|-----------|----------------------------|
| ACCESSION | mnra sequence. |
| VERSION | BF178544 |
| KEYWORDS | BF178544.1 GI:11056686 |
| SOURCE | EST. |
| ORGANISM | Mus musculus (house mouse) |
| | Mus musculus |

ORGANISM: *Mammalia*; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eumetazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 980)
REFERENCE: NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS: National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE: Unpublished (1999)
JOURNAL: Contact: Robert Strausberg, Ph.D.
COMMENT:

Email: cgabbs@omail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9317 row: 5 column: 03
 High quality sequence stop: 647.
 Location/Qualifiers

FEATURES

source
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 /clone="IMAGE:4038626"
 /issue_type="tumor, gross tissue"
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 /clone_id="NCI_CGAP_Mams"
 /note="Organ: mammary; Vector: pCMV-Sport6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

ORIGIN

Query Match 41.3%; Score 526.8; DB 2; Length 980;
 Best Local Similarity 84.8%; Pred. No. 1e-16;
 Matches 626; Conservative 0; Mismatches 107; Indels 5; Gaps 3;

QY 538 TCGCCATCGAAGAGGCTCGGGTGTGGCCCAAGAGCCTGTTGACTGGGTGGCGGCA 597
 DB 1 TCGCCATCGAAGAGGCTCGGGTGTGGCCCAAGAGCCTGTTGACTGGGTGGCGGAA 60
 QY 598 CCAGCACTGGAGGCACTCTGAGCCCTGGCCATTCTGCACAGTAATCCATGCTTACATGC 657
 DB 61 CCAGCACTGGAGGCACTCTGAGCCCTGGCCATTCTGCACAGTAATCCATGCTTATATGC 120
 QY 658 GCGGCATGTACTTTCGATAGAGATGAGGTTCGCGGGCTCCAGGCCCTTACAGATCGG 717
 DB 121 GTGGTGTACTTCCGATAGAGACAGAGGTGTTTCGCGGGCTCCAGGCCCTTATGATCTG 180
 QY 718 GGGCCCTGGAGAGTCTCTGAAGCGGAGTGTGGGAGCACACCAAGATGACGAGCTCA 777
 DB 181 GGGCCCTGGAGAGTCTCTGAAGCGGAGG- TTGGGAGCACACCAAGATGACGAGTCA 239
 QY 778 GGAACCCAAAGTGTGTGACAGGGCACTGTCTGACCGGAGCCGGCTGAATCCACC 837
 DB 240 AAAAACCCAAAGTGTGTGACAGGGCACTGTCTGACCGGAGCCAGAGACTCCACC 299
 QY 838 TCTTCGGAATGATGATGCTCAAGAACTGTCCGGAGCCTCGTTCAACAGAACGTTA 897
 DB 300 TATTCGGAATGATGATGCTCCGAGAGCCGTTGAGAGCCCGCTGCAACCAAACTTA 359
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 DB 360 ACTTCAGGCTCCAGCTCAGCCCTCAGACCAAGTGTGTGGGGGCGGCCGAGCAGTG 419
 QY 958 GGGCAGCTCTTACTTCTTCCGACCAATGGGCGCTTCTGAGCGGTGGCTGTTGGCCA 1017
 DB 420 GGGCAGCTCTTACTTCTTCCGACCAATGGGCGCTTCTGAGTGAAGGCTCTGGC-- 477
 QY 1018 ACAACCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
 DB 478 ACAACCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
 QY 1078 AGGCTCAGGCTCAAGAGTGAAGAACTTCCATCGTGTCTCCCTGGGAGCAGGAGGT 1137
 DB 538 AGGCTCAGGCTCAAGAGTGAAGAACTTCCATCGTGTCTCCCTGGGAGCAGGAAAT 597
 QY 1138 CCCCAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1197
 DB 598 CCCCTCAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 657
 QY 1198 CCAAGACTGTTTGGGGCCAGGAACTGGGCAAGATGATGATGATGATGATGATGATGAT 1257

DB 658 CCCAACTGTTTGGAGGCCAGGAACTGGCA--GAGGCGTGAATGTGACCAAGATC 715
 QY 1258 CAGACGGGCGCCCGGAAT 1275
 DB 716 AGATGGCGGCGCTGGGAT 733

Search completed: December 16, 2004, 15:10:00
 Job time: 4411 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 15, 2004, 13:01:00 ; Search time 35.0255 Seconds
(Without alignments)
1300.780 Million cell updates/sec

Title: US-10-612-668-21

Sequence: 1 MOFGRVLNVTFSGVTLNFSN.....GAKELGMVVDCTDPDGR 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Issued Patents AA:*
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1 | 3620 | 100.0 | 687 | US-08-555-568B-21 | Sequence 21, Appl |
| 2 | 3620 | 100.0 | 687 | US-09-519-223-21 | Sequence 21, Appl |
| 3 | 3620 | 100.0 | 687 | US-09-927-180-21 | Sequence 21, Appl |
| 4 | 3606.5 | 99.6 | 688 | US-08-555-568B-23 | Sequence 23, Appl |
| 5 | 3606.5 | 99.6 | 688 | US-09-519-223-23 | Sequence 23, Appl |
| 6 | 3606.5 | 99.6 | 688 | US-09-927-180-23 | Sequence 23, Appl |
| 7 | 3302.5 | 91.2 | 752 | US-08-281-193-2 | Sequence 2, Appl |
| 8 | 3302.5 | 91.2 | 752 | US-08-422-106-2 | Sequence 2, Appl |
| 9 | 3302.5 | 91.2 | 752 | US-08-735-716-2 | Sequence 2, Appl |
| 10 | 3302.5 | 91.2 | 752 | US-08-555-568B-2 | Sequence 2, Appl |
| 11 | 3302.5 | 91.2 | 752 | US-09-519-223-2 | Sequence 2, Appl |
| 12 | 3302.5 | 91.2 | 752 | US-09-927-180-2 | Sequence 2, Appl |
| 13 | 3302.5 | 91.2 | 752 | PCT-US95-08069-2 | Sequence 2, Appl |
| 14 | 2084 | 57.6 | 394 | US-08-555-568B-17 | Sequence 17, Appl |
| 15 | 2084 | 57.6 | 394 | US-09-519-223-17 | Sequence 17, Appl |
| 16 | 2084 | 57.6 | 394 | US-09-927-180-17 | Sequence 17, Appl |
| 17 | 1531 | 42.3 | 292 | US-08-555-568B-19 | Sequence 19, Appl |
| 18 | 1531 | 42.3 | 292 | US-09-519-223-19 | Sequence 19, Appl |
| 19 | 1531 | 42.3 | 292 | US-09-927-180-19 | Sequence 19, Appl |
| 20 | 1163.5 | 32.1 | 896 | US-09-270-767-46130 | Sequence 46130, A |
| 21 | 902.5 | 24.9 | 545 | US-09-270-767-46130 | Sequence 46130, A |
| 22 | 371 | 10.2 | 143 | US-09-172-977-3 | Sequence 33298, A |
| 23 | 338 | 9.3 | 843 | US-09-404-108-3 | Sequence 3, Appl |
| 24 | 338 | 9.3 | 843 | US-09-404-108-3 | Sequence 3, Appl |
| 25 | 332 | 9.2 | 1839 | US-09-172-977-4 | Sequence 4, Appl |
| 26 | 332 | 9.2 | 1839 | US-09-404-108-4 | Sequence 4, Appl |
| 27 | 332 | 9.2 | 3924 | US-09-538-092-1246 | Sequence 1246, Ap |

| | | | | | | |
|----|-------|-----|------|---|--------------------|-------------------|
| 28 | 305.5 | 8.4 | 1745 | 2 | US-09-031-485-33 | Sequence 33, Appl |
| 29 | 305.5 | 8.4 | 1745 | 2 | US-08-847-429A-33 | Sequence 33, Appl |
| 30 | 305.5 | 8.4 | 1745 | 3 | US-09-065-474-33 | Sequence 33, Appl |
| 31 | 305.5 | 8.4 | 1745 | 3 | US-09-557-034-33 | Sequence 33, Appl |
| 32 | 302 | 8.3 | 786 | 4 | US-09-509-802-2 | Sequence 2, Appl |
| 33 | 302 | 8.3 | 787 | 4 | US-09-188-930-334 | Sequence 334, App |
| 34 | 302 | 8.3 | 787 | 4 | US-09-312-283C-334 | Sequence 334, App |
| 35 | 296 | 8.2 | 1088 | 4 | US-09-082-059-2 | Sequence 2, Appl |
| 36 | 282.5 | 7.8 | 303 | 2 | US-09-031-485-23 | Sequence 23, Appl |
| 37 | 282.5 | 7.8 | 303 | 2 | US-08-847-429A-23 | Sequence 23, Appl |
| 38 | 282.5 | 7.8 | 303 | 3 | US-09-065-474-23 | Sequence 23, Appl |
| 39 | 282.5 | 7.8 | 303 | 3 | US-09-557-034-23 | Sequence 23, Appl |
| 40 | 282.5 | 7.8 | 784 | 4 | US-09-781-882-2 | Sequence 2, Appl |
| 41 | 273.5 | 7.6 | 1704 | 4 | US-09-392-812A-2 | Sequence 2, Appl |
| 42 | 273 | 7.5 | 994 | 4 | US-10-164-595-38 | Sequence 38, Appl |
| 43 | 272.5 | 7.5 | 352 | 3 | US-09-065-474-139 | Sequence 139, App |
| 44 | 272.5 | 7.5 | 352 | 3 | US-09-557-034-139 | Sequence 139, App |
| 45 | 271.5 | 7.5 | 1619 | 4 | US-09-392-812A-4 | Sequence 4, Appl |

ALIGNMENTS

RESULT 1
US-08-555-568B-21
Sequence 21, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-21

Query Match 100.0%; Score 3620; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
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| Qy | 1 | MOFGRVLNVTFSGVTLNFSNPRVKEVAVADYSSDRVREEGQLIFONTPTNTPCCLV | 60 |
| Db | 1 | MOFGRVLNVTFSGVTLNFSNPRVKEVAVADYSSDRVREEGQLIFONTPTNTPCCLV | 60 |
| Qy | 61 | NPNRSGGFLFQLEADALVNPHOYSSQLPFYSSSPQVLTETVLOHTLDIRNHPSW | 120 |
| Db | 61 | NPNRSGGFLFQLEADALVNPHOYSSQLPFYSSSPQVLTETVLOHTLDIRNHPSW | 120 |

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QY 121 SVANLAVELGIRCFHHSRIISCANCAENBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
DB 121 SVANLAVELGIRCFHHSRIISCANCAENBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
QY 181 VTDYKGETVFAVAVQDGNQVQLDLGRNAVAGLNQVNNQGLTPHLACQJGKQEMVRVLL 240
DB 181 VTDYKGETVFAVAVQDGNQVQLDLGRNAVAGLNQVNNQGLTPHLACQJGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNGPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMLKALIVFGAEVDTPNDFGETPTFLASKIGKQDLMLHISRAKRPATILGSMRDEKR 420
DB 361 DNVEMLKALIVFGAEVDTPNDFGETPTFLASKIGKQDLMLHISRAKRPATILGSMRDEKR 420
QY 421 THDHLCLDGGVYKGLIIQLLAIKASGVAATKDLFDWVAGTSTGGIILALILHKSMA 480
DB 421 THDHLCLDGGVYKGLIIQLLAIKASGVAATKDLFDWVAGTSTGGIILALILHKSMA 480
QY 481 YMGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGLTSDRQPAE 540
DB 481 YMGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGLTSDRQPAE 540
QY 541 LHLFRNYDAETVREPRFNQNVNLRPPAOPSDQVWRAARSQGAAPTYFRPNRFLDGL 600
DB 541 LHLFRNYDAETVREPRFNQNVNLRPPAOPSDQVWRAARSQGAAPTYFRPNRFLDGL 600
QY 601 LANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVSLGTGRSPQVPTCVDFRPSNPW 660
DB 601 LANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVSLGTGRSPQVPTCVDFRPSNPW 660
QY 661 ELAKTVFGAKELGKMVVDCCTDPDGRP 687
DB 661 ELAKTVFGAKELGKMVVDCCTDPDGRP 687

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RESULT 2
US-09-519-223-21
; Sequence 21, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-21

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Query Match 100.0%; Score 3620; DB 3; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MOFGRLVNTFSGVTLFNSNPFVKEVAADYSSDRVBEQGLIFONTPNRTMDCVY 60
DB 1 MOFGRLVNTFSGVTLFNSNPFVKEVAADYSSDRVBEQGLIFONTPNRTMDCVY 60
QY 61 NPNNSQSGFRLFQLELEADALVNFQYSSQLPEFYESSPOVLHTEVLQHLTDLIRNHP 120
DB 61 NPNNSQSGFRLFQLELEADALVNFQYSSQLPEFYESSPOVLHTEVLQHLTDLIRNHP 120
QY 121 SVANLAVELGIRCFHHSRIISCANCAENBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
DB 121 SVANLAVELGIRCFHHSRIISCANCAENBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
QY 181 VTDYKGETVFAVAVQDGNQVQLDLGRNAVAGLNQVNNQGLTPHLACQJGKQEMVRVLL 240
DB 181 VTDYKGETVFAVAVQDGNQVQLDLGRNAVAGLNQVNNQGLTPHLACQJGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNGPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAVLLTHGANADARGEHNTPLHLAMSK 360
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DB 361 DNVEMLKALIVFGAEVDTPNDFGETPTFLASKIGKQDLMLHISRAKRPATILGSMRDEKR 420
QY 421 THDHLCLDGGVYKGLIIQLLAIKASGVAATKDLFDWVAGTSTGGIILALILHKSMA 480
DB 421 THDHLCLDGGVYKGLIIQLLAIKASGVAATKDLFDWVAGTSTGGIILALILHKSMA 480
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QY 541 LHLFRNYDAETVREPRFNQNVNLRPPAOPSDQVWRAARSQGAAPTYFRPNRFLDGL 600
DB 541 LHLFRNYDAETVREPRFNQNVNLRPPAOPSDQVWRAARSQGAAPTYFRPNRFLDGL 600
QY 601 LANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVSLGTGRSPQVPTCVDFRPSNPW 660
DB 601 LANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVSLGTGRSPQVPTCVDFRPSNPW 660
QY 661 ELAKTVFGAKELGKMVVDCCTDPDGRP 687
DB 661 ELAKTVFGAKELGKMVVDCCTDPDGRP 687

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RESULT 3
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match      100.0%; Score 3620; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFGRVLTFTSGVTNLFSNPFVKYVAADVYSSDRVEEGQLIFQNTPNRTWDCVY 60
DB 1 MGFGRVLTFTSGVTNLFSNPFVKYVAADVYSSDRVEEGQLIFQNTPNRTWDCVY 60
QY 61 NPNRSOSGFRLLFOLELEADLVNPHOYSSQLPFYESSPOVLTVEVQLTDLIRNPSW 120
DB 61 NPNRSOSGFRLLFOLELEADLVNPHOYSSQLPFYESSPOVLTVEVQLTDLIRNPSW 120
QY 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
DB 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
QY 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
DB 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
QY 181 VTDYKGETVHYAVQGDNSQVLLQILGRNAVAGLNQVNNQGLTPLHLACOLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVQGDNSQVLLQILGRNAVAGLNQVNNQGLTPLHLACOLGKQEMRVLL 240
QY 241 LCNARCCIMPGNPIHSAKFSQKCAEMISMDSSQHSKDPYASPLHAKNAEMA 300
DB 241 LCNARCCIMPGNPIHSAKFSQKCAEMISMDSSQHSKDPYASPLHAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHVGVMNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIGKLODLMHISPAKPAITLGSMDER 420
DB 361 DNVEIMKALIVFGAEVDTNDPFGETPTFLASKIGKLODLMHISPAKPAITLGSMDER 420
QY 421 THDHLCLDGGGAGKLIILQLLAIBKASGVAIKDLFDWYAGTSTGILALAIHSSMA 480
DB 421 THDHLCLDGGGAGKLIILQLLAIBKASGVAIKDLFDWYAGTSTGILALAIHSSMA 480
QY 481 YMGMYFRMKDEVFRGSRPYESGPLEBEFLKREFEHTKMTDVRKPKWMLTGLSDROPAS 540
DB 481 YMGMYFRMKDEVFRGSRPYESGPLEBEFLKREFEHTKMTDVRKPKWMLTGLSDROPAS 540

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QY 541 LHLFRNYDAPETVREPRFNQNVLRPPAPSDQLVMRAASSGAAPTYRPNRFLDGL 600
DB 541 LHLFRNYDAPETVREPRFNQNVLRPPAPSDQLVMRAASSGAAPTYRPNRFLDGL 600
QY 601 LANPPLDANTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNPW 660
DB 601 LANPPLDANTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNPW 660
QY 661 ELAKTVFGAKELGRNVVDCCTDPDGRP 687
DB 661 ELAKTVFGAKELGRNVVDCCTDPDGRP 687

RESULT 4
US-08-555-568B-23
Sequence 23, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-23

Query Match      99.6%; Score 3606.5; DB 2; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGFGRVLTFTSGVTNLFSNPFVKYVAADVYSSDRVEEGQLIFQNTPNRTWDCVY 60
DB 1 MGFGRVLTFTSGVTNLFSNPFVKYVAADVYSSDRVEEGQLIFQNTPNRTWDCVY 60
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DB 61 NPNRSOSGFRLLFOLELEADLVNPHOYSSQLPFYESSPOVLTVEVQLTDLIRNPSW 120
QY 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
DB 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
QY 181 VTDYKGETVHYAVQGDNSQVLLQILGRNAVAGLNQVNNQGLTPLHLACOLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVQGDNSQVLLQILGRNAVAGLNQVNNQGLTPLHLACOLGKQEMRVLL 240

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QY 241 LCNARCNIMGPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDBRYGASPLHMAKNAEMA 300
DB 241 LCNARCNIMGPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDBRYGASPLHMAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHGVNMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVTPNDPFGETPTFLASKIGK-LQDLMHISRAKRPATILGSRDEK 419
DB 361 DNVEMIKALIVFGAEVTPNDPFGETPTFLASKIGK-LQDLMHISRAKRPATILGSRDEK 420
QY 420 RTHDHLCLDGGGVKGLIIIIQLIAIEKASGATKDLFDWAGTSGIILALAILHLSKSM 479
DB 421 RTHDHLCLDGGGVKGLIIIIQLIAIEKASGATKDLFDWAGTSGIILALAILHLSKSM 480
QY 480 AYNRGMVFRMKDEVFRSGRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGILSDRQPA 539
DB 481 AYNRGMVFRMKDEVFRSGRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGILSDRQPA 540
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DB 541 ELHLFRNYDAPEVREPRFNQNVNLRPPAOPSDQLVWRARSSGAAPTYFRPNRFLDGG 600
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DB 601 LLANPFLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WELAKTVFGAKELGKRVVDDCTDPDGRP 687
DB 661 WELAKTVFGAKELGKRVVDDCTDPDGRP 688

RESULT 5

US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridge Park Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-519-223-23

Query Match 99.6%; Score 3606.5; DB 3; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 688; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGFGRVLTNTEGVTNLFSPNPFVKEVAVADYSSDRVREEGQLIFONTNRTWCVLV 60
DB 1 MGFGRVLTNTEGVTNLFSPNPFVKEVAVADYSSDRVREEGQLIFONTNRTWCVLV 60
QY 61 NPNNSGFRFLFQLELEADLVNPHOYSQQLLFYESSPOVLTHTVLQHTDLIRNHPW 120
DB 61 NPNNSGFRFLFQLELEADLVNPHOYSQQLLFYESSPOVLTHTVLQHTDLIRNHPW 120
QY 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELVELVOYCHTQMD 180
DB 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELVELVOYCHTQMD 180
QY 181 VTDYKGETVHYAVQGDNSQVTLQLGNNVAGLNVNNQGLTPLHLACQLGKQEMTVLL 240
DB 181 VTDYKGETVHYAVQGDNSQVTLQLGNNVAGLNVNNQGLTPLHLACQLGKQEMTVLL 240
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QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHGVNMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVTPNDPFGETPTFLASKIGK-LQDLMHISRAKRPATILGSRDEK 419
DB 361 DNVEMIKALIVFGAEVTPNDPFGETPTFLASKIGK-LQDLMHISRAKRPATILGSRDEK 420
QY 420 RTHDHLCLDGGGVKGLIIIIQLIAIEKASGATKDLFDWAGTSGIILALAILHLSKSM 479
DB 421 RTHDHLCLDGGGVKGLIIIIQLIAIEKASGATKDLFDWAGTSGIILALAILHLSKSM 480
QY 480 AYNRGMVFRMKDEVFRSGRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGILSDRQPA 539
DB 481 AYNRGMVFRMKDEVFRSGRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGILSDRQPA 540
QY 540 ELHLFRNYDAPEVREPRFNQNVNLRPPAOPSDQLVWRARSSGAAPTYFRPNRFLDGG 599
DB 541 ELHLFRNYDAPEVREPRFNQNVNLRPPAOPSDQLVWRARSSGAAPTYFRPNRFLDGG 600
QY 600 LLANPFLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 659
DB 601 LLANPFLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WELAKTVFGAKELGKRVVDDCTDPDGRP 687
DB 661 WELAKTVFGAKELGKRVVDDCTDPDGRP 688

RESULT 6

US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridge Park Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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Job time : 123.588 secs

Publication No. US2003010482A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: Bird, Timothy
; APPLICANT: Virca, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
; FILE OF INVENTION: (DAKAR)
; FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/10/299,327
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/509,802
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-299-327-2

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 5.3e-18;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNHPWSVAHLAVELGIRECFHRSRIISCANCAENEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVOYCHTOMDVTYKGETVFHYAVO-GDNSQVLQLLGRNAVAGLNOVNOGTLPLHLACQ 229
DB 491 LLARKTSVNAKDEQWTLHPAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVAQ 548
QY 230 LGQEMVRVLLCNARCINMGNGY-PIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVDVGLQKDAWPLHYAAWQGHLPVKKLAKPGVSVNAQ-TLDGR 607
QY 289 SPLHWAK---NAEMARMLLKRCGNVNSTSAGNTALHVGVMNRFPDCAIVLLTHGANADA 345
DB 608 TPLHAAQQRHYRVARILIDLCSDVNICSLQAQOTPLHVAATGHTSTARLLHHRGAGKEA 667
QY 346 RGEHGNTPHLAMSNDVEMIKALIVFGAEVDTPNDPFGETPTFLASKIGKLGQ----- 397
DB 668 LTSEGYTALHAAQNGHLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVELVSA 727
QY 398 DLMHIS 403
DB 728 DLIDLS 733

RESULT 14
US-10-128-174-13
; Sequence 13, Application US/10128174
; Publication No. US20030109462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-13

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 5.3e-18;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNHPWSVAHLAVELGIRECFHRSRIISCANCAENEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVOYCHTOMDVTYKGETVFHYAVO-GDNSQVLQLLGRNAVAGLNOVNOGTLPLHLACQ 229
DB 491 LLARKTSVNAKDEQWTLHPAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVAQ 548
QY 230 LGQEMVRVLLCNARCINMGNGY-PIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVDVGLQKDAWPLHYAAWQGHLPVKKLAKPGVSVNAQ-TLDGR 607
QY 289 SPLHWAK---NAEMARMLLKRCGNVNSTSAGNTALHVGVMNRFPDCAIVLLTHGANADA 345
DB 608 TPLHAAQQRHYRVARILIDLCSDVNICSLQAQOTPLHVAATGHTSTARLLHHRGAGKEA 667
QY 346 RGEHGNTPHLAMSNDVEMIKALIVFGAEVDTPNDPFGETPTFLASKIGKLGQ----- 397
DB 668 LTSEGYTALHAAQNGHLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVELVSA 727
QY 398 DLMHIS 403
DB 728 DLIDLS 733

RESULT 15
US-10-128-174-31
; Sequence 31, Application US/10128174
; Publication No. US20030109462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-31

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 5.3e-18;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNHPWSVAHLAVELGIRECFHRSRIISCANCAENEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVOYCHTOMDVTYKGETVFHYAVO-GDNSQVLQLLGRNAVAGLNOVNOGTLPLHLACQ 229
DB 491 LLARKTSVNAKDEQWTLHPAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVAQ 548
QY 230 LGQEMVRVLLCNARCINMGNGY-PIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVDVGLQKDAWPLHYAAWQGHLPVKKLAKPGVSVNAQ-TLDGR 607
QY 289 SPLHWAK---NAEMARMLLKRCGNVNSTSAGNTALHVGVMNRFPDCAIVLLTHGANADA 345
DB 608 TPLHAAQQRHYRVARILIDLCSDVNICSLQAQOTPLHVAATGHTSTARLLHHRGAGKEA 667
QY 346 RGEHGNTPHLAMSNDVEMIKALIVFGAEVDTPNDPFGETPTFLASKIGKLGQ----- 397
DB 668 LTSEGYTALHAAQNGHLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVELVSA 727
QY 398 DLMHIS 403
DB 728 DLIDLS 733

Search completed: December 15, 2004, 13:34:57

[illegible]

QY 149 NBEAGCTPLHACRKGDEILVELVOYCHTQMDVTDYKGETVHYAVQGDNSQVQLL--G 206
DB 316 QPEGLSPLMIAVQNTQIETVSMWLDH-GADINILSSEGQNVLHVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLLNCARNCTMGPN--Y 254
DB 375 KKCETMINQTSNGYTPAYVA-----LINACLSNCQTLRGFGGGIQSSDSTQMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSSOIHKSOPRYGASPLHWAKNAEMARMMLKR--GCN 309
DB 425 PIIGAMKRGKLDVSRKMLELQDGLTETPTGNTVHCAINKKCLILLMEKFRDQTD 484
QY 310 VNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
DB 485 PEARNALQOTPLHTFVIKDELGLVMTLSAYGVMDAQDINGNTPLHCAVTRGNTETARM 544
QY 370 IVFGAEVDPNDGPTPLASKIGKQLDLMHISRAR-----KPATF----- 411
DB 545 LCLGAKPDIKNRYKESPRHIAARLTKAEMDIVRALIICGAGACDDGFGICAFGCMHKT 604
QY 412 -----LGSM-----RDEKRT 421
DB 605 GLTSCKTQLGSSSDSQSMEDRVKDIHVSNDNAASAPYFVLPDPTQOLVVEEAERNEIRA 664
QY 422 HDH-----LCLDGGGVKGLIIIIQLLIAIEKASGVATKDL 456
DB 665 FPHEEALKRVKVKELVEKKTSNVINVLGDDGGIRGLVTVMQLICLEAFDLRLIDY 724
QY 457 FOWAGTSTGCIIMSTMTGGSRLKQRYLMFKDQFDSWTRPYDTKTLETFIQRAFGA 784
DB 725 FOWIGATSTGCIIMSTMTGGSRLKQRYLMFKDQFDSWTRPYDTKTLETFIQRAFGA 784
QY 516 HTKMTDVRKPKVMTGLSDROPALHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 575
DB 785 DRLMGDIKPRFFCTTVRADTFFVQLELLNRLPLISEKE---NNDLGF---TDPNELTI 838
QY 576 WRAARSSGAAPTFRPN-GRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI 634
DB 839 WKATRRSSAAPTYSASEGKFIDGGMISNNPVLDMSDIGFYNTTCQKRIPEKMYDMGC 898
QY 635 VVSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGMVVDCTDPPGR 687
DB 899 VLSVGTGITPICVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATAGAP 947

RESULT 9
US-10-369-493-6690
; Sequence 6690, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6690
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6690

Query Match 17.5%; Score 634.5; DB 14; Length 1023;
Best Local Similarity 24.2%; Pred. No. 3.2e-48;
Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

QY 37 RVREBQILFQNTNRTWDCVLPNRNSQSGRFLFQLELEAD--ALNVFHYQSOLLPP 94
DB 204 RAKEEEL--KNKPLYHLAITLYNENNEKYVMSLFRSHKLDADVVALCERCRENPELFRV 260
QY 95 YESSQV--LHTEVLQHLTDLIRNHPWSVAHLAVELGIRECFHH--SRIISCANCAE 148
DB 261 PFKNYNIKDYLT-----IFHELDRNMTWKSVHISKIGLLEFFENKHEKLLKYLNLIV 315
QY 149 NBEAGCTPLHACRKGDEILVELVOYCHTQMDVTDYKGETVHYAVQGDNSQVQLL--G 206
DB 316 QPEGLSPLMIAVQNTQIETVSMWLDH-GADINILSSEGQNVLHVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLLNCARNCTMGPN--Y 254
DB 375 KKCETMINQTSNGYTPAYVA-----LINACLSNCQTLRGFGGGIQSSDSTQMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSSOIHKSOPRYGASPLHWAKNAEMARMMLKR--GCN 309
DB 425 PIIGAMKRGKLDVSRKMLELQDGLTETPTGNTVHCAINKKCLILLMEKFRDQTD 484
QY 310 VNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
DB 485 PEARNALQOTPLHTFVIKDELGLVMTLSAYGVMDAQDINGNTPLHCAVTRGNTETARM 544
QY 370 IVFGAEVDPNDGPTPLASKIGKQLDLMHISRAR-----KPATF----- 411
DB 545 LCLGAKPDIKNRYKESPRHIAARLTKAEMDIVRALIICGAGACDDGFGICAFGCMHKT 604
QY 412 -----LGSM-----RDEKRT 421
DB 605 GLTSCKTQLGSSSDSQSMEDRVKDIHVSNDNAASAPYFVLPDPTQOLVVEEAERNEIRA 664
QY 422 HDH-----LCLDGGGVKGLIIIIQLLIAIEKASGVATKDL 456
DB 665 FPHEEALKRVKVKELVEKKTSNVINVLGDDGGIRGLVTVMQLICLEAFDLRLIDY 724
QY 457 FOWAGTSTGCIIMSTMTGGSRLKQRYLMFKDQFDSWTRPYDTKTLETFIQRAFGA 784
DB 725 FOWIGATSTGCIIMSTMTGGSRLKQRYLMFKDQFDSWTRPYDTKTLETFIQRAFGA 784
QY 516 HTKMTDVRKPKVMTGLSDROPALHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 575
DB 785 DRLMGDIKPRFFCTTVRADTFFVQLELLNRLPLISEKE---NNDLGF---TDPNELTI 838
QY 576 WRAARSSGAAPTFRPN-GRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI 634
DB 839 WKATRRSSAAPTYSASEGKFIDGGMISNNPVLDMSDIGFYNTTCQKRIPEKMYDMGC 898
QY 635 VVSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGMVVDCTDPPGR 687
DB 899 VLSVGTGITPICVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATAGAP 947

RESULT 10
US-10-369-493-4998
; Sequence 4998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4998
; LENGTH: 468

SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match 42.3%; Score 1531; DB 9; Length 292;
Best Local Similarity 100.0%; Pred. No. 5.2e-131; Indels 0; Gaps 0;
Matches 292; Conservative 0; Mismatches 0;

QY 396 LQDLMHISRKAPAFILGSRMRDEKTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 455
Db 1 LQDLMHISRKAPAFILGSRMRDEKTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60

QY 456 LFDWVAGTSTGGILALAILHLSKSMAYRMGMFRMKDEVFRGSRPYSGPLEEFLKREFGE 515
Db 61 LFDWVAGTSTGGILALAILHLSKSMAYRMGMFRMKDEVFRGSRPYSGPLEEFLKREFGE 120

QY 516 HTKMTDVRKPKVMTGTLSDROPALHLPRNYDAPETVREPRENQNVNLRPPAQPDSQLV 575
Db 121 HTKMTDVRKPKVMTGTLSDROPALHLPRNYDAPETVREPRENQNVNLRPPAQPDSQLV 180

QY 576 WRAARSSGAAPTFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKSIV 635
Db 181 WRAARSSGAAPTFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKSIV 240

QY 636 VSLGTGRSPQVPTCVDPVFRPNWELAKTVFGAKELGKMWVDCCTDPPGRP 687
Db 241 VSLGTGRSPQVPTCVDPVFRPNWELAKTVFGAKELGKMWVDCCTDPPGRP 292

RESULT 7
US-10-369-493-6865
; Sequence 6865, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6865
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6865

Query Match 17.9%; Score 647.5; DB 14; Length 1071;
Best Local Similarity 27.0%; Pred. No. 2.3e-49;
Matches 194; Conservative 126; Mismatches 260; Indels 139; Gaps 20;

QY 69 FRLFQLEADALVNFHQSOLLPEYSSPQVLHTEVL---QHLTDLIRNHPWSVAH 124
Db 315 FSFVATDKKDLMLHLCDKESFLTSLDMSTMRADILRSKIEELVQIRLKPHEVMT 374

QY 125 LAVELGIRECFHRSRI-----ISCANCAENESEGTPLHLACRKGDEITLVLQY 174
Db 375 VAIAIDRLDFFSDGMKTNWETLEPESQLRCLCHTENCYPVHLALTMDRQKIVERLLEL 434

QY 175 CHTQMDVTDYKGTVFHYAVQDGNQSVQLLGRNAVAG---LNQVNNQGLTPLHLACQUG 231
Db 435 DPTLFCETDKAGNVVHHV---NSSFCAQIWDRCQPASQHFIDERNMDQGSPLNEAVSTA 491

QY 232 KOEMVRVLLLCNARCINMGPNGYPIHSAMKFSQKCAEMIISM-----DSS 277
Db 492 KPLVATFL-----ICKGAKFTGDRNELFVAMTSKNAQSVVWLTDXP 535

QY 278 QIHSKDPRYGASPLHWAKNAEMARMMLLK-----GCNVNSTSSAGNTALHVGVMNRPDCA 333
Db 536 EIANERDALGNSAIHVALYKESLNALNRKVELGLDIDVKNNAGETALLFITTRKPDLL 595

QY 334 IVLLT---HGANADARGEHNTPLHLAMS-----KONVEMIKALIVFGAEVDTPNDGET 385
Db 596 PLLVTLYAHGANNWATDPHGNTALHKSAAALVDAAKISLBECVKFLISAGSNPNKINLRGES 655

QY 386 PFLASKIKGLQDLMHISRA---RKPAFILG-----SMRDE----- 418
Db 656 PHLAASL-QNQEMLAAILKAAGNTRCPKGYKGRSNCRHDCSSAEDEYBETLQIRIGNE 714

QY 419 -----KRTDHLCLDGGGVKGLIIQLLIAIEKASGVA 452
Db 715 SDYEKTEFTASEKLIQDTLDGSRRGKAKAVNLISMDGGGIRGLVIIQTLLAIEERLGD 774

QY 453 TKDLFDWVAGTSTGGILALAILHLSKSMAYRMGMFRMKDEVFRG-SRPYESGPLEEFLK 511
Db 775 IFKYFDWSAGTSTGSLIMAGLATGKSLREMQQTYLLDKDRVFDGIMPVDTVQLKFIQD 834

QY 512 EFGTKMTDVRKPKVMTGTLSDROPALHLPRNYDAPETVREPRENQNVNLRPPAQP 571
Db 835 QGTGT-VWEIYPRLMISAVNSEKLPVLEWARYKPAKV-----APETPK 881

QY 572 DQLVRAARSSGAAPTFRPN-GRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKV 630
Db 882 EMPLMALARSTAAAPVLPKPESEDYIDGGIISNNPALDLMSEVHAYNRELQLSGRKSDAV 941

QY 631 KLSIVVSLGTGRSPQVPTCVDPFR---PSNPHELAKTVFGAKELGKMWVDCCTDPPGRP 687
Db 942 QMNVLSFGTG---QIPSTVIETLSIDNSPLQSIKTI---KNLAAMFIDQATASEGAP 994

RESULT 8
US-10-369-493-6689
; Sequence 6689, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6689
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6689

Query Match 17.5%; Score 634.5; DB 14; Length 1023;
Best Local Similarity 24.2%; Pred. No. 3.2e-48;
Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

QY 37 RVREBQGLIFQNTNRTWDCVLVNPNSQSGRFLFQLELEAD--ALVNFHQSOLLPP 94
Db 204 RAKEEEL---KNKPLYHLAITYNENNEKYVMSLFRSHKLADVVVALCERCENPELFRV 260

QY 95 YESSQV---LITEVLQHLTDLIRNHPWSVAHLAVELGIRECFHH---SRIISCANCAE 148
Db 261 PPKNVNIKDYLT-----IFHELDRONTWKSVHISKIGLLBYFENMKHKLKYLNLIV 315

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Db 102 LCNARCNIMGPNQPIYSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 161
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 162 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 221
QY 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIGK----- 395
Db 222 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIGRLVTRKAILTLRLTVGAECYCFPPING 281
QY 396 -----LQDLMIHSRARKPAFTILGSMRDEKTRTHDL 425
Db 282 VPBQCSAAPHFHSERAPQPPIISUNLEQLQDLMIHSRARKPAFTILGSMRDEKTRTHDL 341
QY 426 LCLDGGGVKGLIIQLIIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 485
Db 342 LCLDGGGVKGLIIQLIIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 401
QY 486 YFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMLTGLSDRQPAELHLFR 545
Db 402 YFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMLTGLSDRQPAELHLFR 461
QY 546 NYDAPETVREPFRNQNVLNRPAPQSDQLVWRAARSSGAAPTFRPNGRFLDGLLANNP 605
Db 462 NYDAPETVREPFRNQNVLNRPAPQSDQLVWRAARSSGAAPTFRPNGRFLDGLLANNP 521
QY 606 TLDAMTEIHEYNQDLIRKQANKVKLSIWSLGTGRSPQVPTCVDFRPNPNWELAKT 665
Db 522 TLDAMTEIHEYNQDLIRKQANKVKLSIWSLGTGRSPQVPTCVDFRPNPNWELAKT 581
QY 666 VFGAKELGRKVVDCCTDPGR 686
Db 582 VFGAKELGRKVVDCCTDPGR 602

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RESULT 5

```

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid

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RESULT 6

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US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match      57.6%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.3e-161; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0;

QY 1 MOFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MOFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRILPQLEADALNVFHOYSQQLLPFYESSQVLTHTVQLHQLTLIRNHPSW 120
Db 61 NPNRSQSGFRILPQLEADALNVFHOYSQQLLPFYESSQVLTHTVQLHQLTLIRNHPSW 120
QY 121 SVAHLAVELGIRECPHHSRIISCANCAENEECTPLHLACRKGDEGILVELVQYCHTQMD 180
Db 121 SVAHLAVELGIRECPHHSRIISCANCAENEECTPLHLACRKGDEGILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLIQRNAVAGLNQNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVLLIQRNAVAGLNQNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNQPIYSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNQPIYSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIG 394

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QY 600 LLANNPTLDAMTEIHEYNODLRKGOANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNODLRKGOANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

RESULT 3

US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US300201063641
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-927-180-2
Query Match 91.2%; Score 3302.5; DB 9; Length 752;
Best Local Similarity 90.4%; Pred. No. 2.6e-292;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
QY 1 MQPFGRLVNTFSGVTLNFSNPRFRKVAADVTSRDRVEEGQLILFQNTPNRTWDCVLV 60
DB 1 MQPFGRLVNTLSSVTNLFNSNPRFRKVAADVTSRDRVEEGQLILFQNASNRTWDCILV 60
QY 61 NPNRSQSGRLFLQLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHQLTDLIRNHPWS 120
DB 61 SPRNHSIGRLFLQLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHQLTDLIRNHPWS 120
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHLACRKGDSILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRCFHHSRIISCANSTENEBEGCTPLHLACRKGDSILVELVQYCHTQMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNKGETAHYAVQGDNSQVLQLLGNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240

QY 241 LCNARCNIMPGNGYPITHSAMKFSQKCAEMIIISMDSSQIHSKDPRIYCASPLHWAKNAEMA 300
DB 241 LCNARCNIMPGNGYPITHSAMKFSQKCAEMIIISMDSSQIHSKDPRIYCASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRNFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCDVSTSAAGNTALHVGVMNRNFDCAI VLLTHGANAGTPEGHNTPLHLAISK 360
QY 361 DNVEIMIKALIVFGAEVDTNDGETPTFLASKIGK-LQDLMHISRARKPAFILSSMRDEK 419
DB 361 DNVEIMIKALIVFGAEVDTNDGETPTFAFNASKISKQLQDLMFISARKPAFILSSMRDEK 420
QY 420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
DB 421 RTHDHLCLDGGVGKGLVIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEEFKREFGEHTKMTDVRKPKVMLTGTLSRQPA 539
DB 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFLEEFKREFGEHTKMTDVKPKVMLTGTLSRQPA 540
QY 540 ELHLFRNYDAPETVREPQNQNLPPAOPSDOLVWRAARSSGAAPTYFRPNRGLDGG 599
DB 541 ELHLFRNYDAPETVREPQNQNLKPTQPADQLVWRAARSSGAAPTYFRPNRGLDGG 600
QY 600 LLANNPTLDAMTEIHEYNODLRKGOANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNQDMIRKGGCNKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 4

US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 75.2%; Score 2723; DB 15; Length 667;
Best Local Similarity 73.3%; Pred. No. 2e-239;
Matches 543; Conservative 2; Mismatches 2; Indels 194; Gaps 2;

QY 1 MQPFGRLVNTFSGVTLNFSNPRFRKVAADVTSRDRVEEGQLILFQNTPNRTWDCVLV 60
DB 1 MQPFGRLVNTFSGVTLNFSNPRFRKVAADVTSRDRVEEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFLQLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHQLTDLIRNHPWS 120
DB 61 YPRNSQSGRLFLQLEADALVNFHQYSS- - - - - 89
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHLACRKGDSILVELVQYCHTQMD 180
DB 90 - - - - - 89
QY 181 VTDYKGETVPHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 90 - - - - - 101
QY 241 LCNARCNIMPGNGYPITHSAMKFSQKCAEMIIISMDSSQIHSKDPRIYCASPLHWAKNAEMA 300

LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 3620; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MQFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREBQGLILFQNTPTNRTWDCVLV 60
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DB 61 NPNRSQSGFRLFQLEADALVNFHQSQQLPPFYESSQVLHTEVQLHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDGNQVQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDGNQVQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEKR 420
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEKR 420
QY 421 THDHLACLDDGGVKGILIIQLLIAIEKASGATKDLFDWVAGTSTGGIILALAILHKSMA 480
DB 421 THDHLACLDDGGVKGILIIQLLIAIEKASGATKDLFDWVAGTSTGGIILALAILHKSMA 480
QY 481 YMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTLTGTLSDRQPAE 540
DB 481 YMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTLTGTLSDRQPAE 540
QY 541 LHLFRNYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYPFRNGRFLDGGI 600
DB 541 LHLFRNYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYPFRNGRFLDGGI 600
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DB 601 LANNPTLDAMTEHYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPW 660
QY 661 ELAKTVFGAKELGMVVDCCCTDPDGRP 687
DB 661 ELAKTVFGAKELGMVVDCCCTDPDGRP 687
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RESULT 2

US-09-927-180-23
Sequence 23, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:

APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 99.6%; Score 3606.5; DB 9; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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DB 1 MQFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREBQGLILFQNTPTNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLEADALVNFHQSQQLPPFYESSQVLHTEVQLHLDLIRNHPSW 120
DB 61 NPNRSQSGFRLFQLEADALVNFHQSQQLPPFYESSQVLHTEVQLHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDGNQVQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDGNQVQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDDGGVKGILIIQLLIAIEKASGATKDLFDWVAGTSTGGIILALAILHKSMA 479
DB 421 RTHDHLCLDDGGVKGILIIQLLIAIEKASGATKDLFDWVAGTSTGGIILALAILHKSMA 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTLTGTLSDRQPA 539
DB 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYPFRNGRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYPFRNGRFLDGG 600
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 13:13:21 ; Search time 120.588 Seconds
(without alignments)
2034.879 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFFGLVNTFSGVTLFSEN.....GAKELGKVVDDCTDPDGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 3620 | 100.0 | 687 | 9 | US-09-927-180-21 |
| 2 | 3606.5 | 99.6 | 688 | 9 | US-09-927-180-23 |
| 3 | 3302.5 | 91.2 | 752 | 9 | US-09-927-180-2 |
| 4 | 2723 | 75.2 | 667 | 15 | US-10-108-260A-3778 |
| 5 | 2084 | 57.6 | 394 | 9 | US-09-927-180-17 |
| 6 | 1531 | 42.3 | 292 | 9 | US-09-927-180-19 |
| 7 | 647.5 | 17.9 | 1071 | 14 | US-10-369-493-6665 |
| 8 | 634.5 | 17.5 | 1023 | 14 | US-10-369-493-6689 |
| 9 | 634.5 | 17.5 | 1023 | 14 | US-10-369-493-6690 |
| 10 | 324.5 | 9.0 | 468 | 14 | US-10-369-493-4998 |
| 11 | 324 | 9.0 | 1330 | 15 | US-10-108-260A-3237 |
| 12 | 302 | 8.3 | 786 | 14 | US-10-164-080-2 |
| 13 | 302 | 8.3 | 786 | 14 | US-10-299-327-2 |

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|----|-------|-----|------|----|--------------------|
| 14 | 302 | 8.3 | 786 | 14 | US-10-128-174-13 |
| 15 | 302 | 8.3 | 786 | 14 | US-10-128-174-31 |
| 16 | 302 | 8.3 | 786 | 14 | US-10-128-174-32 |
| 17 | 302 | 8.3 | 786 | 14 | US-10-128-174-33 |
| 18 | 301.5 | 8.3 | 787 | 10 | US-09-866-050A-334 |
| 19 | 301.5 | 8.3 | 347 | 14 | US-10-128-174-30 |
| 20 | 300.5 | 8.3 | 1724 | 9 | US-09-964-899-43 |
| 21 | 300 | 8.3 | 1762 | 14 | US-10-205-194-117 |
| 22 | 296 | 8.2 | 3913 | 15 | US-10-334-143-45 |
| 23 | 290 | 8.0 | 720 | 15 | US-10-433-794-20 |
| 24 | 290 | 8.0 | 765 | 14 | US-10-128-174-3 |
| 25 | 290 | 8.0 | 765 | 14 | US-10-128-174-34 |
| 26 | 290 | 8.0 | 765 | 14 | US-10-128-174-35 |
| 27 | 290 | 8.0 | 765 | 14 | US-10-128-174-36 |
| 28 | 290 | 8.0 | 765 | 14 | US-10-128-174-37 |
| 29 | 290 | 8.0 | 765 | 14 | US-10-128-174-38 |
| 30 | 290 | 8.0 | 765 | 14 | US-10-128-174-39 |
| 31 | 290 | 8.0 | 765 | 14 | US-10-128-174-40 |
| 32 | 290 | 8.0 | 765 | 14 | US-10-128-174-41 |
| 33 | 290 | 8.0 | 765 | 14 | US-10-128-174-42 |
| 34 | 290 | 8.0 | 765 | 14 | US-10-128-174-43 |
| 35 | 290 | 8.0 | 765 | 14 | US-10-128-174-44 |
| 36 | 290 | 8.0 | 765 | 15 | US-10-182-243-56 |
| 37 | 284.5 | 7.9 | 784 | 14 | US-10-164-080-7 |
| 38 | 284.5 | 7.9 | 784 | 15 | US-10-258-951-70 |
| 39 | 282.5 | 7.8 | 784 | 14 | US-10-354-358-38 |
| 40 | 282.5 | 7.8 | 784 | 14 | US-10-128-174-12 |
| 41 | 279.5 | 7.7 | 784 | 16 | US-10-648-593-153 |
| 42 | 279.5 | 7.7 | 1053 | 14 | US-10-291-172-343 |
| 43 | 278.5 | 7.7 | 1053 | 15 | US-10-221-278-343 |
| 44 | 278.5 | 7.6 | 1704 | 14 | US-10-369-978-2 |
| 45 | 273.5 | 7.6 | 1704 | 14 | US-10-369-978-2 |

ALIGNMENTS

RESULT 1

US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:

Db 61 NPRNSQSGRLFOLELEADALVNFHQYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
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Db 121 SVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKGDSGRIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFPDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFPDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNPNDFGETPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNPNDFGETPTFLASKIG 394

RESULT 15

US-09-519-223-17
; Sequence 17, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-17

Query Match 57.6%; Score 2084; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.6e-217;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQFFGRLVNTFSGVTNLFNSNPFPRKVEAVADYTSDDRVREGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTFSGVTNLFNSNPFPRKVEAVADYTSDDRVREGQLILFQNTPNRTWDCVLV 60

QY 61 NPRNSQSGRLFOLELEADALVNFHQYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
Db 61 NPRNSQSGRLFOLELEADALVNFHQYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKGDSGRIILVELVOYCHTQMD 180
Db 121 SVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKGDSGRIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFPDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFPDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNPNDFGETPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNPNDFGETPTFLASKIG 394

Search completed: December 15, 2004, 13:15:35
Job time : 37.0255 secs

Db 421 RIHDLHLLCDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHKSMM 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSRQPA 539
Db 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSRQPA 540
QY 540 EHLHFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPGRFLDGG 599
Db 541 EHLHFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPGRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQKANKVKKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNDLIRKQKANKVKKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660
QY 660 WELAKTVFGAKELGKMVVDCCDDPDGR 686
Db 661 WELAKTVFGAKELGKMVVDCCDDPDGR 687

RESULT 13
PCT-US95-08069-2
; Sequence 2, Application PC/TUS9508069
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08069
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08069-2

Query Match 91.2%; Score 3302.5; DB 5; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGRLVNTSGVNTLFSNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MOFFGRLVNTLSVNTLFSNPNFRVKEISVADYTSHERVREEGQLILFQNASRTWDCVLV 60
QY 61 NPNRSQSGFRLQLEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTLIRNHPSW 120
Db 61 SPNPHSGFRLQLESEADALVNFQFSQLPFYESSVQVLHVEVQLHLSDLIRSHPSW 120
QY 121 SVAHLAVALGIRECFHSHRIISCANCAENBECTPLHLACRGDGEIILVELVQYCHTQMD 180
Db 121 TVTHLAVALGIRECFHSHRIISCANSTENEECTPLHLACRGDSEIILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNLPLHLACQLGKQEMVRVLL 240
Db 181 VTDNKGTAHFHYAVQGDNSQVLLGKNASAGLNQVNLPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIIISBDSQIHSKDPYRGASPLHWAKNAEM 300
Db 241 LCNARCNIIMPNGSPFIHTAMKFSQKCAEMIIISBDSQIHSKDPYRGASPLHWAKNAEM 300
QY 301 RMLLRKGCNVNNTSAGNTALHVGWNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRNFDCAIVLLTHGANAGTPGEHNTPLHLAISK 360
QY 361 DNVEMIKALIVFGAEVDTDNDFGETPTFLASKIGK-LQDLMHISRAKPAFILGSMRDEK 419

Db 361 DNVEMIKALIVFGAEVDTDNDFGETPTAFWASKISQQLQDLMPISRARKEPAFILSSMRDEK 420
QY 420 RTHDHLHLLCDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHKSMM 479
Db 421 RIHDLHLLCDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHKSMM 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSRQPA 539
Db 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSRQPA 540
QY 540 EHLHFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPGRFLDGG 599
Db 541 EHLHFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPGRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQKANKVKKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNDLIRKQKANKVKKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660
QY 660 WELAKTVFGAKELGKMVVDCCDDPDGR 686
Db 661 WELAKTVFGAKELGKMVVDCCDDPDGR 687

RESULT 14
US-08-555-568B-17
; Sequence 17, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555.568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-17

Query Match 57.6%; Score 2084; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.68-217;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTSGVNTLFSNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MOFFGRLVNTSGVNTLFSNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLQLEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTLIRNHPSW 120

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-519-223-2

Query Match 91.2%; Score 3302.5; DB 3; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
 QY 1 MQPFGRLVNTSGVTLNFSNPRVKEVAVADYTSDDREEGQLILFQNTNRTWDCVLV 60
 Db 1 MQPFGRLVNTSSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASRTWDCILV 60
 QY 61 NPNRSQSGRLFQLEADALVNFHQSOLLPPFYESSQVLHTEVLOHLTLIRNHP 120
 Db 61 SPNPHSGRLFQLESEADALVNFQSSQLPPFYESSQVLHVEVLQHLSDLRSHPSW 120
 QY 121 SVHLAVELGIRECFHSHRIISCANCAENEEGCTPLHLACRKGDDGILVELVQYCHTQMD 180
 Db 121 TVTHLAVELGIRECFHSHRIISCANSTENEEGCTPLHLACRKGDSILVELVQYCHAQND 180
 QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
 Db 181 VTNKGKETAFAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
 QY 241 LCNARCNMGPNGYPIHSAKMFQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
 Db 241 LCNARCNVMGPGFPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
 QY 301 RMLLKGCVNSTSSAGNTALHVGVRNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLKGCDVDSTSAAGNTALHVAVMNRNFDVCMVLLTYGANAGTPEGHNTPLHLAISK 360
 QY 361 DNMEMIKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSRDEK 419
 Db 361 DNMEMIKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSRDEK 420
 QY 420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKS 479
 Db 421 RIHDHLCLDGGVGKGLVIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKS 480
 QY 480 AYRGMVFRKDVFRGSRPYESGPLEEFLKRFEGEHTKMTDVRKPKVMTGLTSLDRQA 539
 Db 481 AYRGMVFRKDVFRGSRPYESGPLEEFLKRFEGEHTKMTDVRKPKVMTGLTSLDRQA 540
 QY 540 ELHLFRNYDAPETVRPRFNQNLNPPAPQPSQVLVRAARSSGAAPTFRPNGRFLDGG 599
 Db 541 ELHLFRNYDAPETVRPRFNQNLNPPAPQPSQVLVRAARSSGAAPTFRPNGRFLDGG 600
 QY 600 LLANPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659
 Db 601 LLANPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660
 QY 660 WELAKTVFGAKELGKMWVDDCTDPDGR 686
 Db 661 WELAKTVFGAKELGKMWVDDCTDPDGR 687

RESULT 12
 US-09-927-180-2
 ; Sequence 2, Application US/09927180

; Patent No. 6645736
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION NUMBER: US/09/927,180
 ; FILING DATE: 09-Aug-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/519,223
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-09-927-180-2

Query Match 91.2%; Score 3302.5; DB 4; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
 QY 1 MQPFGRLVNTSGVTLNFSNPRVKEVAVADYTSDDREEGQLILFQNTNRTWDCVLV 60
 Db 1 MQPFGRLVNTSSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASRTWDCILV 60
 QY 61 NPNRSQSGRLFQLEADALVNFHQSOLLPPFYESSQVLHTEVLOHLTLIRNHP 120
 Db 61 SPNPHSGRLFQLESEADALVNFQSSQLPPFYESSQVLHVEVLQHLSDLRSHPSW 120
 QY 121 SVHLAVELGIRECFHSHRIISCANCAENEEGCTPLHLACRKGDDGILVELVQYCHTQMD 180
 Db 121 TVTHLAVELGIRECFHSHRIISCANSTENEEGCTPLHLACRKGDSILVELVQYCHAQND 180
 QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
 Db 181 VTNKGKETAFAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
 QY 241 LCNARCNMGPNGYPIHSAKMFQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
 Db 241 LCNARCNVMGPGFPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
 QY 301 RMLLKGCVNSTSSAGNTALHVGVRNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLKGCDVDSTSAAGNTALHVAVMNRNFDVCMVLLTYGANAGTPEGHNTPLHLAISK 360
 QY 361 DNMEMIKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSRDEK 419
 Db 361 DNMEMIKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSRDEK 420
 QY 420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKS 479

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QY 301 RMLKRGCVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLKRGCDVSTSAAGNTALHVAVMNRFDCAI VLLTHGANAGTGEHNTPLHLAISK 360
QY 361 DNVMETKALIVFGAEVDTNDPFGTPTFLASKIGK- LQDLMIHSRARKPAFILGSMRDEK 419
Db 361 DNMEMIKALIVFGAEVDTNDPFGTPTFLASKIGK- LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGVLIIQLLIIAEKASGVATKDLFDWAGTSGGTLALAILHLSKM 479
Db 421 RTHDHLCLDGGVKGVLIIQLLIIAEKASGVATKDLFDWAGTSGGTLALAILHLSKM 480
QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFKREFEGEHTKMTDVRKPKVMTLGTLSDRQA 539
Db 481 AYMRGVYFRMKDEVPFRGSRPYESGPLEEFKREFEGEHTKMTDVRKPKVMTLGTLSDRQA 540
QY 540 ELHLFRNYDAPETVREPRFNQNVLRPPAQSDQLVWRAARSSGAAPTFRPNRFLDGG 599
Db 541 ELHLFRNYDAPETVREPRFNQNVLRPPAQSDQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI VVSLGTGRSPQVPTCDVFRPSPNP 659
Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI VVSLGTGRSPQVPTCDVFRPSPNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
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RESULT 10

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US-08-555-568B-2
; Sequence 2, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
```

CLASSIFICATION: 435

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ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-2
```

```
Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
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QY 1 MQFFGRLVNTLSSVNLFSNPRVKEISVADYTSHERVREEGQLILFQNSRNTWDCILV 60
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Db 1 MQFFGRLVNTLSSVNLFSNPRVKEISVADYTSHERVREEGQLILFQNSRNTWDCILV 60
QY 61 NPNRSGSFRLLPQLELEADALVNFHOYSQQLLPFFYESSQVLTHTVQLHQLTDLIRNHPWS 120
Db 61 SPRNPHSGFRLLPQLESEADALVNFQFSSQLPFPFYESSQVLTHTVQLHQLTDLIRNHPWS 120
QY 121 SYAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDGGEILVELVOYCHTQMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDSILVELVOYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDNRGETAFHYAVQGDNSQVLQLLGRNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNMGPNGYPIHSAMKFSQGCABMIISMSSQIHSKDPYKASPLHWAKNAEMA 300
Db 241 LCNARCNMGPSGFPPIHTAMKFSQGCABMIISMSSQIHSKDPYKASPLHWAKNAEMA 300
QY 301 RMLLXRGCVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLXRGCDVSTSAAGNTALHVAVMNRFDCAI VLLTHGANAGTGEHNTPLHLAISK 360
QY 361 DNVMETKALIVFGAEVDTNDPFGTPTFLASKIGK- LQDLMIHSRARKPAFILGSMRDEK 419
Db 361 DNMEMIKALIVFGAEVDTNDPFGTPTFLASKIGK- LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGVLIIQLLIIAEKASGVATKDLFDWAGTSGGTLALAILHLSKM 479
Db 421 RTHDHLCLDGGVKGVLIIQLLIIAEKASGVATKDLFDWAGTSGGTLALAILHLSKM 480
QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFKREFEGEHTKMTDVRKPKVMTLGTLSDRQA 539
Db 481 AYMRGVYFRMKDEVPFRGSRPYESGPLEEFKREFEGEHTKMTDVRKPKVMTLGTLSDRQA 540
QY 540 ELHLFRNYDAPETVREPRFNQNVLRPPAQSDQLVWRAARSSGAAPTFRPNRFLDGG 599
Db 541 ELHLFRNYDAPETVREPRFNQNVLRPPAQSDQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI VVSLGTGRSPQVPTCDVFRPSPNP 659
Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI VVSLGTGRSPQVPTCDVFRPSPNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
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RESULT 11

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US-09-519-223-2
; Sequence 2, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
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Db 541 ELHLFRNYDAPEVIREPRFNQINLKPTQPADQLVWRAARSSGAAPTFRNGRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 8
US-08-422-106-2
; Sequence 2, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-422-106-2

Query Match 91.2%; Score 3302.5; DB 1; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGLVNTFSQVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
Db 1 MQFFGLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60

QY 61 NPNRSQSGFRLFOLELEADALVNFHQYSSQLLPFYESSQVLTHTVQLHLDLIRNHPWS 120
Db 61 SPNPHSGFRLFOLESEADALVNFQFSSQLPPFYESSQVLTHTVQLHLDLIRNHPWS 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
Db 181 VTDNKGETAHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240

QY 241 LCNARCNMGPNGYPIHSAKFSQKCAEMIIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNMGPSGFPPIHTAMKFSQKCAEMIIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLKGCNNVSTSSAGNTALHGVNRNFDCAI VLLTHCANADARGEHNTPLHLAMSK 360
Db 301 RMLLKGCDDVSTSSAGNTALHGVNRNFDCAI VLLTHCANADARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFAEVDTPNDFGETPTFLASKIGK-LQDLMIHSRARKPAFIIIGSNRDEK 419
Db 361 DNMEMIKALIVFAEVDTPNDFGETPAFWASKISKQLQDLMLPISRARKPAFIIIGSNRDEK 420

QY 420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFQWVAGTSTGGIILAILHKSMM 479

Db 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFQWVAGTSTGGIILAILHKSMM 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGEHTKMTDVRKPKVMLTGTLSRQPA 539
Db 481 AYMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGEHTKMTDVRKPKVMLTGTLSRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQINLKPTQPADQLVWRAARSSGAAPTFRNGRFLDGG 599
Db 541 ELHLFRNYDAPETVREPRFNQINLKPTQPADQLVWRAARSSGAAPTFRNGRFLDGG 600

QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 9
US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGLVNTFSQVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
Db 1 MQFFGLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60

QY 61 NPNRSQSGFRLFOLELEADALVNFHQYSSQLLPFYESSQVLTHTVQLHLDLIRNHPWS 120
Db 61 SPNPHSGFRLFOLESEADALVNFQFSSQLPPFYESSQVLTHTVQLHLDLIRNHPWS 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
Db 181 VTDNKGETAHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240

QY 241 LCNARCNMGPNGYPIHSAKFSQKCAEMIIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNMGPSGFPPIHTAMKFSQKCAEMIIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-927-180-23

Query Match 99.6%; Score 3606.5; DB 4; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTFSGVTNLFNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSGQGRLLPQLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHTDLIRNHPWS 120
DB 61 NPNRSGQGRLLPQLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHTDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPYTHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIIMPNGYPYTHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGTILALAILHKSXM 479
DB 420 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGTILALAILHKSXM 480
QY 480 AYMRGWYFRMKDEVPFRGSRPYSGPLEEFLEKFEFGHTKMTDVRPKVMTCTGLSDRQPA 539
DB 480 AYMRGWYFRMKDEVPFRGSRPYSGPLEEFLEKFEFGHTKMTDVRPKVMTCTGLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPREFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPNGRFLDGG 599
DB 540 ELHLFRNYDAPETVREPREFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPNGRFLDGG 600
QY 600 LLANNPTLDAMTEIHYNDLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP 659
DB 600 LLANNPTLDAMTEIHYNDLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP 660

QY 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

RESULT 7

US-08-281-193-2

; Sequence 2, Application US/08281193

; Patent No. 5466595

; GENERAL INFORMATION:

; APPLICANT: Jones, Simon

; APPLICANT: Tang, Jim

; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

; NUMBER OF SEQUENCES: 15

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/281,193

; FILING DATE:

; CLASSIFICATION: 435

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 752 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-281-193-2

Query Match 91.2%; Score 3302.5; DB 1; Length 752;

Best Local Similarity 90.4%; Pred. No. 0;

Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTFSGVTNLFNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTLSSVNTLNFNPFVRKEISVADYTSHERVEEGQLILFQNASRTWDCILV 60
QY 61 NPNRSGQGRLLPQLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHTDLIRNHPWS 120
DB 61 SPRNPHSGRLLPQLESEADALVNFQFSQSLPFYESSQVLTHTVQLHTDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFPHHSRIISCANSTENEECTPLHLACRKGDSILLVELVOYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVQGDNSQVLLQGLKNASAGLNQVKNQGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPYTHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIIMPNGSPFIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRNFDCAIVLLTHGANADARGEHNTPLHLAISK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDFGETPAFWASKISQQLQDLMPISRARKPAFTILSSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGTILALAILHKSXM 479
DB 421 RTHDHLCLDGGVKGKLIILQIIAIEKASGVATKDLFDWVAGTSTGGTILALAILHKSXM 480
QY 480 AYMRGWYFRMKDEVPFRGSRPYSGPLEEFLEKFEFGHTKMTDVRPKVMTCTGLSDRQPA 539
DB 481 AYMRGWYFRMKDEVPFRGSRPYSGPLEEFLEKFEFGHTKMTDVRPKVMTCTGLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPREFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPNGRFLDGG 599
DB 540 ELHLFRNYDAPETVREPREFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPNGRFLDGG 599